

## SEARCH REQUEST FORM

## Scientific and Technical Information Center

Requester's Full Name: Man-Tam DAVIS Examiner #: 13422 Date: 2/12/2003  
 Art Unit: 1042 Phone Number 305-8008 Serial Number: 091403440  
 Mail Box and Bldg/Room Location: 8E12 8A01 Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

\*\*\*\*\*

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: \_\_\_\_\_

Inventors (please provide full names): \_\_\_\_\_

Earliest Priority Filing Date: \_\_\_\_\_

*\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

newly checked  
04/97

Jan Delaval  
Reference Librarian  
Library & Chemical Library  
C&E 1207 - 703-308-4493  
jdelaval@uspis.gov

## STAFF USE ONLY

Searcher: Man-Tam DAVIS

Searcher Phone #: 305-8008

Searcher Location: \_\_\_\_\_

Date Searcher Picked Up: 2/12/03

Date Completed: 2/12/03

Searcher Prep & Review Time: \_\_\_\_\_

Clerical Prep Time: 70

Online Time: 70

## Type of Search

NA Sequence (#) \_\_\_\_\_

AA Sequence (#) ✓

Structure (#) \_\_\_\_\_

Bibliographic \_\_\_\_\_

Litigation \_\_\_\_\_

Fulltext \_\_\_\_\_

Patent Family \_\_\_\_\_

Other \_\_\_\_\_

## Vendors and cost where applicable

STN \_\_\_\_\_

Dialog \_\_\_\_\_

Questel/Orbit \_\_\_\_\_

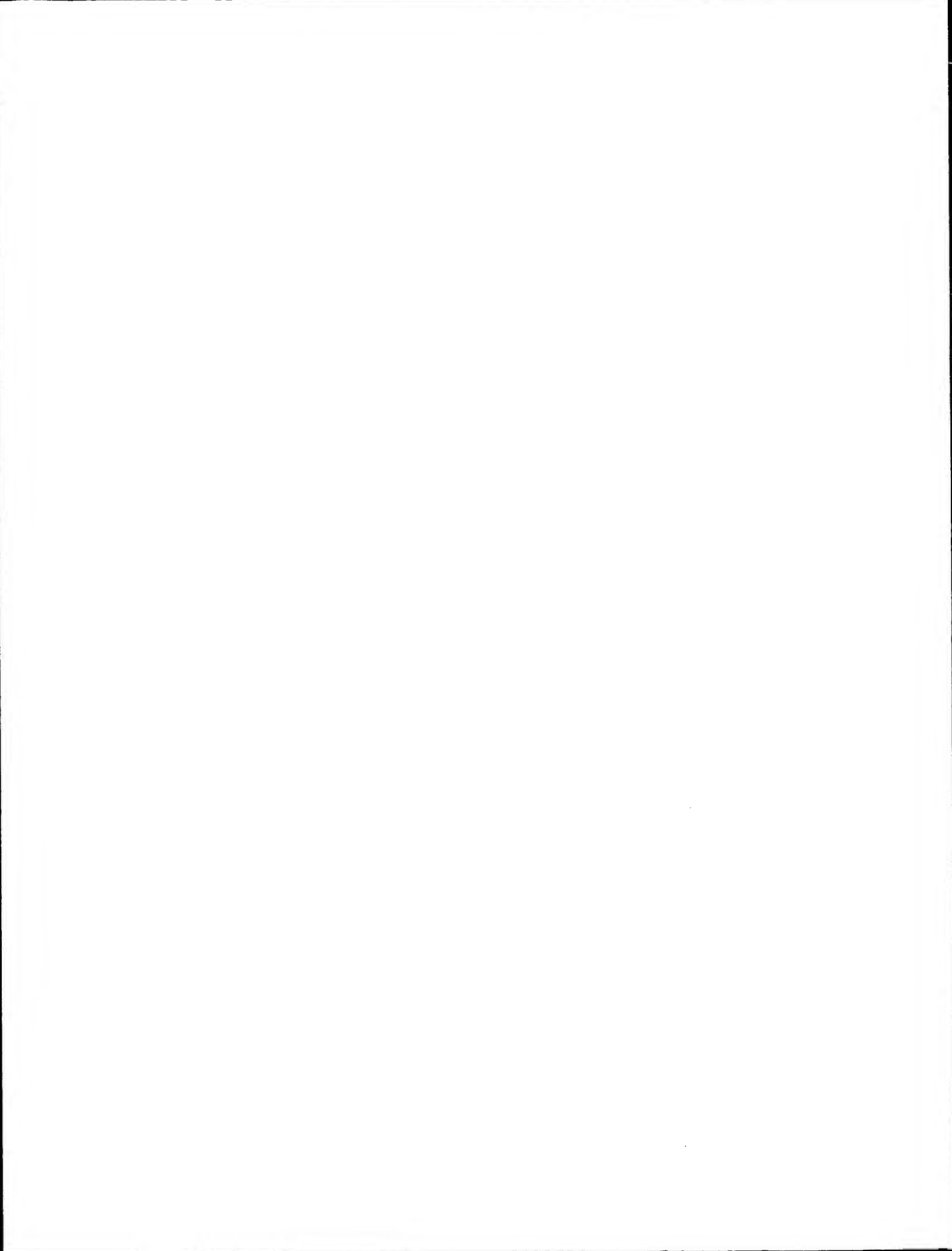
Dr.Link \_\_\_\_\_

Lexis/Nexis \_\_\_\_\_

Sequence Systems ✓

WWW/Internet \_\_\_\_\_

Other (specify) \_\_\_\_\_





GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 12, 2003, 11:12:42 ; Search time 17.4167 Seconds  
(without alignments)  
32.098 Million cell updates/sec

Title: US-09-403-440A-2

Perfect score: 105

Sequence: 1 PPLSQTFSDMLKLLPENG 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 147762

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA: \*  
1: /cgn2\_6/prodata/1/iaa/5A COMB.pap:\*  
2: /cgn2\_6/prodata/1/iaa/5B COMB.pap:\*  
3: /cgn2\_6/prodata/1/iaa/6A COMB.pap:\*  
4: /cgn2\_6/prodata/1/iaa/6B COMB.pap:\*  
5: /cgn2\_6/prodata/1/iaa/PCTUS COMB.pap:\*  
6: /cgn2\_6/prodata/1/iaa/backfiles1.pap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	99	94.3	20	4	US-09-081-975-8
2	99	94.3	20	4	US-09-081-975-10
3	99	94.3	20	4	US-09-081-975-11
4	99	94.3	20	4	US-09-081-975-16
5	94	89.5	20	4	US-09-081-975-14
6	94	89.5	20	4	US-09-081-975-15
7	90	85.7	19	4	US-09-081-975-13
8	86	81.9	20	4	US-09-081-975-19
9	77	73.3	15	1	US-08-277-660A-1
10	77	73.3	15	1	US-08-277-660A-4
11	77	73.3	15	1	US-08-424-957-1
12	77	73.3	15	1	US-08-424-957-20
13	77	73.3	15	4	US-09-035-686-1
14	77	73.3	15	4	US-09-035-686-20
15	74	70.5	15	1	US-08-277-660A-5
16	74	70.5	15	1	US-08-424-957-21
17	74	70.5	15	4	US-09-035-686-21
18	74	70.5	16	4	US-09-081-975-23
19	74	70.5	20	4	US-09-081-975-20
20	72	68.6	20	4	US-09-081-975-18
21	65	61.9	15	3	US-09-280-047-6
22	65	61.9	15	4	US-08-208-573B-6
23	65	61.9	15	5	PCT-US95-02856-6
24	60	57.1	18	4	US-09-081-975-22
25	59	56.2	11	1	US-08-277-660A-9
26	59	56.2	11	1	US-08-424-957-17
27	59	56.2	11	4	US-09-035-686-17

28	59	56.2	13	4	US-09-236-415-5	Sequence 5, Appl
29	57	54.3	11	1	US-08-424-957-45	Sequence 45, Appl
30	57	54.3	11	1	US-08-424-957-46	Sequence 45, Appl
31	57	54.3	11	4	US-09-035-686-45	Sequence 45, Appl
32	57	54.3	11	4	US-09-035-686-46	Sequence 46, Appl
33	57	54.3	14	4	US-09-400-653A-7	Sequence 7, Appl
34	57	54.3	14	4	US-09-248-061B-7	Sequence 7, Appl
35	56	53.3	11	1	US-08-277-660A-10	Sequence 10, Appl
36	56	53.3	11	1	US-08-277-660A-15	Sequence 15, Appl
37	56	53.3	11	1	US-08-424-957-23	Sequence 23, Appl
38	56	53.3	11	1	US-08-424-957-28	Sequence 28, Appl
39	56	53.3	11	1	US-08-424-957-40	Sequence 40, Appl
40	56	53.3	11	4	US-09-035-686-23	Sequence 23, Appl
41	56	53.3	11	4	US-09-035-686-28	Sequence 28, Appl
42	56	53.3	11	4	US-09-035-686-40	Sequence 40, Appl
43	55	52.4	10	1	US-08-277-660A-7	Sequence 7, Appl
44	55	52.4	10	1	US-08-424-957-11	Sequence 11, Appl
45	55	52.4	10	4	US-09-035-686-11	Sequence 11, Appl

## ALIGNMENTS

## RESULT 1

US-09-081-975-8  
; Sequence 8, Application US/09081975  
; Patent No. 6451979

## GENERAL INFORMATION:

; APPLICANT: Kaelin, William  
; TITLE OF INVENTION: METHODS OF TREATMENT USING  
; TITLE OF INVENTION: NBS-1, ANTIBODIES AND PROTEINS THERETO, AND USES OF THE  
; TITLE OF INVENTION: ANTIBODIES  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Nixon Peabody LLP  
; STREET: 101 Federal Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/081,975  
; FILING DATE: 12-MAY-1998  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/046,207  
; FILING DATE: 12-MAY-1997

; ATTORNEY/AGENT INFORMATION:  
; NAME: Eisenstein, Ronald I  
; REGISTRATION NUMBER: 30,628  
; REFERENCE/DOCKET NUMBER: 47400

; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-345-6054  
; TELEFAX: 617-345-1300

; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

US-09-081-975-8

Query Match 94.3%; Score 99; DB 4; Length 20;  
Best Local Similarity 100.0%; Pred.No. 1.6e-09;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18  
 |||||  
 Db 2 PPLSQETFSDLWKLLPEN 19

## RESULT 2

US-09-081-975-10  
 ; Sequence 10, Application US/09081975  
 ; Patent No. 6451979  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kaelin, William  
 ; APPLICANT: Jost, Christine  
 ; TITLE OF INVENTION: METHODS OF TREATMENT USING  
 ; NBS-1, ANTIBODIES AND PROTEINS THEREO, AND USES OF THE  
 ; TITLE OF INVENTION: ANTIBODIES  
 ; NUMBER OF SEQUENCES: 27  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Nixon Peabody LLP  
 ; STREET: 101 Federal Street  
 ; CITY: Boston  
 ; STATE: MA  
 ; COUNTRY: USA  
 ; ZIP: 02110  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: Windows  
 ; SOFTWARE: FastSeq for Windows Version 2.0b  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/081.975  
 ; FILING DATE: 12-MAY-1998  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 60/046,207  
 ; FILING DATE: 12-MAY-1997  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Eisenstein, Ronald I  
 ; REGISTRATION NUMBER: 30,628  
 ; REFERENCE/DOCKET NUMBER: 47400  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 617-345-6054  
 ; TELEFAX: 617-345-1300  
 ; TELEX:  
 ; INFORMATION FOR SEQ ID NO: 10:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 20 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ;

Query Match 94.3%; Score 99; DB 4; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-09;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18  
 |||||  
 Db 2 PPLSQETFSDLWKLLPEN 19

## RESULT 3

US-09-081-975-11  
 ; Sequence 11, Application US/09081975  
 ; Patent No. 6451979  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kaelin, William  
 ; APPLICANT: Jost, Christine  
 ; TITLE OF INVENTION: METHODS OF TREATMENT USING  
 ; NBS-1, ANTIBODIES AND PROTEINS THEREO, AND USES OF THE  
 ; TITLE OF INVENTION: ANTIBODIES  
 ; NUMBER OF SEQUENCES: 27  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Nixon Peabody LLP

; STREET: 101 Federal Street  
 ; CITY: Boston  
 ; STATE: MA  
 ; COUNTRY: USA  
 ; ZIP: 02110  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: Windows  
 ; SOFTWARE: FastSeq for Windows Version 2.0b  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/081.975  
 ; FILING DATE: 12-MAY-1998  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 60/046,207  
 ; FILING DATE: 12-MAY-1997  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Eisenstein, Ronald I  
 ; REGISTRATION NUMBER: 30,628  
 ; REFERENCE/DOCKET NUMBER: 47400  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 617-345-6054  
 ; TELEFAX: 617-345-1300  
 ; TELEX:  
 ; INFORMATION FOR SEQ ID NO: 11:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 20 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ;

Query Match 94.3%; Score 99; DB 4; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-09;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18  
 |||||  
 Db 2 PPLSQETFSDLWKLLPEN 19

## RESULT 4

US-09-081-975-16  
 ; Sequence 16, Application US/09081975  
 ; Patent No. 6451979  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kaelin, William  
 ; APPLICANT: Jost, Christine  
 ; TITLE OF INVENTION: METHODS OF TREATMENT USING  
 ; NBS-1, ANTIBODIES AND PROTEINS THEREO, AND USES OF THE  
 ; TITLE OF INVENTION: ANTIBODIES  
 ; NUMBER OF SEQUENCES: 27  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Nixon Peabody LLP  
 ; STREET: 101 Federal Street  
 ; CITY: Boston  
 ; STATE: MA  
 ; COUNTRY: USA  
 ; ZIP: 02110  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: Windows  
 ; SOFTWARE: FastSeq for Windows Version 2.0b  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/081.975  
 ; FILING DATE: 12-MAY-1998  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 60/046,207  
 ; FILING DATE: 12-MAY-1997  
 ; ATTORNEY/AGENT INFORMATION:

NAME: Eisenstein, Ronald I  
 REGISTRATION NUMBER: 30,628  
 REFERENCE/DOCKET NUMBER: 47400  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617-345-6054  
 TELEFAX: 617-345-1300  
 TELEX:  
 INFORMATION FOR SEQ ID NO: 16:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 20 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-09-081-975-16

Query Match 94.3%; Score 99; DB 4; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-09;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18  
 |||||  
 Db 2 PPLSQETFSDLWKLLPEN 19

## RESULT 5

US-09-081-975-14  
 Sequence 14, Application US/09081975  
 Patent No. 6451979  
 GENERAL INFORMATION:  
 APPLICANT: Kaelin, William  
 APPLICANT: Jost, Christine  
 TITLE OF INVENTION: METHODS OF TREATMENT USING  
 TITLE OF INVENTION: NBS-1, ANTIBODIES AND PROTEINS THEREO, AND USES OF THE  
 TITLE OF INVENTION: ANTIBODIES  
 NUMBER OF SEQUENCES: 27  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Nixon Peabody LLP  
 STREET: 101 Federal Street  
 CITY: Boston  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02110  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: Windows  
 SOFTWARE: FastSeq for Windows Version 2.0b  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/081,975  
 FILING DATE: 12-MAY-1998  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 60/046,207  
 FILING DATE: 12-MAY-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Eisenstein, Ronald I  
 REGISTRATION NUMBER: 30,628  
 REFERENCE/DOCKET NUMBER: 47400  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617-345-6054  
 TELEFAX: 617-345-1300  
 TELEX:  
 INFORMATION FOR SEQ ID NO: 14:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 20 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-09-081-975-14

Query Match 89.5%; Score 94; DB 4; Length 20;  
 Best Local Similarity 94.4%; Pred. No. 1e-08;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18  
 |||||  
 Db 2 PPLSQETFSDLWKLLPEN 19

## RESULT 6

US-09-081-975-15  
 Sequence 15, Application US/09081975  
 Patent No. 6451979  
 GENERAL INFORMATION:  
 APPLICANT: Kaelin, William  
 APPLICANT: Jost, Christine  
 TITLE OF INVENTION: METHODS OF TREATMENT USING  
 TITLE OF INVENTION: NBS-1, ANTIBODIES AND PROTEINS THEREO, AND USES OF THE  
 TITLE OF INVENTION: ANTIBODIES  
 NUMBER OF SEQUENCES: 27  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Nixon Peabody LLP  
 STREET: 101 Federal Street  
 CITY: Boston  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02110  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: Windows  
 SOFTWARE: FastSeq for Windows Version 2.0b  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/081,975  
 FILING DATE: 12-MAY-1998  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 60/046,207  
 FILING DATE: 12-MAY-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Eisenstein, Ronald I  
 REGISTRATION NUMBER: 30,628  
 REFERENCE/DOCKET NUMBER: 47400  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617-345-6054  
 TELEFAX: 617-345-1300  
 TELEX:  
 INFORMATION FOR SEQ ID NO: 15:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 20 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-09-081-975-15

Query Match 89.5%; Score 94; DB 4; Length 20;  
 Best Local Similarity 94.4%; Pred. No. 1e-08;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18  
 |||||  
 Db 2 PPLSQETFSDLWKLLPEN 19

## RESULT 7

US-09-081-975-13  
 Sequence 13, Application US/09081975  
 Patent No. 6451979  
 GENERAL INFORMATION:  
 APPLICANT: Kaelin, William  
 APPLICANT: Jost, Christine  
 TITLE OF INVENTION: METHODS OF TREATMENT USING  
 TITLE OF INVENTION: NBS-1, ANTIBODIES AND PROTEINS THEREO, AND USES OF THE  
 TITLE OF INVENTION: ANTIBODIES  
 NUMBER OF SEQUENCES: 27  
 CORRESPONDENCE ADDRESS:

```

ADDRESSSEE: Nixon Peabody LLP
STREET: 101 Federal Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICANT: FastSEQ for Windows Version 2.0b
APPLICANT NUMBER: US/09/081,975
FILING DATE: 12-MAY-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/046,207
FILING DATE: 12-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Eisenstein, Ronald I
REGISTRATION NUMBER: 30,628
REFERENCE/DOCKET NUMBER: 47400
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-345-6054
TELEFAX: 617-345-1300
TELEX:
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-081-975-13
Query Match 85.7%; Score 90; DB 4; Length 19;
Best Local Similarity 88.9%; Pred. No. 4.2e-08;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0
QY 1 PPLSQETFDLWKLLEN 18
Db 1 PPLSQETFDLWKLLEN 18
RESULT 8
US-09-081-975-19
; Sequence 19, Application US/09081975
; Patent No 6451979
; GENERAL INFORMATION:
; APPLICANT: Kaelin, William
; APPLICANT: Joest, Christine
; TITLE OF INVENTION: METHODS OF TREATMENT USING
; TITLE OF INVENTION: NBS-1, ANTIBODIES AND PROTEINS THEREO, AND USES OF THE
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon Peabody LLP
; STREET: 101 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/081,975
; FILING DATE: 12-MAY-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/046,207
; FILING DATE: 12-MAY-1997

```

Db 1 QETFDLWKLLEN 14

RESULT 10

US-08-277-660A-4

; Sequence 4, Application US/08277660A

; Patent No. 5702908

; GENERAL INFORMATION:

; APPLICANT: Picklesley, Steven M.

; APPLICANT: Lane, David P.

; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53

; TITLE OF INVENTION: Protein and Therapeutic Application Thereof

; NUMBER OF SEQUENCES: 27

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert

; STREET: Four Embarcadero Center, Suite 3400

; CITY: San Francisco

; STATE: California

; COUNTRY: United States

; ZIP: 94111-4187

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/277,660A

; FILING DATE: 20-JUL-1994

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: Dreger, Walter H.

; REGISTRATION NUMBER: 24,190

; REFERENCE/DOCKET NUMBER: A-60244/WH

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 781-1989

; TELEFAX: (415) 398-3249

; TELEX: 910 277299

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 15 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

US-08-277-660A-4

Query Match

Best Local Similarity 100.0%; Pred. No. 3.8e-06;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFDLWKL 14

Db 2 PPLSQETFDLWKL 15

RESULT 11

US-08-424-957-1

; Sequence 1, Application US/08424957

; Patent No. 5770377

; GENERAL INFORMATION:

; APPLICANT: Picklesley, Steven M.

; APPLICANT: Lane, David P.

; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53

; TITLE OF INVENTION: Protein and Therapeutic Application Thereof

; NUMBER OF SEQUENCES: 50

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert

; STREET: Four Embarcadero Center, Suite 3400

; CITY: San Francisco

; STATE: California

; COUNTRY: United States

; ZIP: 94111-4187

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/424,957

; FILING DATE: 19-APR-1995

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/277,660

; FILING DATE: 20-JUL-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Dreger, Walter H.

; REGISTRATION NUMBER: 24,190

; REFERENCE/DOCKET NUMBER: A-61228/WH

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 781-1989

; TELEFAX: (415) 398-3249

; TELEX: 910 277299

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 15 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: unknown

US-08-424-957-1

Query Match 73.3%; Score 77; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 3.8e-06;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QETFDLWKLLEN 18

Db 1 QETFDLWKLLEN 14

RESULT 12

US-08-424-957-20

; Sequence 20, Application US/08424957

; Patent No. 5770377

; GENERAL INFORMATION:

; APPLICANT: Picklesley, Steven M.

; APPLICANT: Lane, David P.

; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53

; TITLE OF INVENTION: Protein and Therapeutic Application Thereof

; NUMBER OF SEQUENCES: 50

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert

; STREET: Four Embarcadero Center, Suite 3400

; CITY: San Francisco

; STATE: California

; COUNTRY: United States

; ZIP: 94111-4187

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/424,957

; FILING DATE: 19-APR-1995

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/277,660

; FILING DATE: 20-JUL-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Dreger, Walter H.

; REGISTRATION NUMBER: 24,190

; REFERENCE/DOCKET NUMBER: A-61228/WH

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 781-1989

; TELEFAX: (415) 398-3249

; TELEX: 910 277299

; INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 15 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: unknown  
 US-08-424-957-20

Query Match 73.3%; Score 77; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKL 14  
 |||||  
 Db 2 PPLSQETFSDLWKL 15

## RESULT 13

US-09-035-686-1

; Sequence 1, Application US/09035686  
 ; Patent No. 6153391  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Picksley, Steven M.  
 ; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53  
 ; TITLE OF INVENTION: Protein and Therapeutic Application Thereof  
 ; NUMBER OF SEQUENCES: 50  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert  
 ; STREET: Four Embarcadero Center, Suite 3400  
 ; CITY: San Francisco  
 ; STATE: California  
 ; COUNTRY: United States  
 ; ZIP: 94111-4187  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/035,686  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/424,957  
 ; FILING DATE: 19-APR-1995  
 ; APPLICATION NUMBER: US 08/277,660  
 ; FILING DATE: 20-JUL-1994  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Dreger, Walter H.  
 ; REGISTRATION NUMBER: 24,190  
 ; REFERENCE/DOCKET NUMBER: A-61228/WH  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (415) 398-3249  
 ; TELEFAX: (415) 398-3249  
 ; TELEX: 910 277299  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 15 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS:  
 ; TOPOLOGY: unknown  
 ; US-09-035-686-1

Query Match 73.3%; Score 77; DB 4; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QETFSDLWKLLEN 18  
 |||||  
 Db 1 QETFSDLWKLLEN 14

## RESULT 14

US-09-035-686-20  
 ; Sequence 20, Application US/09035686  
 ; Patent No. 6153391  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Picksley, Steven M.  
 ; APPLICANT: Lane, David P.  
 ; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53  
 ; TITLE OF INVENTION: Protein and Therapeutic Application Thereof  
 ; NUMBER OF SEQUENCES: 50  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert  
 ; STREET: Four Embarcadero Center, Suite 3400  
 ; CITY: San Francisco  
 ; STATE: California  
 ; COUNTRY: United States  
 ; ZIP: 94111-4187  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/035,686  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/424,957  
 ; FILING DATE: 19-APR-1995  
 ; APPLICATION NUMBER: US 08/277,660  
 ; FILING DATE: 20-JUL-1994  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Dreger, Walter H.  
 ; REGISTRATION NUMBER: 24,190  
 ; REFERENCE/DOCKET NUMBER: A-61228/WH  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (415) 398-3249  
 ; TELEFAX: (415) 398-3249  
 ; TELEX: 910 277299  
 ; INFORMATION FOR SEQ ID NO: 20:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 15 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS:  
 ; TOPOLOGY: unknown  
 ; US-09-035-686-20

Query Match 73.3%; Score 77; DB 4; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKL 14  
 |||||  
 Db 2 PPLSQETFSDLWKL 15

## RESULT 15

US-08-277-660A-5

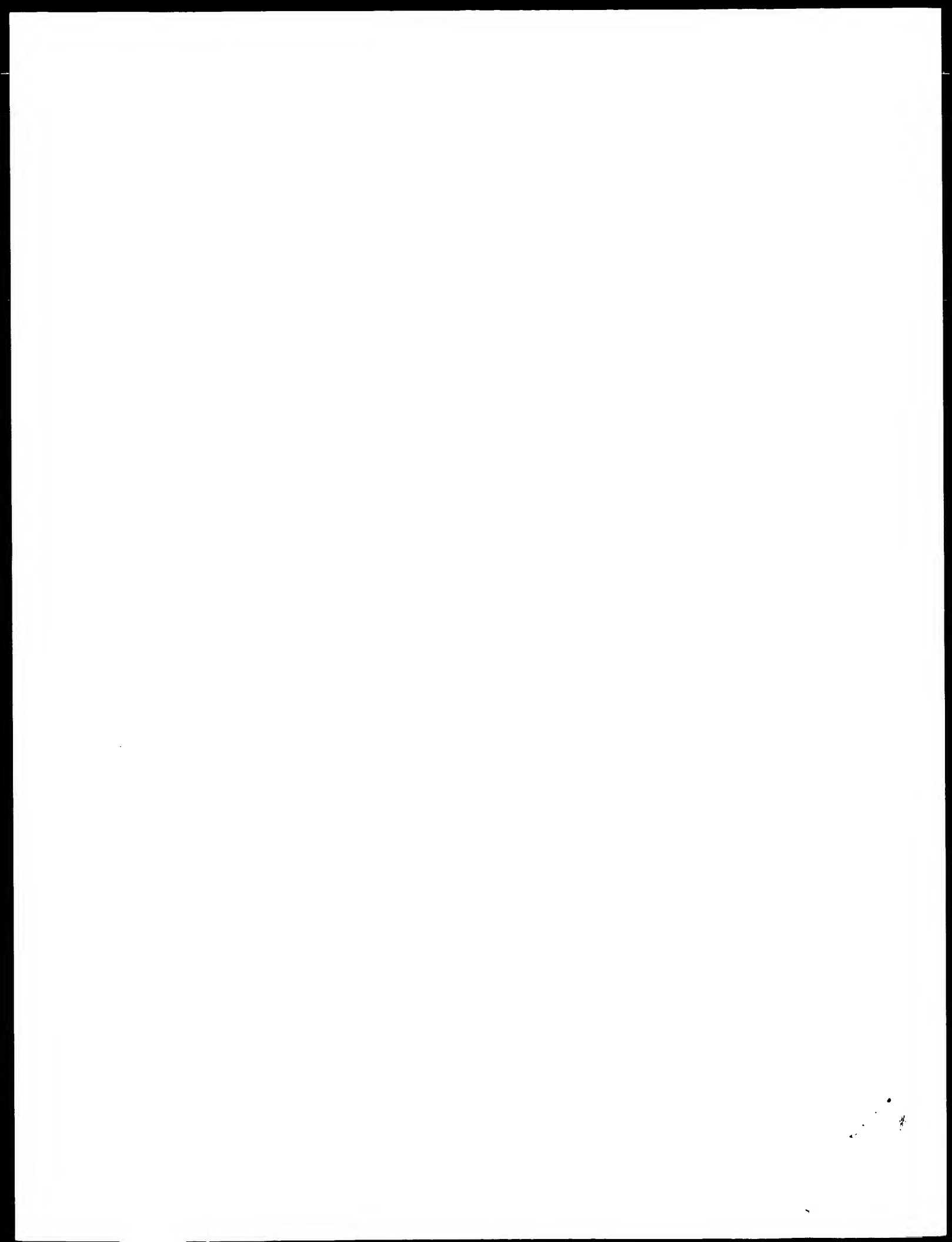
; Sequence 5, Application US/08277660A  
 ; Patent No. 5702908  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Picksley, Steven M.  
 ; APPLICANT: Lane, David P.  
 ; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53  
 ; TITLE OF INVENTION: Protein and Therapeutic Application Thereof  
 ; NUMBER OF SEQUENCES: 27  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert  
 ; STREET: Four Embarcadero Center, Suite 3400  
 ; CITY: San Francisco  
 ; STATE: California  
 ; COUNTRY: United States  
 ; ZIP: 94111-4187  
 ; COMPUTER READABLE FORM:  
 ; US-08-277-660A-5

;  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/277,660A  
; FILING DATE: 20-JUL-1994  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dreger, Walter H.  
; REGISTRATION NUMBER: 24,190  
; REFERENCE/DOCKET NUMBER: A-60244/WHI  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 781-1989  
; TELEFAX: (415) 398-3249  
; TELEX: 910 277299  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; US-08-277-660A-5

Query Match 70.5%; Score 74; DB 1; Length 15;  
Best Local Similarity 93.3%; Pred. No. 1.2e-05;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PLSQETFSGLWKLLP 16  
| | | | | | | | | | | | | | | |  
Db 1 PLSQETFSGLWKLLP 15

Search completed: February 12, 2003, 11:15:59  
Job time : 17.9167 secs





GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 12, 2003, 11:14:12 ; Search time 26.9167 Seconds  
(without alignments)  
59.144 Million cell updates/sec

Title: US-09-403-440A-2

Perfect score: 105

Sequence: 1 PLSQETFSDLWKLLPEN 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425801 seqs, 83787487 residues

Total number of hits satisfying chosen parameters: 159213

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending Patents AA New.\*

- 1: /cgn2\_6/prodata/1/paa/PCT\_NEW\_COMB.pep.\*
- 2: /cgn2\_6/prodata/1/paa/US06\_NEW\_COMB.pep.\*
- 3: /cgn2\_6/prodata/1/paa/US07\_NEW\_COMB.pep.\*
- 4: /cgn2\_6/prodata/1/paa/US08\_NEW\_COMB.pep.\*
- 5: /cgn2\_6/prodata/1/paa/US09\_NEW\_COMB.pep.\*
- 6: /cgn2\_6/prodata/1/paa/US10\_NEW\_COMB.pep.\*
- 7: /cgn2\_6/prodata/1/paa/US60\_NEW\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	92	87.6	19	7	US-60-438-805-9
2	81	77.1	15	6	US-10-211-088-141
3	70	66.7	13	5	US-09-701-080C-22
4	70	66.7	13	5	US-09-701-080C-27
5	59	56.2	11	5	US-09-189-702A-286
6	41	39.0	14	6	US-10-049-428-6
7	40	38.1	7	5	US-09-701-080C-12
8	35	33.3	14	6	US-10-049-428-7
9	31.5	30.0	14	6	US-10-268-332-53
10	31.5	30.0	16	6	US-10-225-567A-1177
11	31	29.5	9	5	US-09-189-702A-7
12	31	29.5	12	5	US-09-281-717A-31
13	31	29.5	12	5	US-09-281-717A-33
14	31	29.5	12	5	US-09-281-717A-35
15	31	29.5	12	5	US-09-830-693B-6
16	31	29.5	12	5	US-09-830-693B-8
17	31	29.5	22	6	US-10-203-138A-12722
18	31	29.5	24	6	US-10-212-499-23
19	30	28.6	16	6	US-10-348-131-49
20	30	28.6	22	6	US-10-283-599-28
21	30	28.6	22	6	US-10-263-162-61
22	29	27.6	15	6	US-10-169-026-3
23	29	27.6	16	6	US-10-225-567A-942
24	29	27.6	17	1	PCT-US02-28371-70
25	29	27.6	17	6	US-10-236-878-70
26	29	27.6	18	5	US-09-552-802B-30

27 29 27.6 20 6 US-10-319-786-54 Sequence 54, Appli  
28 29 27.6 21 6 US-10-190-866A-6 Sequence 6, Appli  
29 29 27.6 22 6 US-10-283-599-149 Sequence 149, App  
30 28.5 27.1 18 5 US-09-632-036E-11 Sequence 11, Appl  
31 28.5 27.1 20 7 US-60-438-805-3 Sequence 3, Appli  
32 28 26.7 16 7 US-10-174-717A-36 Sequence 36, Appl  
33 28 26.7 18 6 US-10-283-599-219 Sequence 219, App  
34 28 26.7 18 6 US-10-332-410-9 Sequence 9, Appli  
35 28 26.7 20 6 US-10-299-867-60 Sequence 60, Appl  
36 28 26.7 22 6 US-10-203-138A-15194 Sequence 15194, A  
37 28 26.7 22 6 US-09-641-528-25751 Sequence 25751, A  
38 27 25.7 9 5 US-09-641-528-29042 Sequence 29042, A  
39 27 25.7 9 5 US-09-641-528A-25751 Sequence 25751, A  
40 27 25.7 9 5 US-09-641-528A-29042 Sequence 29042, A  
41 27 25.7 9 6 US-10-029-206A-67 Sequence 67, Appl  
42 27 25.7 9 6 US-10-301-644-18 Sequence 18, Appl  
43 27 25.7 9 6 US-10-028-075B-67 Sequence 67, Appl  
44 27 25.7 10 5 US-09-641-528-463 Sequence 463, App  
45 27 25.7

#### ALIGNMENTS

RESULT 1  
US-60-438-805-9  
; Sequence 9, Application US/60438805  
; GENERAL INFORMATION: THOMAS  
; APPLICANT: KODAREK, THOMAS  
; TITLE OF INVENTION: MIXED ELEMENT CAPTURE AGENTS  
; FILE REFERENCE: UTSD:935USPI  
; CURRENT APPLICATION NUMBER: US/60/438,805  
; CURRENT FILING DATE: 2003-01-09  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 9  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
US-60-438-805-9

Query Match 87.6%; Score 92; DB 7; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.5e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLSQETFSDLWKLLPEN 18  
| | | | | | | | | | | | | | | | | |  
Db 1 PLSQETFSDLWKLLPEN 17

RESULT 2  
US-10-211-088-141  
; Sequence 141, Application US/10211088  
; GENERAL INFORMATION:  
; APPLICANT: Bright, Gary R.  
; APPLICANT: Premkumar, D. David  
; APPLICANT: Chen, Yih-Tai  
; TITLE OF INVENTION: Novel Fusion Proteins And Assays For Molecular Binding  
; FILE REFERENCE: 01-1022-US  
; CURRENT APPLICATION NUMBER: US/10/211,088  
; CURRENT FILING DATE: 2002-10-15  
; PRIOR APPLICATION NUMBER: 60/309,395  
; PRIOR FILING DATE: 2001-08-01  
; PRIOR APPLICATION NUMBER: 60/341,589  
; PRIOR FILING DATE: 2001-12-13  
; NUMBER OF SEQ ID NOS: 366  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 141  
; LENGTH: 15  
; TYPE: PRT

```
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Binding domain
US-10-211-088-141

Query Match      77.1%; Score 81; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKL 15
Db 1 PPLSQETFSDLWKL 15

RESULT 3
US-09-701-080C-22
; Sequence 22, Application US/09701080C
; GENERAL INFORMATION:
; APPLICANT: INSTITUTE OF MOLECULAR AND CELL BIOLOGY
; TITLE OF INVENTION: POLYPEPTIDES FROM CREB BINDING PROTEIN AND RELATED PROTEIN P300 F
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATION
; FILE REFERENCE: N73477C GCW
; CURRENT APPLICATION NUMBER: US/09/701,080C
; CURRENT FILING DATE: 2001-02-27
; PRIOR FILING DATE: 1998-05-26
; PRIOR APPLICATION NUMBER: GB 9811303.8
; PRIOR FILING DATE: 1998-05-26
; PRIOR APPLICATION NUMBER: GB 9900157.0
; PRIOR FILING DATE: 1999-01-05
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: derived from p53
US-09-701-080C-22

Query Match      66.7%; Score 70; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.6e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SQETFSDLWKLLP 16
Db 1 SQETFSDLWKLLP 13

RESULT 4
US-09-701-080C-27
; Sequence 27, Application US/09701080C
; GENERAL INFORMATION:
; APPLICANT: INSTITUTE OF MOLECULAR AND CELL BIOLOGY
; TITLE OF INVENTION: POLYPEPTIDES FROM CREB BINDING PROTEIN AND RELATED PROTEIN P300 F
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATION
; FILE REFERENCE: N73477C GCW
; CURRENT APPLICATION NUMBER: US/09/701,080C
; CURRENT FILING DATE: 2001-02-27
; PRIOR FILING DATE: 1998-05-26
; PRIOR APPLICATION NUMBER: GB 9811303.8
; PRIOR FILING DATE: 1998-05-26
; PRIOR APPLICATION NUMBER: GB 9900157.0
; PRIOR FILING DATE: 1999-01-05
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: derived from p53
US-09-701-080C-27

Query Match      66.7%; Score 70; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.6e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SQETFSDLWKLLP 16
Db 1 SQETFSDLWKLLP 13

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SQETFSDLWKLLP 16
Db 1 SQETFSDLWKLLP 13

RESULT 5
US-09-189-702A-286
; Sequence 286, Application US/09189702A
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Kast, W. Martin
; APPLICANT: Southwood, Scott
; APPLICANT: Epimmune, Inc.
; TITLE OF INVENTION: HLA Binding Peptides and Their Uses
; FILE REFERENCE: 39963-20019.20
; CURRENT APPLICATION NUMBER: US/09/189,702A
; CURRENT FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 286
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: p53.14 peptide 34.0324
US-09-189-702A-286

Query Match      56.2%; Score 59; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0046;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LSQETFSDLWK 13
Db 1 LSQETFSDLWK 11

RESULT 6
US-10-049-428-6
; Sequence 6, Application US/10049428
; GENERAL INFORMATION:
; APPLICANT: Charles, Ian G.
; APPLICANT: Xu, Weiming
; APPLICANT: Liu, Lizhi
; TITLE OF INVENTION: Unducible Screen for Drug Discovery
; FILE REFERENCE: HO-P02380US0
; CURRENT APPLICATION NUMBER: US/10/049,428
; CURRENT FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: GB 9918077
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: GB 0016171.1
; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 14
; TYPE: PRT
; ORGANISM: HUMAN
; OTHER INFORMATION:
US-10-049-428-6

Query Match      39.0%; Score 41; DB 6; Length 14;
Best Local Similarity 69.2%; Pred. No. 4.3;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWK 13
Db 2 PPLSQEAFALLKK 14
```

RESULT 7  
 US-09-701-080C-12  
 ; Sequence 12, Application US/09701080C  
 ; GENERAL INFORMATION:  
 ; APPLICANT: INSTITUTE OF MOLECULAR AND CELL BIOLOGY  
 ; TITLE OF INVENTION: POLYPEPTIDES FROM CREB BINDING PROTEIN AND RELATED PROTEIN P300 P  
 ; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATION  
 ; FILE REFERENCE: N73477C GCW  
 ; CURRENT APPLICATION NUMBER: US/09/701,080C  
 ; CURRENT FILING DATE: 2001-02-27  
 ; PRIOR APPLICATION NUMBER: GB 9811303.8  
 ; PRIOR FILING DATE: 1998-05-26  
 ; PRIOR APPLICATION NUMBER: GB 9900157.0  
 ; PRIOR FILING DATE: 1999-01-05  
 ; NUMBER OF SEQ ID NOS: 36  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 12  
 ; LENGTH: 7  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: derived from p53  
 US-09-701-080C-12

Query Match 38.1%; Score 40; DB 5; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 FSDLWKL 14  
 |||||  
 Db 1 FSDLWKL 7

RESULT 8  
 US-10-049-428-7  
 ; Sequence 7, Application US/10049428  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Charles, Ian G.  
 ; APPLICANT: Xu, Weiming  
 ; APPLICANT: Liu, Lishi  
 ; TITLE OF INVENTION: Unducible Screen for Drug Discovery  
 ; FILE REFERENCE: HO-P02380US0  
 ; CURRENT APPLICATION NUMBER: US/10/049,428  
 ; CURRENT FILING DATE: 2000-07-28  
 ; PRIOR APPLICATION NUMBER: GB 9918077  
 ; PRIOR FILING DATE: 1999-07-30  
 ; PRIOR APPLICATION NUMBER: GB 0016171.1  
 ; PRIOR FILING DATE: 2000-06-30  
 ; NUMBER OF SEQ ID NOS: 7  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 7  
 ; LENGTH: 14  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Mutagen  
 US-10-049-428-7

Query Match 33.3%; Score 35; DB 6; Length 14;  
 Best Local Similarity 53.8%; Pred. No. 38;  
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWK 13  
 |||||  
 Db 2 PPLSEQAFALLKK 14

RESULT 9  
 US-10-268-332-53  
 ; Sequence 53, Application US/10268332  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bristol-Myers Squibb Company  
 ; TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBWY3, EXPRESSED HIGHLY

; TITLE OF INVENTION: IMMUNE- AND COLON- RELATED TISSUES  
 ; FILE REFERENCE: D0042A CIP  
 ; CURRENT APPLICATION NUMBER: US/10/268,332  
 ; CURRENT FILING DATE: 2002-10-10  
 ; PRIOR APPLICATION NUMBER: U.S. 60/235,713  
 ; PRIOR FILING DATE: 2000-09-27  
 ; PRIOR APPLICATION NUMBER: U.S. 60/261,783  
 ; PRIOR FILING DATE: 2001-01-16  
 ; PRIOR APPLICATION NUMBER: U.S. 60/305,085  
 ; PRIOR FILING DATE: 2001-07-13  
 ; PRIOR APPLICATION NUMBER: U.S. 60/313,171  
 ; PRIOR FILING DATE: 2001-08-17  
 ; PRIOR APPLICATION NUMBER: U.S. 09/964,821  
 ; PRIOR FILING DATE: 2001-09-26  
 ; NUMBER OF SEQ ID NOS: 66  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 53  
 ; LENGTH: 14  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; OTHER INFORMATION: US-10-268-332-53

Query Match 30.0%; Score 31.5; DB 6; Length 14;  
 Best Local Similarity 77.8%; Pred. No. 1.4e+02;  
 Matches 7; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Qy 6 BTFSDELWK 13  
 |||||  
 Db 5 ESFSDWLWK 13

RESULT 10  
 US-10-225-567A-1177  
 ; Sequence 1177, Application US/10225567A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: LifeSpan Biosciences  
 ; APPLICANT: Brown, Joseph P.  
 ; APPLICANT: Burner, Glenna C.  
 ; APPLICANT: Roush, Christine L.  
 ; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS  
 ; FILE REFERENCE: 1920-4-4  
 ; CURRENT APPLICATION NUMBER: US/10/225,567A  
 ; CURRENT FILING DATE: 2001-12-19  
 ; PRIOR APPLICATION NUMBER: 60/257,144  
 ; PRIOR FILING DATE: 2000-12-19  
 ; NUMBER OF SEQ ID NOS: 2292  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 1177  
 ; LENGTH: 16  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; OTHER INFORMATION: US-10-225-567A-1177

Query Match 30.0%; Score 31.5; DB 6; Length 16;  
 Best Local Similarity 53.3%; Pred. No. 1.6e+02;  
 Matches 8; Conservative 2; Mismatches 2; Indels 3; Gaps 1;

Qy 4 SQETFSDLWKLLEN 18  
 |||||  
 Db 5 SQENHS---RLPEN 16

RESULT 11  
 US-09-189-702A-7  
 ; Sequence 7, Application US/09189702A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Sette, Alessandro  
 ; APPLICANT: Sidney, John  
 ; APPLICANT: Kast, W. Martin  
 ; APPLICANT: Southwood, Scott  
 ; APPLICANT: Epimmune, Inc.  
 ; TITLE OF INVENTION: HLA Binding Peptides and Their Uses  
 ; FILE REFERENCE: 39963-20019.20

; CURRENT APPLICATION NUMBER: US/09/189,702A  
; CURRENT FILING DATE: 1998-11-10  
; PRIOR APPLICATION NUMBER: US 08/205,713  
; PRIOR FILING DATE: 1994-03-04  
; NUMBER OF SEQ ID NOS: 380  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 7  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: p53.24V9 peptide 1323.02  
US-09-189-702A-7

Query Match 29.5%; Score 31; DB 5; Length 9;  
Best Local Similarity 100.0%; Pred. No. 3.5e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 KLLPEN 18  
|||  
Db 1 KLLPEN 6

## RESULT 12

US-09-281-717A-31  
; Sequence 31, Application US/09281717A

; GENERAL INFORMATION:  
; APPLICANT: Baxter, John  
; APPLICANT: Darimont, Beatrice  
; APPLICANT: Feng, Weijun  
; APPLICANT: Fletterick, Robert  
; APPLICANT: Kushner, Peter  
; APPLICANT: West, Brian  
; APPLICANT: Wagner, Richard  
; APPLICANT: Yamamoto, Keith

; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING NUCLEAR RECEPTOR  
; FILE REFERENCE: 9811-008-999  
; CURRENT APPLICATION NUMBER: US/09/281,717A

; CURRENT FILING DATE: 1999-03-30

; PRIOR APPLICATION NUMBER: US 60/079,956

; PRIOR FILING DATE: 1998-03-30

; NUMBER OF SEQ ID NOS: 60

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 31

; LENGTH: 12

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: MUTAGEN

; LOCATION: (5)..(5)

; OTHER INFORMATION: Leu --> Arg (L454R)

; FEATURE:

; NAME/KEY: MUTAGEN

; LOCATION: (7)..(7)

; OTHER INFORMATION: Leu --> Arg (L456R)

; FEATURE:

; NAME/KEY: MUTAGEN

; LOCATION: (8)..(8)

; OTHER INFORMATION: Glu --> Lys (E457K)

US-09-281-717A-31

Query Match 29.5%; Score 31; DB 5; Length 12;  
Best Local Similarity 60.0%; Pred. No. 1.4e+02;  
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 PPLSQETFS 10  
|||  
Db 3 PPLFLEVPED 12

## RESULT 13

US-09-281-717A-33

; Sequence 33, Application US/09281717A

; GENERAL INFORMATION:

; APPLICANT: Baxter, John

; APPLICANT: Darimont, Beatrice

; APPLICANT: Feng, Weijun

; APPLICANT: Fletterick, Robert

; APPLICANT: Kushner, Peter

; APPLICANT: West, Brian

; APPLICANT: Wagner, Richard

; APPLICANT: Yamamoto, Keith

; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING NUCLEAR RECEPTOR

; FILE REFERENCE: 9811-008-999

; CURRENT APPLICATION NUMBER: US/09/281,717A

; CURRENT FILING DATE: 1999-03-30

; PRIOR APPLICATION NUMBER: US 60/079,956

; PRIOR FILING DATE: 1998-03-30

; NUMBER OF SEQ ID NOS: 60

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 33

; LENGTH: 12

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-281-717A-33

Query Match 29.5%; Score 31; DB 5; Length 12;

Best Local Similarity 60.0%; Pred. No. 1.4e+02;

Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 PPLSQETFS 10  
|||  
Db 3 PPLFLEVPED 12

## RESULT 14

US-09-281-717A-35

; Sequence 35, Application US/09281717A

; GENERAL INFORMATION:

; APPLICANT: Baxter, John

; APPLICANT: Darimont, Beatrice

; APPLICANT: Feng, Weijun

; APPLICANT: Fletterick, Robert

; APPLICANT: Kushner, Peter

; APPLICANT: West, Brian

; APPLICANT: Wagner, Richard

; APPLICANT: Yamamoto, Keith

; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING NUCLEAR RECEPTOR

; FILE REFERENCE: 9811-008-999

; CURRENT APPLICATION NUMBER: US/09/281,717A

; CURRENT FILING DATE: 1999-03-30

; PRIOR APPLICATION NUMBER: US 60/079,956

; PRIOR FILING DATE: 1998-03-30

; NUMBER OF SEQ ID NOS: 60

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 35

; LENGTH: 12

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-281-717A-35

Query Match 29.5%; Score 31; DB 5; Length 12;

Best Local Similarity 60.0%; Pred. No. 1.4e+02;

Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 PPLSQETFS 10  
|||  
Db 3 PPLFLEVPED 12

## RESULT 15

US-09-830-693B-6

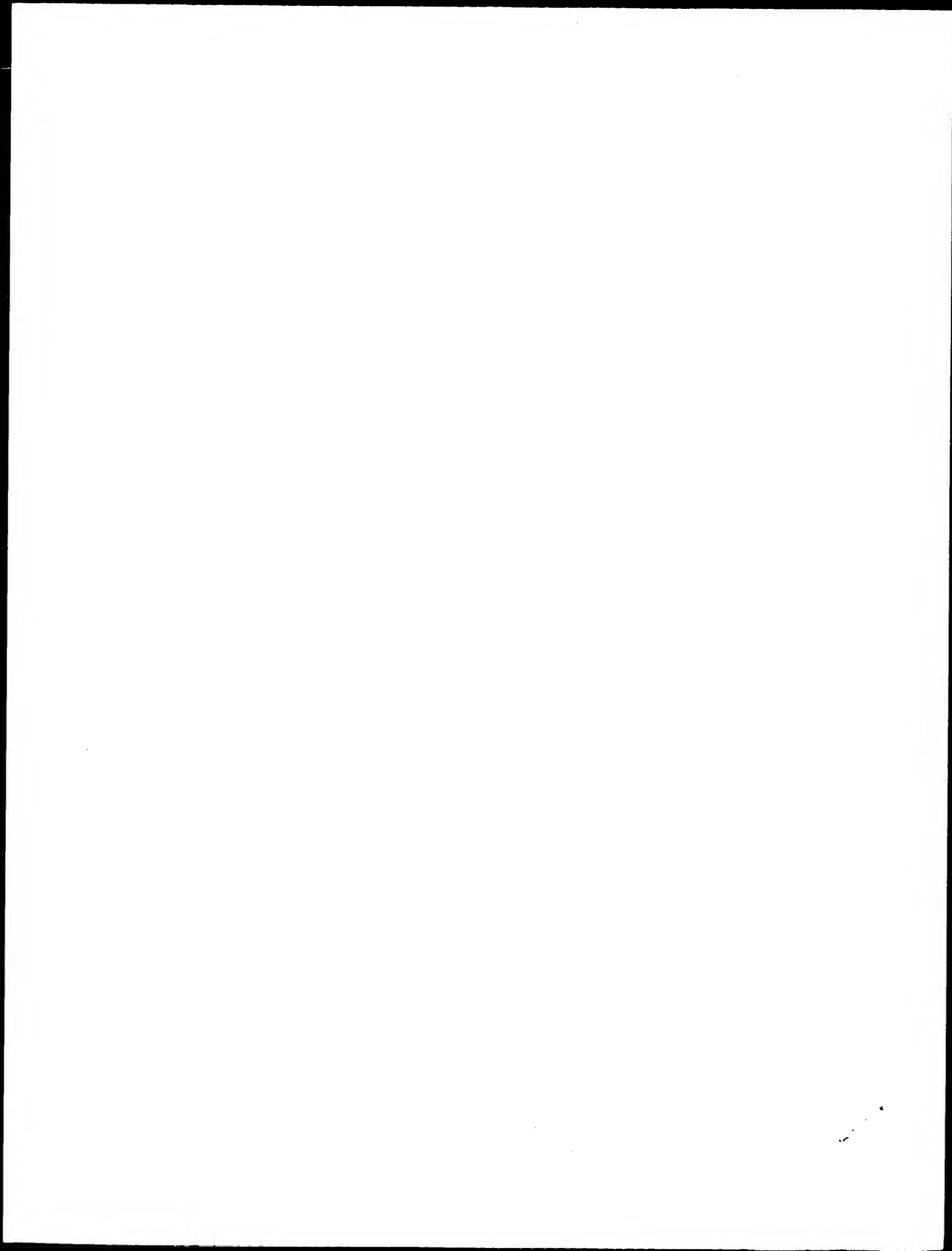
; Sequence 6, Application US/09830693B

```
; GENERAL INFORMATION:
; APPLICANT: Shiau, Andrew
; APPLICANT: Kushner, Peter
; APPLICANT: Agard, David
; APPLICANT: Greene, Geoffrey
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING NUCLEAR RECEPTOR
; TITLE OF INVENTION: ACTIVITY
; FILE REFERENCE: 9811-013-999
; CURRENT APPLICATION NUMBER: US/09/830,693B
; CURRENT FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: PCT/US99/06937
; PRIOR FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: US 60/079,956
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: US 60/113,146
; PRIOR FILING DATE: 1998-12-16
; PRIOR APPLICATION NUMBER: US 60/113,014
; PRIOR FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-830-693B-6

Query Match      29.5%; Score 31; DB 5; Length 12;
Best Local Similarity 60.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 PPLSOFTSD 10
Db 3 PPLFLEVFED 12

Search completed: February 12, 2003, 11:24:44
Job time : 26.9167 secs
```



GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 12, 2003, 11:13:52 ; Search time 377.625 Seconds  
(without alignments)  
32.439 Million cell updates/sec

Title: US-09-403-440A-2

Perfect score: 105

Sequence: 1 PPLSQETFSDLWKLLPENG 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters: 2260083

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending Patents AA.Main.\*  
1: /cgn2\_6/ptodata/1/paa/PCTUS\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/paa/US06\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/paa/US07\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/paa/US08\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/paa/US081\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/paa/US082\_COMB.pep.\*  
7: /cgn2\_6/ptodata/1/paa/US083\_COMB.pep.\*  
8: /cgn2\_6/ptodata/1/paa/US084\_COMB.pep.\*  
9: /cgn2\_6/ptodata/1/paa/US085\_COMB.pep.\*  
10: /cgn2\_6/ptodata/1/paa/US086\_COMB.pep.\*  
11: /cgn2\_6/ptodata/1/paa/US087\_COMB.pep.\*  
12: /cgn2\_6/ptodata/1/paa/US088\_COMB.pep.\*  
13: /cgn2\_6/ptodata/1/paa/US089\_COMB.pep.\*  
14: /cgn2\_6/ptodata/1/paa/US090\_COMB.pep.\*  
15: /cgn2\_6/ptodata/1/paa/US091\_COMB.pep.\*  
16: /cgn2\_6/ptodata/1/paa/US092\_COMB.pep.\*  
17: /cgn2\_6/ptodata/1/paa/US093\_COMB.pep.\*  
18: /cgn2\_6/ptodata/1/paa/US094\_COMB.pep.\*  
19: /cgn2\_6/ptodata/1/paa/US095\_COMB.pep.\*  
20: /cgn2\_6/ptodata/1/paa/US096\_COMB.pep.\*  
21: /cgn2\_6/ptodata/1/paa/US097\_COMB.pep.\*  
22: /cgn2\_6/ptodata/1/paa/US098\_COMB.pep.\*  
23: /cgn2\_6/ptodata/1/paa/US099\_COMB.pep.\*  
24: /cgn2\_6/ptodata/1/paa/US100\_COMB.pep.\*  
25: /cgn2\_6/ptodata/1/paa/US101\_COMB.pep.\*  
26: /cgn2\_6/ptodata/1/paa/US102\_COMB.pep.\*  
27: /cgn2\_6/ptodata/1/paa/US60\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	105	100.0	19	US-09-403-440A-2	Sequence 2, Appli
2	99	94.3	18	US-09-214-371-74	Sequence 74, Appli
3	99	94.3	20	US-10-155-059-8	Sequence 8, Appli
4	99	94.3	20	US-10-155-059-10	Sequence 10, Appli
5	99	94.3	20	US-10-155-059-11	Sequence 11, Appli
6	99	94.3	20	US-10-155-059-16	Sequence 16, Appli

7	99	94.3	25	6	US-08-244-476-18	Sequence 18, Appli
8	99	94.3	25	8	US-08-424-273-1	Sequence 1, Appli
9	94	89.5	20	25	US-10-155-059-14	Sequence 14, Appli
10	94	89.5	20	25	US-10-155-059-15	Sequence 15, Appli
11	93	88.6	22	16	US-09-214-371-73	Sequence 73, Appli
12	92	87.6	19	21	US-09-732-384-7	Sequence 7, Appli
13	90	85.7	19	25	US-10-155-059-13	Sequence 13, Appli
14	89	84.8	19	16	US-09-214-371-1	Sequence 1, Appli
15	86	81.9	20	25	US-10-155-059-19	Sequence 19, Appli
16	77	73.3	15	6	US-08-277-660-1	Sequence 1, Appli
17	77	73.3	15	6	US-08-277-660-4	Sequence 4, Appli
18	77	73.3	15	8	US-08-424-273-3	Sequence 3, Appli
19	77	73.3	15	8	US-08-424-273-4	Sequence 4, Appli
20	77	73.3	15	18	US-09-458-297-1109	Sequence 1109, Ap
21	77	73.3	15	18	US-09-458-297-1469	Sequence 1469, Ap
22	77	73.3	15	18	US-09-458-297A-1109	Sequence 1109, Ap
23	77	73.3	15	18	US-09-458-297A-1469	Sequence 1469, Ap
24	77	73.3	15	21	US-09-732-384-6	Sequence 6, Appli
25	77	73.3	15	23	US-09-936-956-2	Sequence 2, Appli
26	77	73.3	15	23	US-09-936-956-3	Sequence 3, Appli
27	77	73.3	15	23	US-09-936-956-4	Sequence 4, Appli
28	77	73.3	17	16	US-09-265-927-3	Sequence 3, Appli
29	77	73.3	25	27	US-60-397-136-2	Sequence 2, Appli
30	74	70.5	15	6	US-08-277-660-5	Sequence 5, Appli
31	74	70.5	15	23	US-09-936-956-5	Sequence 5, Appli
32	74	70.5	15	23	US-09-936-956-9	Sequence 9, Appli
33	74	70.5	16	25	US-10-155-059-23	Sequence 23, Appli
34	74	70.5	18	20	US-09-695-437A-63	Sequence 63, Appli
35	74	70.5	20	25	US-10-155-059-20	Sequence 20, Appli
36	73	69.5	15	5	US-08-132-284-8	Sequence 8, Appli
37	73	69.5	15	7	US-08-398-139B-8	Sequence 8, Appli
38	73	69.5	15	20	US-09-695-437A-8	Sequence 8, Appli
39	73	69.5	15	23	US-09-936-956-13	Sequence 13, Appli
40	73	69.5	24	5	US-08-132-284-26	Sequence 26, Appli
41	73	69.5	25	5	US-08-132-284-4	Sequence 4, Appli
42	73	69.5	25	7	US-08-398-139B-4	Sequence 4, Appli
43	73	69.5	25	20	US-09-695-437A-4	Sequence 4, Appli
44	72	68.6	20	25	US-10-155-059-18	Sequence 18, Appli
45	71	67.6	15	23	US-09-936-956-6	Sequence 6, Appli

#### ALIGNMENTS

RESULT 1  
US-09-403-440A-2  
; Sequence 2, Application US/09403440A  
; GENERAL INFORMATION:  
; APPLICANT: Lane, David Philip  
; TITLE OF INVENTION: MATERIALS AND METHODS RELATING TO  
; TITLE OF INVENTION: INHIBITING THE INTERACTION OF P53 AND MDM2  
; FILE REFERENCE: MEMB25.001APC  
; CURRENT APPLICATION NUMBER: US/09/403,440A  
; CURRENT FILING DATE: 2000-01-19  
; PRIOR APPLICATION NUMBER: PCT/GB98/01144  
; PRIOR FILING DATE: 1998-04-20  
; PRIOR APPLICATION NUMBER: GB 9708092.3  
; PRIOR FILING DATE: 1997-04-22  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-403-440A-2

Query Match 100.0%; Score 105; DB 18; Length 19;  
Best Local Similarity 100.0%; Pred. No. 7.8e-09;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 PPLSQETFSDLWKLLPENG 19  
Db 1 PPLSQETFSDLWKLLPENG 19

```

RESULT 2
US-09-214-371-74
; Sequence 74, Application US/09214371B
; GENERAL INFORMATION:
; APPLICANT: Lane, David
; APPLICANT: Bottger, Volker
; APPLICANT: Bottger, Angelica
; APPLICANT: Pickseley, Stephen
; APPLICANT: Chene, Patrick
; APPLICANT: Hochkeppel, Heinz-Kurt
; APPLICANT: Garcia-Scheverria, Carlos
; APPLICANT: Furet, Pascal
; TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2
; FILE REFERENCE: 4-20937/A/PCT
; CURRENT APPLICATION NUMBER: US/09/214,371B
; CURRENT FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: PCT/EP97/03549
; PRIOR FILING DATE: 1997-07-04
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 74
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:peptide
US-09-214-371-74

Query Match          94.3%; Score 99; DB 16; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLPEN 18
Db 1 PPLSQETFSDLWKLLPEN 18

RESULT 3
US-10-155-059-8
; Sequence 8, Application US/10155059
; GENERAL INFORMATION:
; APPLICANT: Kaelin, William
; APPLICANT: Jost, Christine
; TITLE OF INVENTION: METHODS OF TREATMENT USING
; NBS-1, ANTIBODIES AND PROTEINS THERETO, AND USES OF THE
; ANTIBODIES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon Peabody LLP
; STREET: 101 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/155,059
; FILING DATE: 24-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/081,975
; FILING DATE: 12-MAY-1998
; APPLICATION NUMBER: 60/046,207
; FILING DATE: 12-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Eisenstein, Ronald I
; REGISTRATION NUMBER: 30,628
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-345-6054
; TELEFAX: 617-345-1300
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 8
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-155-059-8

Query Match          94.3%; Score 99; DB 25; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLPEN 18
Db 2 PPLSQETFSDLWKLLPEN 19

RESULT 4
US-10-155-059-10
; Sequence 10, Application US/10155059
; GENERAL INFORMATION:
; APPLICANT: Kaelin, William
; APPLICANT: Jost, Christine
; TITLE OF INVENTION: METHODS OF TREATMENT USING
; NBS-1, ANTIBODIES AND PROTEINS THERETO, AND USES OF THE
; ANTIBODIES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon Peabody LLP
; STREET: 101 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/155,059
; FILING DATE: 24-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/081,975
; FILING DATE: 12-MAY-1998
; APPLICATION NUMBER: 60/046,207
; FILING DATE: 12-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Eisenstein, Ronald I
; REGISTRATION NUMBER: 30,628
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-345-6054
; TELEFAX: 617-345-1300
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 10
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-155-059-10

Query Match          94.3%; Score 99; DB 25; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.2e-08;

```

```

; REFERENCE/DOCKET NUMBER: 47400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-345-6054
; TELEFAX: 617-345-1300
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 8
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-155-059-8

Query Match          94.3%; Score 99; DB 25; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLPEN 18
Db 2 PPLSQETFSDLWKLLPEN 19

RESULT 4
US-10-155-059-10
; Sequence 10, Application US/10155059
; GENERAL INFORMATION:
; APPLICANT: Kaelin, William
; APPLICANT: Jost, Christine
; TITLE OF INVENTION: METHODS OF TREATMENT USING
; NBS-1, ANTIBODIES AND PROTEINS THERETO, AND USES OF THE
; ANTIBODIES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon Peabody LLP
; STREET: 101 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/155,059
; FILING DATE: 24-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/081,975
; FILING DATE: 12-MAY-1998
; APPLICATION NUMBER: 60/046,207
; FILING DATE: 12-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Eisenstein, Ronald I
; REGISTRATION NUMBER: 30,628
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-345-6054
; TELEFAX: 617-345-1300
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 10
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-155-059-10

Query Match          94.3%; Score 99; DB 25; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.2e-08;

```



Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18  
| | | | | | | | | | | | | | | | | | | | | |  
Db 2 PPLSQETFSDLWKLLPEN 19

RESULT 5  
US-10-155-059-11  
; Sequence 11, Application US/10155059  
; GENERAL INFORMATION:  
; APPLICANT: Kaelin, William  
; Jost, Christine  
; TITLE OF INVENTION: METHODS OF TREATMENT USING  
; NBS-1, ANTIBODIES AND PROTEINS THEREO, AND USES OF THE  
; ANTIBODIES  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Nixon Peabody LLP  
; STREET: 101 Federal Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/155,059  
; FILING DATE: 24-May-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/081,975  
; FILING DATE: 12-MAY-1998  
; APPLICATION NUMBER: 60/046,207  
; FILING DATE: 12-MAY-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Eisenstein, Ronald I  
; REGISTRATION NUMBER: 30,628  
; REFERENCE/DOCKET NUMBER: 47400  
; TELEPHONE: 617-345-6054  
; TELEFAX: 617-345-1300  
; TELEX: <Unknown>  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
US-10-155-059-11

Query Match 94.3%; Score 99; DB 25; Length 20;  
Best Local Similarity 100.0%; Pred. No. 7.2e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18  
| | | | | | | | | | | | | | | | | | | | | |  
Db 2 PPLSQETFSDLWKLLPEN 19

RESULT 6  
US-10-155-059-16  
; Sequence 16, Application US/10155059  
; GENERAL INFORMATION:  
; APPLICANT: Kaelin, William  
; Jost, Christine  
; TITLE OF INVENTION: METHODS OF TREATMENT USING  
; NBS-1, ANTIBODIES AND PROTEINS THEREO, AND USES OF THE  
; ANTIBODIES

NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nixon Peabody LLP  
STREET: 101 Federal Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/155,059  
FILING DATE: 24-May-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/081,975  
FILING DATE: 12-MAY-1998  
APPLICATION NUMBER: 60/046,207  
FILING DATE: 12-MAY-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Eisenstein, Ronald I  
REGISTRATION NUMBER: 30,628  
REFERENCE/DOCKET NUMBER: 47400  
TELEPHONE: 617-345-6054  
TELEFAX: 617-345-1300  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 16:  
US-10-155-059-16

Query Match 94.3%; Score 99; DB 25; Length 20;  
Best Local Similarity 100.0%; Pred. No. 7.2e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18  
| | | | | | | | | | | | | | | | | | | | | |  
Db 2 PPLSQETFSDLWKLLPEN 19

RESULT 7  
US-08-244-476-18  
; Sequence 18, Application US/08244476  
; GENERAL INFORMATION:  
; APPLICANT: Zentgraf, Hanswalter  
; APPLICANT: Schranz, Peter  
; APPLICANT: Volkman, Martin  
; APPLICANT: Tessmer, Claudia  
; APPLICANT: Klein, Ralf  
; TITLE OF INVENTION: METHOD OF DETECTING p53-SPECIFIC  
; TITLE OF INVENTION: ANTIBODIES  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
; STREET: 1201 New York Avenue, N.W., Suite 1000  
; CITY: Washington  
; STATE: DC  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:

```

; APPLICATION NUMBER: US/08/244,476
; FILING DATE: 15-SEP-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO 94/08241
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 42 32 823.3
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 18644-94281-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-244-476-18

```

```

Query Match          94.3%; Score 99; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 9.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLPEN 18
   |||||
Db 4 PPLSQETFSDLWKLLPEN 21

```

```

RESULT 8
US-08-424-273-1
; Sequence 1, Application US/08424273
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: P53 PROTEIN FRAGMENTS AND USE THEREOF FOR
; TITLE OF INVENTION: DETECTING AND MONITORING DISEASED CONDITIONS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern, PLLC
; STREET: 400 Seventh Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 5.1 (ASC III)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,273
; FILING DATE: 28-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 9213110
; FILING DATE: 2-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR 9301082
; FILING DATE: 2-NOV-1993
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens

```

```

US-08-424-273-1
Query Match          94.3%; Score 99; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 9.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLPEN 18
   |||||
Db 2 PPLSQETFSDLWKLLPEN 19

```

```

RESULT 9
US-10-155-059-14
; Sequence 14, Application US/10155059
; GENERAL INFORMATION:
; APPLICANT: Kaelin, William
; Jost, Christine
; TITLE OF INVENTION: METHODS OF TREATMENT USING
; NBS-1, ANTIBODIES AND PROTEINS THERETO, AND USES OF THE
; ANTIBODIES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon Peabody LLP
; STREET: 101 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/155,059
; FILING DATE: 24-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/081,975
; FILING DATE: 12-MAY-1998
; APPLICATION NUMBER: 60/046,207
; FILING DATE: 12-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Eisenstein, Ronald I
; REGISTRATION NUMBER: 30,628
; REFERENCE/DOCKET NUMBER: 47400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-345-6054
; TELEFAX: 617-345-1300
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-155-059-14

```

```

Query Match          89.5%; Score 94; DB 25; Length 20;
Best Local Similarity 94.4%; Pred. No. 4.3e-07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLPEN 18
   |||||
Db 2 PPLSQETFSDLWKLLPEN 19

```

```

RESULT 10
US-10-155-059-15
; Sequence 15, Application US/10155059
; GENERAL INFORMATION:
; APPLICANT: Kaelin, William

```

```
; Jost, Christine
;
; TITLE OF INVENTION: METHODS OF TREATMENT USING
; NBS-1, ANTIBODIES AND PROTEINS THEREO, AND USES OF THE
; ANTIBODIES
;
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon Peabody LLP
; STREET: 101 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/155,059
; FILING DATE: 24-May-2002
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/081,975
; FILING DATE: 12-MAY-1998
; APPLICATION NUMBER: 60/046,207
; FILING DATE: 12-MAY-1997
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Eisenstein, Ronald I
; REGISTRATION NUMBER: 30,628
; REFERENCE/DOCKET NUMBER: 47400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-345-6054
; TELEFAX: 617-345-1300
; TELEX: <Unknown>
;
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
;
; US-10-155-059-15
;
; Query Match 89.5%; Score 94; DB 25; Length 20;
; Best Local Similarity 94.4%; Pred. No. 4.3e-07;
; Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; QY 1 PPLSQETFSDLWKLLPEN 18
; | | | | | | | | | | | | | | | | | |
; Db 2 PPLSQETFSDLWNLLPEN 19
; | | | | | | | | | | | | | | | | | |
;
; RESULT 11
; US-09-214-371-73
; Sequence 73, Application US/09214371B
; GENERAL INFORMATION:
; APPLICANT: Lane, David
; APPLICANT: Bottger, Volker
; APPLICANT: Bottger, Angelica
; APPLICANT: Pickseley, Stephen
; APPLICANT: Chene, Patrick
; APPLICANT: Hochkeppel, Heinz-Kurt
; APPLICANT: Garcia-Echeverria, Carlos
; APPLICANT: Furet, Pascal
;
; TITLE OF INVENTION: Inhibitors of the Interaction of p53 and MDM2
;
; FILE REFERENCE: 4-20937/A/PCT
; CURRENT APPLICATION NUMBER: US/09/214,371B
; CURRENT FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: PCT/EP97/03549
; PRIOR FILING DATE: 1997-07-04
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 73
```

```
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:peptide
; NAME/KEY: VARIANT
; LOCATION: (1)
; OTHER INFORMATION: X = Biotin-Ser
;
; US-09-214-371-73
;
; Query Match 88.6%; Score 93; DB 16; Length 22;
; Best Local Similarity 100.0%; Pred. No. 6.9e-07;
; Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 PPLSQETFSDLWKLLPE 17
; | | | | | | | | | | | | | | | | | |
; Db 6 PPLSQETFSDLWKLLPE 22
; | | | | | | | | | | | | | | | | | |
;
; RESULT 12
; US-09-732-384-7
; Sequence 7, Application US/09732384
; GENERAL INFORMATION:
; APPLICANT: Yuan, Zhi-Min
; APPLICANT: Gu, JiJie
; TITLE OF INVENTION: Inhibition of p53 Degradation
; FILE REFERENCE: 21508-044
; CURRENT APPLICATION NUMBER: US/09/732,384
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 60/169,816
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Protein
; OTHER INFORMATION: fragment not in inhibitory p53 polypeptide
;
; US-09-732-384-7
;
; Query Match 87.6%; Score 92; DB 21; Length 19;
; Best Local Similarity 100.0%; Pred. No. 8.4e-07;
; Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 2 PLSQETFSDLWKLLPEN 18
; | | | | | | | | | | | | | | | | | |
; Db 1 PLSQETFSDLWKLLPEN 17
; | | | | | | | | | | | | | | | | | |
;
; RESULT 13
; US-10-155-059-13
; Sequence 13, Application US/10155059
; GENERAL INFORMATION:
; APPLICANT: Kaelin, William
; APPLICANT: Jost, Christine
;
; TITLE OF INVENTION: METHODS OF TREATMENT USING
; NBS-1, ANTIBODIES AND PROTEINS THEREO, AND USES OF THE
; ANTIBODIES
;
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon Peabody LLP
; STREET: 101 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; SEQ ID NO 73
```

;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/10/155,059  
;; FILING DATE: 24-May-2002  
;; CLASSIFICATION: <Unknown>  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/081,975  
;; FILING DATE: 12-MAY-1998  
;; APPLICATION NUMBER: 60/046,207  
;; FILING DATE: 12-MAY-1997  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Eisenstein, Ronald I  
;; REGISTRATION NUMBER: 30,628  
;; REFERENCE/DOCKET NUMBER: 47400  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 617-345-6054  
;; TELEFAX: 617-345-1300  
;; TELEX: <Unknown>  
;; INFORMATION FOR SEQ ID NO: 13:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 19 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 13:  
US-10-155-059-13

Query Match 85.7%; Score 90; DB 25; Length 19;  
Best Local Similarity 88.9%; Pred. No. 1.7e-06;  
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PLSQETFSDLWKLLPEN 18  
| | | | | | | | | | | | | | | | | |  
Db 1 PLSQETFSDLWKLLPEN 18

## RESULT 14

US-09-214-371-1  
;; Sequence 1, Application US/09214371B  
;; GENERAL INFORMATION:  
;; APPLICANT: Lane, David  
;; APPLICANT: Bottger, Volker  
;; APPLICANT: Bottger, Angelica  
;; APPLICANT: Pickaley, Stephen  
;; APPLICANT: Chene, Patrick  
;; APPLICANT: Hochkeppel, Heinz-Kurt  
;; APPLICANT: Garcia-Echeverria, Carlos  
;; APPLICANT: Furet, Pascal  
;; TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2  
;; FILE REFERENCE: 4-20937/A/PCT  
;; CURRENT APPLICATION NUMBER: US/09/214,371B  
;; CURRENT FILING DATE: 1999-03-26  
;; PRIOR APPLICATION NUMBER: PCT/EP97/03549  
;; PRIOR FILING DATE: 1997-07-04  
;; NUMBER OF SEQ ID NOS: 83  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 1  
;; LENGTH: 19  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence:peptide  
US-09-214-371-1

Query Match 84.8%; Score 89; DB 16; Length 19;  
Best Local Similarity 94.1%; Pred. No. 2.5e-06;  
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLSQETFSDLWKLLPEN 18  
| | | | | | | | | | | | | | | | | |  
Db 1\* PLSQETFSDLWKLLPEN 17

## RESULT 15

US-10-155-059-19  
;; Sequence 19, Application US/10155059  
;; GENERAL INFORMATION:  
;; APPLICANT: Kaelin, William  
;; Jost, Christine  
;; TITLE OF INVENTION: METHODS OF TREATMENT USING  
;; NBS-1, ANTIBODIES AND PROTEINS THERETO, AND USES OF THE  
;; ANTIBODIES  
;; NUMBER OF SEQUENCES: 27  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Nixon Peabody LLP  
;; STREET: 101 Federal Street  
;; CITY: Boston  
;; STATE: MA  
;; COUNTRY: USA  
;; ZIP: 02110  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Diskette  
;; COMPUTER: IBM Compatible  
;; OPERATING SYSTEM: Windows  
;; SOFTWARE: FastSeq for Windows Version 2.0b  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/10/155,059  
;; FILING DATE: 24-May-2002  
;; CLASSIFICATION: <Unknown>  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/081,975  
;; FILING DATE: 12-MAY-1998  
;; APPLICATION NUMBER: 60/046,207  
;; FILING DATE: 12-MAY-1997  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Eisenstein, Ronald I  
;; REGISTRATION NUMBER: 30,628  
;; REFERENCE/DOCKET NUMBER: 47400  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 617-345-6054  
;; TELEFAX: 617-345-1300  
;; TELEX: <Unknown>  
;; INFORMATION FOR SEQ ID NO: 19:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 20 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 19:  
US-10-155-059-19

Query Match 81.9%; Score 86; DB 25; Length 20;  
Best Local Similarity 94.1%; Pred. No. 7.7e-06;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PLSQETFSDLWKLLPEN 18  
| | | | | | | | | | | | | | | | | |  
Db 3 PLSQETFSDLWKLLPPN 19

Search completed: February 12, 2003, 11:24:05  
Job time : 378.625 secs

GenCore version 5.1.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 12, 2003, 11:15:02 ; Search time 12.6667 Seconds  
(without alignments)  
38.323 Million cell updates/sec

Title: US-09-403-440A-2

Perfect score: 105

Sequence: 1 PPLSQETFSDLWKLLPEN 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 140259 seqs, 25548876 residues

Total number of hits satisfying chosen parameters: 42882

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

#### Database :

Published Applications AA.\*  
1: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*  
8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*  
12: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep.\*  
13: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
14: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	ID	Description
1	99	94.3	18	US-09-214-371-74
2	99	94.3	20	US-10-155-059-8
3	99	94.3	20	US-10-155-059-10
4	99	94.3	20	US-10-155-059-11
5	99	94.3	20	US-10-155-059-12
6	94	89.5	20	US-10-155-059-16
7	94	89.5	20	US-10-155-059-14
8	93	88.6	22	US-10-155-059-15
9	92	87.6	19	US-09-214-371-73
10	90	85.7	19	US-09-732-384-7
11	89	84.8	19	US-10-155-059-13
12	86	81.9	20	US-09-214-371-1
13	77	73.3	15	US-10-155-059-19
14	74	70.5	16	US-09-732-384-6
15	74	70.5	20	US-10-155-059-23
16	72	68.6	20	US-10-155-059-20
17	66	62.9	12	US-10-155-059-18
18	65	61.9	15	US-09-214-371-17
19	60	57.1	18	US-09-950-692-6
			18	US-10-155-059-22

20	59	56.2	16	10	US-09-214-371-39	Sequence 39, Appl
21	57	54.3	14	9	US-10-024-123-7	Sequence 7, Appl
22	55	52.4	12	10	US-09-214-371-7	Sequence 7, Appl
23	54	51.4	12	10	US-09-214-371-24	Sequence 24, Appl
24	54	51.4	16	10	US-09-214-371-41	Sequence 41, Appl
25	53	50.5	16	10	US-09-214-371-40	Sequence 40, Appl
26	49	46.7	12	10	US-09-214-371-25	Sequence 25, Appl
27	49	46.7	12	10	US-09-214-371-26	Sequence 26, Appl
28	48	45.7	14	10	US-09-214-371-33	Sequence 33, Appl
29	48	45.7	14	10	US-09-214-371-34	Sequence 34, Appl
30	47	44.8	10	12	US-10-155-059-17	Sequence 17, Appl
31	47	44.8	16	10	US-09-019-679-3	Sequence 3, Appl
32	44	41.9	11	12	US-10-155-059-21	Sequence 21, Appl
33	44	41.9	12	10	US-09-214-371-20	Sequence 20, Appl
34	42	40.0	15	12	US-10-155-059-24	Sequence 24, Appl
35	36	34.3	6	10	US-09-214-371-83	Sequence 83, Appl
36	36	34.3	6	12	US-09-732-384-4	Sequence 4, Appl
37	36	34.3	6	12	US-10-155-059-1	Sequence 1, Appl
38	36	34.3	9	10	US-09-214-371-37	Sequence 37, Appl
39	36	34.3	9	10	US-09-214-371-38	Sequence 38, Appl
40	36	34.3	10	10	US-09-214-371-35	Sequence 35, Appl
41	36	34.3	10	10	US-09-214-371-36	Sequence 36, Appl
42	32	30.5	6	12	US-10-155-059-2	Sequence 2, Appl
43	32	30.5	12	9	US-09-840-277-66	Sequence 66, Appl
44	32	30.5	17	10	US-09-920-552-110	Sequence 110, App
45	31	29.5	8	10	US-09-214-371-13	Sequence 13, Appl

#### ALIGNMENTS

RESULT 1  
US-09-214-371-74  
; Sequence 74, Application US/09214371B  
; Patent No. US2001001851A1  
; GENERAL INFORMATION:  
; APPLICANT: Lane, David  
; APPLICANT: Bottger, Volker  
; APPLICANT: Bottger, Angelica  
; APPLICANT: Pickaley, Stephen  
; APPLICANT: Chene, Patrick  
; APPLICANT: Hochkeppel, Heinz-Kurt  
; APPLICANT: Garcia-Echeverria, Carlos  
; APPLICANT: Furet, Pascal  
; TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2  
; FILE REFERENCE: 4-20937/A/PCT  
; CURRENT APPLICATION NUMBER: US/09/214,371B  
; PRIOR FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: PCT/EP97/03549  
; NUMBER OF SEQ ID NOS: 83  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 74  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:peptide  
US-09-214-371-74

Query Match 94.3%; Score 99; DB 10; Length 18;  
Best Local Similarity 100.0%; Pred. No. 5.5e-09;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLPEN 18  
Db 1 PPLSQETFSDLWKLLPEN 18

RESULT 2  
US-10-155-059-8  
; Sequence 8, Application US/10155059  
; Patent No. US20020147173A1

```

; GENERAL INFORMATION:
; APPLICANT: Kaelin, William
; Jost, Christine
; TITLE OF INVENTION: METHODS OF TREATMENT USING
; NBS-1, ANTIBODIES AND PROTEINS THERETO, AND USES OF THE
; ANTIBODIES
;
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon Peabody LLP
; STREET: 101 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/155,059
; FILING DATE: 24-May-2002
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/081,975
; FILING DATE: 12-MAY-1998
; APPLICATION NUMBER: 60/046,207
; FILING DATE: 12-MAY-1997
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Eisenstein, Ronald I
; REGISTRATION NUMBER: 30,628
; REFERENCE/DOCKET NUMBER: 47400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-345-1300
; TELEFAX: 617-345-1300
; TELEX: <Unknown>
;
; INFORMATION FOR SEQ ID NO: 8:
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
;
; US-10-155-059-8
;
; Query Match 94.3%; Score 99; DB 12; Length 20;
; Best Local Similarity 100.0%; Pred. No. 6.2e-09;
; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; Qy 1 PPLSQETFSDLWKLLEN 18
; Db 2 PPLSQETFSDLWKLLEN 19
;
; RESULT 3
; US-10-155-059-10
; Sequence 10, Application US/10155059
; Patent No. US20020147173A1
; GENERAL INFORMATION:
; APPLICANT: Kaelin, William
; Jost, Christine
; TITLE OF INVENTION: METHODS OF TREATMENT USING
; NBS-1, ANTIBODIES AND PROTEINS THERETO, AND USES OF THE
; ANTIBODIES
;
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon Peabody LLP
; STREET: 101 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/155,059
; FILING DATE: 24-May-2002
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/081,975
; FILING DATE: 12-MAY-1998
; APPLICATION NUMBER: 60/046,207
; FILING DATE: 12-MAY-1997
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Eisenstein, Ronald I
; REGISTRATION NUMBER: 30,628
; REFERENCE/DOCKET NUMBER: 47400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-345-1300
; TELEFAX: 617-345-1300
; TELEX: <Unknown>
;
; INFORMATION FOR SEQ ID NO: 8:
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
;
; US-10-155-059-11
; Sequence 11, Application US/10155059
; Patent No. US20020147173A1
; GENERAL INFORMATION:
; APPLICANT: Kaelin, William
; Jost, Christine
; TITLE OF INVENTION: METHODS OF TREATMENT USING
; NBS-1, ANTIBODIES AND PROTEINS THERETO, AND USES OF THE
; ANTIBODIES
;
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon Peabody LLP
; STREET: 101 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/155,059
; FILING DATE: 24-May-2002
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/081,975
; FILING DATE: 12-MAY-1998
; APPLICATION NUMBER: 60/046,207
; FILING DATE: 12-MAY-1997
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Eisenstein, Ronald I

```

```

; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/155,059
; FILING DATE: 24-May-2002
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/081,975
; FILING DATE: 12-MAY-1998
; APPLICATION NUMBER: 60/046,207
; FILING DATE: 12-MAY-1997
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Eisenstein, Ronald I
; REGISTRATION NUMBER: 30,628
; REFERENCE/DOCKET NUMBER: 47400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-345-6054
; TELEFAX: 617-345-1300
; TELEX: <Unknown>
;
; INFORMATION FOR SEQ ID NO: 10:
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
;
; US-10-155-059-10
;
; Query Match 94.3%; Score 99; DB 12; Length 20;
; Best Local Similarity 100.0%; Pred. No. 6.2e-09;
; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; Qy 1 PPLSQETFSDLWKLLEN 18
; Db 2 PPLSQETFSDLWKLLEN 19
;
; RESULT 4
; US-10-155-059-11
; Sequence 11, Application US/10155059
; Patent No. US20020147173A1
; GENERAL INFORMATION:
; APPLICANT: Kaelin, William
; Jost, Christine
; TITLE OF INVENTION: METHODS OF TREATMENT USING
; NBS-1, ANTIBODIES AND PROTEINS THERETO, AND USES OF THE
; ANTIBODIES
;
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon Peabody LLP
; STREET: 101 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/155,059
; FILING DATE: 24-May-2002
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/081,975
; FILING DATE: 12-MAY-1998
; APPLICATION NUMBER: 60/046,207
; FILING DATE: 12-MAY-1997
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Eisenstein, Ronald I

```

; REGISTRATION NUMBER: 30,628  
 ; REFERENCE/DOCKET NUMBER: 47400  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 617-345-6054  
 ; TELEFAX: 617-345-1300  
 ; TELEX: <Unknown>  
 ; INFORMATION FOR SEQ ID NO: 11:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 20 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
 US-10-155-059-11

Query Match 94.3%; Score 99; DB 12; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 6.2e-09;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLPEN 18  
 Db 2 PPLSQETFSDLWKLLPEN 19

## RESULT 5

US-10-155-059-16  
 ; Sequence 16, Application US/10155059  
 ; Patent No. US20020147173A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kaelin, William

; TITLE OF INVENTION: METHODS OF TREATMENT USING  
 ; NBS-1, ANTIBODIES AND PROTEINS THERETO, AND USES OF THE  
 ; ANTIBODIES

; NUMBER OF SEQUENCES: 27  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Nixon Peabody LLP  
 ; STREET: 101 Federal Street  
 ; CITY: Boston  
 ; STATE: MA  
 ; COUNTRY: USA  
 ; ZIP: 02110

; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: Windows  
 ; SOFTWARE: FastSeq for Windows Version 2.0b  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/10/155,059  
 ; FILING DATE: 24-May-2002  
 ; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/081,975  
 ; FILING DATE: 12-MAY-1998  
 ; APPLICATION NUMBER: 60/046,207  
 ; FILING DATE: 12-MAY-1997  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Eisenstein, Ronald I

; REGISTRATION NUMBER: 30,628  
 ; REFERENCE/DOCKET NUMBER: 47400  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 617-345-6054  
 ; TELEFAX: 617-345-1300  
 ; TELEX: <Unknown>

; INFORMATION FOR SEQ ID NO: 16:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 20 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 16:  
 US-10-155-059-16

Query Match 94.3%; Score 99; DB 12; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 6.2e-09;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLPEN 18  
 Db 2 PPLSQETFSDLWKLLPEN 19

## RESULT 6

US-10-155-059-14  
 ; Sequence 14, Application US/10155059  
 ; Patent No. US20020147173A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kaelin, William

; TITLE OF INVENTION: METHODS OF TREATMENT USING  
 ; NBS-1, ANTIBODIES AND PROTEINS THERETO, AND USES OF THE  
 ; ANTIBODIES

; NUMBER OF SEQUENCES: 27  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Nixon Peabody LLP  
 ; STREET: 101 Federal Street  
 ; CITY: Boston  
 ; STATE: MA  
 ; COUNTRY: USA  
 ; ZIP: 02110

; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: Windows  
 ; SOFTWARE: FastSeq for Windows Version 2.0b  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/10/155,059  
 ; FILING DATE: 24-May-2002  
 ; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/081,975  
 ; FILING DATE: 12-MAY-1998  
 ; APPLICATION NUMBER: 60/046,207  
 ; FILING DATE: 12-MAY-1997  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Eisenstein, Ronald I

; REGISTRATION NUMBER: 30,628  
 ; REFERENCE/DOCKET NUMBER: 47400  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 617-345-6054  
 ; TELEFAX: 617-345-1300  
 ; TELEX: <Unknown>

; INFORMATION FOR SEQ ID NO: 14:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 20 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 14:  
 US-10-155-059-14

Query Match 89.5%; Score 94; DB 12; Length 20;  
 Best Local Similarity 94.4%; Pred. No. 3.5e-08;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLPEN 18  
 Db 2 PPLSQETFSDLWKLLPEN 19

## RESULT 7

US-10-155-059-15  
 ; Sequence 15, Application US/10155059  
 ; Patent No. US20020147173A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kaelin, William





COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: Fast-Seq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/155,059  
FILING DATE: 24-May-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/081,975  
FILING DATE: 12-MAY-1998  
FILING DATE: 12-MAY-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Eisenstein, Ronald I  
REGISTRATION NUMBER: 30,628  
REFERENCE/DOCKET NUMBER: 47400  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-345-6054  
TELEFAX: 617-345-1300  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 13:  
US-10-155-059-13

Db 1 PLSQOTFSDWLKLLPEN 17  
RESULT 12  
US-10-155-059-19  
Sequence 19, Application US/10155059  
Patent No. US20020147173A1  
GENERAL INFORMATION:  
APPLICANT: Kaelin, William  
Jost, Christine  
TITLE OF INVENTION: METHODS OF TREATMENT USING  
NBS-1, ANTIBODIES AND PROTEINS THERETO, AND USES OF THE  
ANTIBODIES  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nixon Peabody LLP  
STREET: 101 Federal Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/155,059  
FILING DATE: 24-May-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/081,975  
FILING DATE: 12-MAY-1998  
FILING DATE: 12-MAY-1997  
FILING DATE: 12-MAY-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Eisenstein, Ronald I  
REGISTRATION NUMBER: 30,628  
REFERENCE/DOCKET NUMBER: 47400  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-345-6054  
TELEFAX: 617-345-1300  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 19:  
US-10-155-059-19

Query Match 81.9%; Score 86; DB 12; Length 20;  
Best Local Similarity 94.1%; Pred. No. 5.6e-07;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 2 PLSQOTFSDWLKLLPEN 18  
Db 3 PLSQOTFSDWLKLLPEN 19  
RESULT 13  
US-09-732-384-6  
Sequence 6, Application US/09732384  
Patent No. US20020132977A1  
GENERAL INFORMATION:  
APPLICANT: Yuan, Zhi-Min  
APPLICANT: Gu, JiJie  
TITLE OF INVENTION: Inhibition of p53 Degradation  
FILE REFERENCE: 21508-044  
CURRENT APPLICATION NUMBER: US/09/732,384  
CURRENT FILING DATE: 2000-12-07  
PRIOR APPLICATION NUMBER: 60/169,816

Query Match 85.7%; Score 90; DB 12; Length 19;  
Best Local Similarity 88.9%; Pred. No. 1.3e-07;  
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 PLSQOTFSDWLKLLPEN 18  
Db 1 PLSQOTFSELNLLPEN 18

RESULT 11  
US-09-214-371-1  
Sequence 1, Application US/09214371B  
Patent No. US20010018511A1  
GENERAL INFORMATION:  
APPLICANT: Lane, David  
APPLICANT: Bottger, Volker  
APPLICANT: Bottger, Angelica  
APPLICANT: Pickseley, Stephen  
APPLICANT: Chene, Patrick  
APPLICANT: Hochkeppel, Heinz-Kurt  
APPLICANT: Garcia-Echeverria, Carlos  
APPLICANT: Furet, Pascal  
TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2  
FILE REFERENCE: 4-20937/A/PCT  
CURRENT APPLICATION NUMBER: US/09/214,371B  
CURRENT FILING DATE: 1999-03-26  
PRIOR APPLICATION NUMBER: PCT/EP97/03549  
PRIOR FILING DATE: 1997-07-04  
NUMBER OF SEQ ID NOS: 83  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1  
LENGTH: 19  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:peptide  
US-09-214-371-1

Query Match 84.8%; Score 89; DB 10; Length 19;  
Best Local Similarity 94.1%; Pred. No. 1.9e-07;  
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 2 PLSQOTFSDWLKLLPEN 18  
Db 1 PLSQOTFSDWLKLLPEN 18

;; PRIOR FILING DATE: 1999-12-08  
;; NUMBER OF SEQ ID NOS: 10  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 6  
;; LENGTH: 15  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence:Protein  
;; OTHER INFORMATION: fragment not in inhibitory p53 polypeptide  
US-09-732-384-6

Query Match 73.3%; Score 77; DB 10; Length 15;  
Best Local Similarity 100.0%; Pred. No. 9.4e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QETFDLWKLLEN 18  
Db 1 QETFDLWKLLEN 14

## RESULT 14

US-10-155-059-23  
; Sequence 23, Application US/10155059  
; Patent No. US20020147173A1  
; GENERAL INFORMATION:  
; APPLICANT: Kaelin, William  
; Jost, Christine

;; TITLE OF INVENTION: METHODS OF TREATMENT USING  
;; NBS-1, ANTIBODIES AND PROTEINS THEREO, AND USES OF THE  
;; ANTIBODIES

;; NUMBER OF SEQUENCES: 27  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Nixon Peabody LLP  
;; STREET: 101 Federal Street  
;; CITY: Boston  
;; STATE: MA  
;; COUNTRY: USA  
;; ZIP: 02110

;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Diskette  
;; COMPUTER: IBM Compatible  
;; OPERATING SYSTEM: Windows

;; SOFTWARE: FastSeq for Windows Version 2.0b  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/10/155,059  
;; FILING DATE: 24-May-2002  
;; CLASSIFICATION: <Unknown>

;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/081,975  
;; FILING DATE: 12-MAY-1998  
;; APPLICATION NUMBER: 60/046,207  
;; FILING DATE: 12-MAY-1997

;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Eisenstein, Ronald I  
;; REGISTRATION NUMBER: 30,628  
;; REFERENCE/DOCKET NUMBER: 47400  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 617-345-6054  
;; TELEFAX: 617-345-1300  
;; TELEX: <Unknown>

;; INFORMATION FOR SEQ ID NO: 23:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 16 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear

;; SEQUENCE DESCRIPTION: SEQ ID NO: 23:  
US-10-155-059-23

Query Match 70.5%; Score 74; DB 12; Length 16;  
Best Local Similarity 81.2%; Pred. No. 2.8e-05;  
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PLSQETFDLWKLLE 17  
Db 1 PLSQETFDLWKLLE 16

## RESULT 15

US-10-155-059-20  
; Sequence 20, Application US/10155059  
; Patent No. US20020147173A1  
; GENERAL INFORMATION:  
; APPLICANT: Kaelin, William  
; Jost, Christine

;; TITLE OF INVENTION: METHODS OF TREATMENT USING  
;; NBS-1, ANTIBODIES AND PROTEINS THEREO, AND USES OF THE  
;; ANTIBODIES

;; NUMBER OF SEQUENCES: 27  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Nixon Peabody LLP  
;; STREET: 101 Federal Street  
;; CITY: Boston  
;; STATE: MA  
;; COUNTRY: USA  
;; ZIP: 02110

;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Diskette  
;; COMPUTER: IBM Compatible  
;; OPERATING SYSTEM: Windows

;; SOFTWARE: FastSeq for Windows Version 2.0b  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/10/155,059  
;; FILING DATE: 24-May-2002  
;; CLASSIFICATION: <Unknown>

;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/081,975  
;; FILING DATE: 12-MAY-1998  
;; APPLICATION NUMBER: 60/046,207  
;; FILING DATE: 12-MAY-1997

;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Eisenstein, Ronald I  
;; REGISTRATION NUMBER: 30,628  
;; REFERENCE/DOCKET NUMBER: 47400  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 617-345-6054  
;; TELEFAX: 617-345-1300  
;; TELEX: <Unknown>

;; INFORMATION FOR SEQ ID NO: 20:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 20 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear

;; SEQUENCE DESCRIPTION: SEQ ID NO: 20:  
US-10-155-059-20

Query Match 70.5%; Score 74; DB 12; Length 20;  
Best Local Similarity 93.3%; Pred. No. 3.6e-05;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PLSQETFDLWKLLE 16  
Db 3 PLSQETFDLWKLLE 17

Search completed: February 12, 2003, 11:25:07  
Job time : 12.6667 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 12, 2003, 11:10:52 ; Search time 47.5 Seconds  
(without alignments)  
53.300 Million cell updates/sec

Title: US-09-403-440A-2

Perfect score: 105

Sequence: 1 PFLSQTFSDLKLLPENG 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 320064

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_101002:\*

- 1: /SID22/gcgdata/geneseq/geneseq-embl/AA1980.DAT:\*
- 2: /SID22/gcgdata/geneseq/geneseq-embl/AA1981.DAT:\*
- 3: /SID22/gcgdata/geneseq/geneseq-embl/AA1982.DAT:\*
- 4: /SID22/gcgdata/geneseq/geneseq-embl/AA1983.DAT:\*
- 5: /SID22/gcgdata/geneseq/geneseq-embl/AA1984.DAT:\*
- 6: /SID22/gcgdata/geneseq/geneseq-embl/AA1985.DAT:\*
- 7: /SID22/gcgdata/geneseq/geneseq-embl/AA1986.DAT:\*
- 8: /SID22/gcgdata/geneseq/geneseq-embl/AA1987.DAT:\*
- 9: /SID22/gcgdata/geneseq/geneseq-embl/AA1988.DAT:\*
- 10: /SID22/gcgdata/geneseq/geneseq-embl/AA1989.DAT:\*
- 11: /SID22/gcgdata/geneseq/geneseq-embl/AA1990.DAT:\*
- 12: /SID22/gcgdata/geneseq/geneseq-embl/AA1991.DAT:\*
- 13: /SID22/gcgdata/geneseq/geneseq-embl/AA1992.DAT:\*
- 14: /SID22/gcgdata/geneseq/geneseq-embl/AA1993.DAT:\*
- 15: /SID22/gcgdata/geneseq/geneseq-embl/AA1994.DAT:\*
- 16: /SID22/gcgdata/geneseq/geneseq-embl/AA1995.DAT:\*
- 17: /SID22/gcgdata/geneseq/geneseq-embl/AA1996.DAT:\*
- 18: /SID22/gcgdata/geneseq/geneseq-embl/AA1997.DAT:\*
- 19: /SID22/gcgdata/geneseq/geneseq-embl/AA1998.DAT:\*
- 20: /SID22/gcgdata/geneseq/geneseq-embl/AA1999.DAT:\*
- 21: /SID22/gcgdata/geneseq/geneseq-embl/AA2000.DAT:\*
- 22: /SID22/gcgdata/geneseq/geneseq-embl/AA2001.DAT:\*
- 23: /SID22/gcgdata/geneseq/geneseq-embl/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	105	100.0	19	AAW82321	p53 homologue TIP
2	105	100.0	19	AAW82319	p53 homologue TIP
3	99	94.3	18	AAW37228	p53 N-terminal pep
4	99	94.3	25	AAW54907	Immunodominant epi
5	99	94.3	25	AAW54907	Human p53 amino ac
6	97	92.4	19	AAW47074	p53/RB interaction
7	93	88.6	22	AAW37227	p53 biotinylated N
8	81	77.1	15	AAW06310	Human p53 peptide
9	77	73.3	15	AAW54909	Immunodominant epi
10	77	73.3	15	AAW54910	Immunodominant epi

11	77	73.3	15	17	AAW89914	p53 protein bindin
12	77	73.3	15	21	AAW29157	Peptide #1. Unide
13	77	73.3	15	22	AAW89500	p53 DR3 3a motif bi
14	77	73.3	15	22	AAW89730	p53 DR3 binding pe
15	77	73.3	17	20	AAW45227	p53 peptide 9-25.
16	74	70.5	15	21	AAW29159	Peptide #3. Unide
17	74	70.5	15	21	AAW29163	Peptide #7. Unide
18	73	69.5	14	23	ABW05528	Biotinylated pepi
19	73	69.5	15	21	AAW29167	Peptide #11. Unid
20	71	67.6	15	21	AAW29160	Peptide #4. Unide
21	71	67.6	15	21	AAW29161	Peptide #5. Unide
22	71	67.6	15	21	AAW99001	HLA class II bindi
23	70	66.7	13	21	AAW57799	TRAM-interaction m
24	69	65.7	15	21	AAW29162	Peptide #6. Unide
25	69	65.7	15	21	AAW29164	Peptide #8. Unide
26	66.5	63.3	16	21	AAW29149	Ligand #1. Uniden
27	66.5	63.3	16	21	AAW29158	Peptide #2. Unide
28	66	62.9	12	19	AAW37181	Human p53 wild-typ
29	66	62.9	12	19	AAW37188	Human oncogenic pr
30	66	62.9	12	21	AAW17075	Mdm/hdm antagonist
31	66	62.9	12	21	AAW17087	Mdm/hdm antagonist
32	66	62.9	12	23	ABW73170	Mdm/hdm antagonist
33	66	62.9	12	23	ABW73182	Mdm/hdm antagonist
34	66	62.9	16	19	AAW37201	Human oncogenic pr
35	65	61.9	15	16	AAW83012	Promega protein ki
36	65	61.9	15	21	AAW95859	Tumour suppressor
37	65	61.9	15	23	ABW09246	Target activatable
38	62	59.0	15	22	AAW89447	p53-DR supermotif
39	61	58.1	11	23	AAW52269	Miniature protein
40	61	58.1	12	19	AAW37190	Human oncogenic pr
41	61	58.1	12	21	AAW17077	Mdm/hdm antagonist
42	61	58.1	12	21	AAW17089	Mdm/hdm antagonist
43	61	58.1	12	23	ABW73172	Mdm/hdm antagonist
44	61	58.1	12	23	ABW73184	Mdm/hdm antagonist
45	61	58.1	16	19	AAW37203	Human oncogenic pr

#### ALIGNMENTS

RESULT 1  
AAW82321  
ID AAW82321 standard; Peptide; 19 AA.  
AC AAW82321;  
XX  
XX  
DT 22-FEB-1999 (first entry)  
XX  
DE p53 homologue TIP peptide.  
XX  
KW p53; mdm2; inhibitor; therapy; activator; treatment; cancer; medicament.  
XX  
OS Synthetic.  
XX  
XX WO9847919-A1.  
XX  
XX 29-OCT-1998.  
XX  
PF 20-APR-1998; 98WO-GB01140.  
XX  
XX 22-APR-1997; 97GB-0008089.  
XX  
XX (UVDU-) UNIV DUNDEE.  
PA  
XX  
XX  
PI Lane DP;  
XX  
DR WPI; 1998-603975/51.  
XX  
PT New substance with a mdm2 binding domain and coupling partner  
PT useful for stabilising in cells without an efficient mdm2-mediated  
PT degradation pathway  
XX  
PS Disclosure; Fig 1; 52pp; English.

XX This sequence is a peptide homologue of a region of p53 which binds  
 CC to mdm2. This peptide is used in the construction of a novel agent  
 CC capable of disrupting the binding of p53 and mdm2 or inhibiting the  
 CC production of mdm2 in a population of cells. This agent is also used in  
 CC the preparation of a therapeutic for activating p53, where the population  
 CC of cells do not overexpress mdm2. Inhibiting mdm2 production and/or  
 CC inhibiting the binding of mdm2 to p53 allows levels of p53 to increase by  
 CC reducing the clearance of p53 by mdm2, and can be used to activate p53  
 CC function. The agents for use in therapeutics for activating p53 can be  
 CC used for the treatment of cancer, viral conditions or other conditions  
 CC associated with non-functional p53.

XX SQ Sequence 19 AA;

Query Match 100.0%; Score 105; DB 19; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 5.7e-10;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLPPENG 19  
 |||||  
 Db 1 PPLSQETFSDLWKLPPENG 19

## RESULT 2

AAW82319  
 ID AAW82319 standard; Peptide; 19 AA.

AC AAW82319;

DT 22-FEB-1999 (first entry)

DE p53 homologue TIP peptide.

XX p53; mdm2; inhibitor; therapy; activator; treatment; cancer; medicament.

XX Synthetic.

XX WO9847525-A1.

XX 29-OCT-1998.

XX 20-APR-1998; 98WO-GB01144.

XX 22-APR-1997; 97GB-0008092.

XX (UYDU-) UNIV DUNDEE.

XX Lane DP;

XX WPI; 1998-609932/51.

XX New agents which inhibit interaction of p53 and mdm2 - useful for  
 PT activating p53, e.g. for treating cancers, viral conditions or other  
 PT conditions associated with non functional p53 or mdm2

XX Disclosure; Fig 1; 52pp; English.

XX This sequence is a peptide homologue of a region of p53 which binds  
 CC to mdm2. This peptide is used in the construction of a novel agent  
 CC capable of disrupting the binding of p53 and mdm2 or inhibiting the  
 CC production of mdm2 in a population of cells. This agent is also used in  
 CC the preparation of a therapeutic for activating p53, where the population  
 CC of cells do not overexpress mdm2. Inhibiting mdm2 production and/or  
 CC inhibiting the binding of mdm2 to p53 allows levels of p53 to increase by  
 CC reducing the clearance of p53 by mdm2, and can be used to activate p53  
 CC function. The agents for use in therapeutics for activating p53 can be  
 CC used for the treatment of cancer, viral conditions or other conditions  
 CC associated with non-functional p53.

XX SQ Sequence 19 AA;

Query Match 100.0%; Score 105; DB 19; Length 19;

Best Local Similarity 100.0%; Pred. No. 5.7e-10;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLPPENG 19  
 |||||  
 Db 1 PPLSQETFSDLWKLPPENG 19

## RESULT 3

AAW37228

ID AAW37228 standard; peptide; 18 AA.

XX AAW37228;

XX 20-JUL-1998 (first entry)

XX p53 N-terminal peptide fragment for Elisa TIP assay.

XX MDM2; oncogenic protein; p53; human; inhibition; interaction; cancer;  
 KW tumor; diagnosis; binding; viral infection; Elisa TIP assay.

XX Homo sapiens.

XX WO9801467-A2.

XX 15-JAN-1998.

XX 04-JUL-1997; 97WO-EP03549.

XX 07-APR-1997; 97GB-0007041.

XX 05-JUL-1996; 96GB-0014197.

XX (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.

XX (NOVS) NOVARTIS AG.

XX Boettger A, Boettger V, Chene P, Furet P, Garcia-echeverria C;

XX Hochkeppel H, Lane D, Pickesley S;

XX WPI; 1998-100996/09.

XX Compounds binding to MDM2 protein and inhibit its interaction with  
 PT p53 - useful in, e.g. diagnosis and treatment of cancer and viral  
 PT infections and identifying binding agents

XX Disclosure; Page 34; 45pp; English.

XX This represents a p53 N-terminal peptide fragment used in an Elisa TIP  
 CC assay for analysing the interaction between human oncogenic protein MDM2  
 CC and p53. The invention provides peptide derivatives capable of binding to  
 CC the human MDM2. These peptides can specifically inhibit or block the  
 CC binding of MDM2 to the human p53 protein, in vitro or in vivo. Inhibiting  
 CC the interaction between the p53 and MDM2 can induce growth arrest or  
 CC apoptosis in tumour cells comprising a wild-type p53 and non-elevated  
 CC levels of MDM2. The peptides may be used to identify molecules that bind  
 CC to MDM2 and to identify and design inhibitors of MDM2/p53 binding. They  
 CC may also be used to purify binding partners especially MDM2, diagnose  
 CC disease by measuring levels of MDM2 in blood of cancer and leukaemia  
 CC patients and for treatment or prevention of disease involving p53/MDM2  
 CC interactions, especially tumours and viral infections. The peptides can  
 CC be administered nasally, rectally, orally or by injection. By interfering  
 CC with MDM2/p53 interaction, the peptides can activate p53 function and  
 CC accumulation in normal cells. The peptides which mimic the MDM2 binding  
 CC site in p53, have a significantly greater blocking activity compared  
 CC with wild-type p53.

XX SQ Sequence 18 AA;

Query Match 94.3%; Score 99; DB 19; Length 18;

Best Local Similarity 100.0%; Pred. No. 4.9e-09;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLPPEN 18  
 |||||

Db 1 PPLSQETFSDLWKLLPEN 18

# RESULT 4

AAR54907

ID AAR54907 standard; peptide; 25 AA.

XX AC AAR54907;

XX DT 29-NOV-1994 (first entry)

XX DE Immunodominant epitope from p53 N-terminal.

XX KW cancer; pre-cancerous state; detection; diagnosis; human p53 gene;

XX KW immunodominant epitope; human cellular tumour antigen;

XX KW transformation-associated protein.

XX OS Homo sapiens.

XX PN WO9410306-A.

XX PD 11-MAY-1994.

XX PF 02-NOV-1993; 93WO-FR01082.

XX PR 02-NOV-1992; 92FR-0013110.

XX PA (EURO-) LAB EURO BIO SA.

XX PI Legros Y, Lubin R, Soussi T;

XX DR WPI; 1994-167463/20.

XX PT New immuno-dominant epitope(s) of protein p53 - for detecting and

XX PT monitoring antibodies indicative of cancer and precancerous

XX PT states

XX PS Claim 4; Page 42; 62pp; French.

XX CC Peptides derived from the N-terminal (amino acids 1-112) or the C-

XX CC terminal (amino acids 350-393) of protein p53 which specifically

XX CC react with anti-p53 antibodies in patients with cancer or

XX CC precancerous conditions are claimed. The peptides (AAR54907-R54921)

XX CC are useful for detecting and monitoring cancerous and precancerous

XX CC conditions.

XX SQ Sequence 25 AA;

Query Match 94.3%; Score 99; DB 15; Length 25;

Best Local Similarity 100.0%; Pred. No. 7.1e-09;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLPEN 18

Db 2 PPLSQETFSDLWKLLPEN 19

# RESULT 5

AAR51879

ID AAR51879 standard; Protein; 25 AA.

XX AC AAR51879;

XX DT 18-NOV-1994 (first entry)

XX DE Human p53 amino acids 9-33.

XX KW Human nuclear phosphoprotein p53; tumour suppressor gene product;

XX KW anti-oncogene; cancer; tumour; antibody binding region; epitope.

XX OS Homo sapiens.

XX PN WO9408241-A.

Query Match 94.3%; Score 99; DB 15; Length 25;

Best Local Similarity 100.0%; Pred. No. 7.1e-09;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLPEN 18

Db 2 PPLSQETFSDLWKLLPEN 19

# RESULT 6

AAW47074

ID AAW47074 standard; peptide; 19 AA.

XX AC AAW47074;

XX DT 19-MAY-1998 (first entry)

XX DE p53/RB interaction inhibiting peptide 6 (residues 11-29 of human p53).

XX KW Retinoblastoma gene; RB; p53 protein; interaction; inhibitor;

XX KW tumour; apoptosis; modulator; medicine; veterinary; human.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN WO9741433-A1.

XX PD 06-NOV-1997.

XX PF 29-APR-1997; 97WO-GB01168.

XX PR 29-APR-1996; 96GB-0008937.

XX PA (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.

XX PI Kouzarides T;

XX DR WPI; 1997-549887/50.

XX PT Identifying compounds that modulate interaction of p53 and Rb

XX PT protein - or those that bind to Rb protein, used to induce

XX PT apoptosis, specifically for treatment of tumours

XX PS Claim 36; Page 63; 83pp; English.

XX

PD 14-APR-1994.

XX PF 30-SEP-1993; 93WO-EP02666.

XX PR 30-SEP-1992; 92DE-4232823.

XX PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM STIFTUNG.

XX PI Klein R, Schranz P, Tessmer C, Volkmann M, Zentgraf H;

XX DR WPI; 1994-135732/16.

XX DR N-PSDB; AAQ62365.

XX PT Non-radioactive detection of p53 specific antibodies - by capture

XX PT on immobilised p53 or its fragments, then reaction with labelled

XX PT second antibody, for diagnosis of tumours and suitable for

XX PT screening

XX PS Claim 11; Page 19; 35pp; German.

XX CC Antibodies specific for p53 are detected by binding to immobilised

XX CC fragments of the p53 gene product containing the antibody-binding

XX CC region. Preferred fragments contain amino acids 1-241, 40-349,

XX CC 40-393, 66-241, 66-393, 237-349, 237-393 and esp. 9-33, 37-52 or

XX CC 368-386. See AAR51872-R51881 for sequences of these fragments.

XX SQ Sequence 25 AA;

Query Match 94.3%; Score 99; DB 15; Length 25;

Best Local Similarity 100.0%; Pred. No. 7.1e-09;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLPEN 18

Db 4 PPLSQETFSDLWKLLPEN 21

XX This peptide fragment of p53 is an inhibitor of the interaction between  
 CC a p53 protein and a retinoblastoma (RB) protein. This peptide  
 CC corresponds to residues 11-29 of human p53 (AAW47079). The interaction  
 CC between p53 and Rb is found to be critical for determining whether or not  
 CC a cell enters apoptosis. Apoptosis is prevented if interaction occurs.  
 CC The interaction is between regions 1-71 or 290-393 of p53 and region  
 CC 379-928 of Rb. The invention provides methods to identify compounds able  
 CC to modulate interaction or binding between p53 and Rb protein. The method  
 CC comprises combining p53 and Rb, or their fragments, with a test compound  
 CC and detecting interaction/binding between them. These inhibitory  
 CC compounds are used in human or veterinary medicine to modulate p53  
 CC activity and processes, specifically for inducing apoptosis in tumour  
 CC cells (possibly also in cells infected by virus), in vivo or in vitro.  
 CC Expression of these modulators by gene therapy methods is also  
 CC contemplated. Other activities that can be affected are transcription  
 CC repression, G1 arrest, DNA repair, homologous recombination and  
 CC 3'-5'-exonuclease activity. Modulation of interaction with Rb may also  
 CC stabilise p53.

XX SQ Sequence 19 AA;

Query Match 92.4%; Score 97; DB 18; Length 19;  
 Best Local Similarity 94.4%; Pred. No. 1.1e-08;  
 Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLEN 18  
 |||||  
 Db 2 PPLSQETFSDLWKLLEN 19

RESULT 7  
 AAW37227  
 ID AAW37227 standard; peptide; 22 AA.

XX AC AAW37227;

XX DT 20-JUL-1998 (first entry)

XX DE p53 biotinylated N-terminal peptide fragment for Elisa P2 assay.

XX KW MDM2; oncogenic protein; p53; human; inhibition; interaction; cancer;  
 KW tumour; diagnosis; binding; viral infection; Elisa P2 assay.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers  
 FT Modified-site 1 /note= "biotinylated"

XX PN WO9801467-A2.

XX PD 15-JAN-1998.

XX PF 04-JUL-1997; 97WO-EP03549.

XX PR 07-APR-1997; 97GB-0007041.

XX PR 05-JUL-1996; 96GB-0014197.

XX PA (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.

XX PA (NOVS) NOVARTIS AG.

XX PI Boettger A, Boettger V, Chene P, Furet P, Garcia-echeverria C;  
 PI Hochkeppel H, Lane D, Picklesley S;

XX DR WPI; 1998-100996/09.

XX FT Compounds binding to MDM2 protein and inhibit its interaction with  
 FT p53 - useful in, e.g. diagnosis and treatment of cancer and viral  
 FT infections and identifying binding agents

XX PS Disclosure; Page 34; 45pp; English.

CC This p53 biotinylated N-terminal peptide fragment is used in an Elisa P2  
 CC assay for analysing the interaction between human oncogenic protein MDM2  
 CC and p53. The invention provides peptide derivatives capable of binding to  
 CC the human MDM2. These peptides can specifically inhibit or block the  
 CC binding of MDM2 to the human p53 protein, in vitro or in vivo. Inhibiting  
 CC the interaction between the p53 and MDM2 can induce growth arrest or  
 CC apoptosis in tumour cells comprising a wild-type p53 and non-elevated  
 CC levels of MDM2. The peptides may be used to identify molecules that bind  
 CC to MDM2 and to identify and design inhibitors of MDM2/p53 binding. They  
 CC may also be used to purify binding partners especially MDM2, diagnose  
 CC disease by measuring levels of MDM2 in blood of cancer and leukaemia  
 CC patients and for treatment or prevention of disease involving p53/MDM2  
 CC interactions, especially tumours and viral infections. The peptides can  
 CC be administered nasally, rectally, orally or by injection. By interfering  
 CC with MDM2/p53 interaction, the peptides can activate p53 function and  
 CC accumulation in normal cells. The peptides which mimic the MDM2 binding  
 CC site in p53, have a significantly greater blocking activity compared  
 CC with wild-type p53.

XX SQ Sequence 22 AA;

Query Match 88.6%; Score 93; DB 19; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 5.7e-08;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLE 17  
 |||||  
 Db 6 PPLSQETFSDLWKLLE 22

RESULT 8  
 AAY06310  
 ID AAY06310 standard; Peptide; 15 AA.

XX AC AAY06310;

XX DT 06-SEP-1999 (first entry)

XX DE Human p53 peptide (aa13-27).

XX KW RB18A; p53 regulatory protein; apoptosis; neoplasia; inflammation;  
 KW wound healing; graft rejection; reperfusion injury;  
 KW myocardial infarction; stroke; traumatic brain injury;  
 KW neurodegenerative disease; ischaemia; toxemia; infection; AIDS;  
 KW hepatitis; breast cancer; ovarian cancer; colon cancer; diagnosis;  
 KW therapy; human.

XX OS Homo sapiens.

XX PN WO9931231-A1.

XX PD 24-JUN-1999.

XX PF 14-DEC-1998; 98WO-EP08560.

XX PR 15-DEC-1997; 97EP-0403051.

XX PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.

XX PI Frade R;

XX DR WPI; 1999-395177/33.

XX PT New p53 regulatory protein (RB18A) useful as, e.g. sources of probes  
 PT and primers to detect the transcription rate and abundance of RB18A  
 PT mRNA in lymphocytes

XX PS Example 1; Page 25; 87pp; English.

XX CC This synthetic peptide corresponds to amino acids 13-27 of human  
 CC p53. It was used to raise anti-peptide p53.1 and anti-RB18A  
 CC antibodies in rabbit. RB18A (see AAY06310) is a novel p53  
 CC regulatory protein of the invention. The antibodies were used in

CC immunoscreenings that led to the isolation of a cDNA clone (see  
 CC AAX59124) encoding human RB18A. The invention provides methods and  
 CC compositions for the diagnostic and therapeutic applications of  
 CC RB18A, in particular for the diagnosis, prevention or treatment of  
 CC neoplasia.

XX SQ Sequence 15 AA;

Query Match 77.1%; Score 81; DB 20; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLSQETFSDLWKLLP 16  
 | | | | | | | | | | | | | | |  
 Db 1 PLSQETFSDLWKLLP 15

## RESULT 9

AAR54909  
 ID AAR54909 standard; peptide; 15 AA.

XX AC AAR54909;

XX DT 29-NOV-1994 (first entry)

XX DE Immunodominant epitope from p53 N-terminal.

XX KW cancer; pre-cancerous state; detection; diagnosis; human p53 gene;  
 XX KW immunodominant epitope; human cellular tumour antigen;  
 XX KW transformation-associated protein.

XX OS Homo sapiens.

XX PN WO9410306-A.

XX PD 11-MAY-1994.

XX PF 02-NOV-1993; 93WO-FR01082.

XX PR 02-NOV-1992; 92FR-0013110.

XX PA (EURO-) LAB EURO BIO SA.

XX PI Legros Y, Lubin R, Soussi T;

XX WPI; 1994-167463/20.

XX DR New immuno:dominant epitope(s) of protein p53 - for detecting and  
 XX PT monitoring antibodies indicative of cancer and precancerous  
 XX PT states

XX PS Claim 5; Page 42; 62pp; French.

XX CC Peptides derived from the N-terminal (amino acids 1-112) or the C-  
 CC terminal (amino acids 350-393) of protein p53 which specifically  
 CC react with anti-p53 antibodies in patients with cancer or  
 CC precancerous conditions are claimed. The peptides (AAR54907-R54921)  
 CC are useful for detecting and monitoring cancerous and precancerous  
 CC conditions.

XX SQ Sequence 15 AA;

Query Match 73.3%; Score 77; DB 15; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKL 14  
 | | | | | | | | | | | | | | |  
 Db 2 PPLSQETFSDLWKL 15

## RESULT 10

AAR54910

ID AAR54910 standard; peptide; 15 AA.

XX AC AAR54910;

XX DT 29-NOV-1994 (first entry)

XX DE Immunodominant epitope from p53 N-terminal.

XX KW cancer; pre-cancerous state; detection; diagnosis; human p53 gene;  
 XX KW immunodominant epitope; human cellular tumour antigen;  
 XX KW transformation-associated protein.

XX OS Homo sapiens.

XX PN WO9410306-A.

XX PD 11-MAY-1994.

XX PF 02-NOV-1993; 93WO-FR01082.

XX PR 02-NOV-1992; 92FR-0013110.

XX PA (EURO-) LAB EURO BIO SA.

XX PI Legros Y, Lubin R, Soussi T;

XX WPI; 1994-167463/20.

XX PT New immuno:dominant epitope(s) of protein p53 - for detecting and  
 XX PT monitoring antibodies indicative of cancer and precancerous  
 XX PT states

XX PS Claim 5; Page 42; 62pp; French.

XX CC Peptides derived from the N-terminal (amino acids 1-112) or the C-  
 CC terminal (amino acids 350-393) of protein p53 which specifically  
 CC react with anti-p53 antibodies in patients with cancer or  
 CC precancerous conditions are claimed. The peptides (AAR54907-R54921)  
 CC are useful for detecting and monitoring cancerous and precancerous  
 CC conditions.

XX SQ Sequence 15 AA;

Query Match 73.3%; Score 77; DB 15; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QETFSDLWKLLPEN 18  
 | | | | | | | | | | | | | | | | | |  
 Db 1 QETFSDLWKLLPEN 14

## RESULT 11

AAR89914

ID AAR89914 standard; peptide; 15 AA.

XX AC AAR89914;

XX DT 10-SEP-1996 (first entry)

XX DE p53 protein binding motif corresp. to residues 16-30.

XX KW Interference; binding; p53; tumour suppressor; MDM2; oncogene; cancer;  
 XX KW inhibition; diagnosis; treatment; malignancy; consensus.

XX OS Synthetic.

XX PN WO9602642-A1.

XX PD 01-FEB-1996.

XX PF 20-JUL-1995; 95WO-GB01719.

PR 19-APR-1995; 95US-0424957.  
 XX 20-JUL-1994; 94US-0277660.  
 PA (UYDU-) UNIV DUNDEE.  
 PI Lane DP, Picklesley SM;  
 XX WPI; 1996-105905/11.  
 DR New cpds. which interfere with binding of MDM2 and p53 - used to  
 PT develop prods. for use in the diagnosis and treatment of cancer and  
 PT other malignancies  
 XX  
 PS Disclosure; Page 1; 46pp; English.  
 XX  
 CC New peptides of the invention which interfere with the binding of the  
 CC p53 tumour suppressor protein and the MDM2 oncogene protein contain  
 CC the peptide sequences AAR89911-3 which form part of the p53 protein  
 CC binding motif between amino acids 16-33 (AAR89914). The peptides were  
 CC identified by modifying the p53 consensus binding sequence by  
 CC substitution of an Alanine at each pos. and identifying which amino  
 CC acid changes altered binding to expressed MDM2. The peptides and  
 CC methods of identifying similar inhibitory peptides can be used to  
 CC diagnose and treat e.g. cancer and other malignancies.  
 XX  
 SQ Sequence 15 AA;  
 XX  
 Query Match 73.3%; Score 77; DB 17; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 QETFSDLWKLPEN 18  
 DB 1 QETFSDLWKLPEN 14  
 |||||  
 RESULT 12  
 AAB29157  
 ID AAB29157 standard; Peptide; 15 AA.  
 AC AAB29157;  
 XX  
 DT 02-FEB-2001 (first entry)  
 DE Peptide #1.  
 XX  
 KW Fork head associated; FHA; domain; transcriptional control;  
 KW DNA replication; DNA repair; cell cycle control.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200057184-A2.  
 PD 28-SEP-2000.  
 XX  
 PF 17-MAR-2000; 2000WO-GB01024.  
 XX  
 PR 19-MAR-1999; 99GB-0006432.  
 PR 28-JUN-1999; 99GB-0015075.  
 XX  
 PA (KUDO-) KUDOS PHARM LTD.  
 XX  
 PI Jackson SP, Durocher D;  
 XX WPI; 2000-664872/64.  
 DR  
 XX Assays and screening methods based on direct interaction between FHA  
 PT domains and phosphopeptides, useful for characterizing binding and to  
 PT identify binding partners and modulators of FHA domain-phosphopeptide  
 PT binding -  
 XX  
 PS Disclosure; Fig 2; 92pp; English.  
 XX

CC The present invention relates to assays and screening methods based on  
 CC a direct interaction between fork head associated (FHA) domains and  
 CC phosphorylated polypeptides, for characterizing the binding of these  
 CC molecules. FHA peptides may be useful for treating medical conditions  
 CC associated with defects in transcriptional control, DNA replication,  
 CC DNA repair, cell cycle control or other cellular process. The method  
 CC may provide valuable insights into checkpoint signalling, has important  
 CC implications for the functions of other FHA domain-containing  
 CC proteins and provides basis for new lines of therapy. The present  
 CC sequence is a peptide used in the present invention.  
 XX  
 SQ Sequence 15 AA;  
 XX  
 Query Match 73.3%; Score 77; DB 21; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 PPLSQETFSDLWLK 14  
 DB 2 PPLSQETFSDLWLK 15  
 |||||  
 RESULT 13  
 AAG89500  
 ID AAG89500 standard; Peptide; 15 AA.  
 AC AAG89500;  
 XX  
 DT 11-SEP-2001 (first entry)  
 DE p53 DR 3a motif binding peptide exemplary sequence #3.  
 XX  
 KW Human; p53; tumour suppressor; human leukocyte antigen; HLA; CTL;  
 KW cytotoxic T lymphocyte; T cell; immune response; tumour; cancer;  
 KW vaccine; epitope; cytostatic.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200141788-A1.  
 XX  
 PD 14-JUN-2001.  
 XX  
 PF 11-DEC-2000; 2000WO-US33629.  
 XX  
 PR 10-DEC-1999; 99US-0458297.  
 XX  
 PA (EPIM-) EPIMUNE INC.  
 XX  
 PI Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;  
 PI Keogh E;  
 XX  
 DR WPI; 2001-381493/40.  
 XX  
 PT Epitope-based vaccines comprising p53 epitope having a specified  
 PT sequences, useful for treating and preventing cancer, the epitopic  
 PT peptides is useful as diagnostic agents and for evaluating immune  
 PT response -  
 XX  
 PS Disclosure; Page 113; 138pp; English.  
 XX  
 CC The present invention describes isolated prepared p53 epitopes (I). Also  
 CC described are: (1) a cytotoxic T lymphocyte (CTL) that is cultured  
 CC in vivo and binds to a complex of (I); (2) a peptide (II) comprising (I)  
 CC and a second epitope and has less than 50 contiguous amino acids; (3) a  
 CC vaccine composition comprising (II), a unit dose of a peptide with less  
 CC than 50 contiguous amino acids with 100% identity to the native peptide  
 CC sequence of p53, and a pharmaceutical excipient; (4) an isolated nucleic  
 CC acid encoding (I); and (5) an isolated nucleic acid encoding (II). (I)  
 CC has cytostatic activity and can be used in vaccines. The vaccine  
 CC composition is useful for treating or preventing cancer. (I) and (II)  
 CC are useful as diagnostic agents and for evaluating immune responses.  
 CC Unlike conventional epitopes, immunosuppressive epitopes that may be



CC present in whole antigens can be avoided with the use of the vaccine  
CC composition of (I). The ability to combine selected epitopes and  
CC further, to modify the composition of the epitopes enhances the  
CC immunogenicity. The possible pathological side effects caused by  
CC infectious agents or whole protein antigens, which might have their own  
CC intrinsic biological activity, are eliminated. AAG89363 to AAG89747  
CC represent amino acid sequences used in the exemplification of the  
CC present invention.  
XX  
SQ Sequence 15 AA;  
Query Match 73.3%; Score 77; DB 22; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 PPLSQETFSDLWKL 14  
DB 2 PPLSQETFSDLWKL 15  
RESULT 14  
AAG89730  
ID AAG89730 standard; Peptide; 15 AA.  
XX  
AC AAG89730;  
DT 11-SEP-2001 (first entry)  
XX  
DE p53 DR3 binding peptide #1.  
XX  
KW Human; p53; tumour suppressor; human leukocyte antigen; HLA; CTL;  
KW cytotoxic T lymphocyte; T cell; immune response; tumour; cancer;  
KW vaccine; epitope; cytostatic.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200141788-A1.  
PD 14-JUN-2001.  
XX  
PF 11-DEC-2000; 2000WO-US33629.  
XX  
PR 10-DEC-1999; 99US-0458297.  
XX  
PA (EPIM-) EPIMUNE INC.  
XX  
PI Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;  
PI Keogh E;  
XX  
DR WPI; 2001-381493/40.  
XX  
PT Epitope-based vaccines comprising p53 epitope having a specified  
PT sequences, useful for treating and preventing cancer, the epitopic  
PT peptides is useful as diagnostic agents and for evaluating immune  
PT response -  
XX  
PS Example 5; Page 131; 138pp; English.  
XX  
CC The present invention describes isolated prepared p53 epitopes (I). Also  
CC described are: (1) a cytotoxic T lymphocyte (CTL) that is cultured  
CC in vivo and binds to a complex of (I); (2) a peptide (II) comprising (I)  
CC and a second epitope and has less than 50 contiguous amino acids; (3) a  
CC vaccine composition comprising (II), a unit dose of a peptide with less  
CC than 50 contiguous amino acids with 100% identity to the native peptide  
CC sequence of p53, and a pharmaceutical excipient; (4) an isolated nucleic  
CC acid encoding (I); and (5) an isolated nucleic acid encoding (II). (I)  
CC has cytostatic activity and can be used in vaccines. The vaccine  
CC composition is useful for treating or preventing cancer. (I) and (II)  
CC are useful as diagnostic agents and for evaluating immune responses.  
CC Unlike conventional epitopes, immunosuppressive epitopes that may be  
CC present in whole antigens can be avoided with the use of the vaccine  
CC composition of (I). The ability to combine selected epitopes and

CC further, to modify the composition of the epitopes enhances the  
CC immunogenicity. The possible pathological side effects caused by  
CC infectious agents or whole protein antigens, which might have their own  
CC intrinsic biological activity, are eliminated. AAG89363 to AAG89747  
CC represent amino acid sequences used in the exemplification of the  
CC present invention.  
XX  
SQ Sequence 15 AA;  
Query Match 73.3%; Score 77; DB 22; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 PPLSQETFSDLWKL 14  
DB 2 PPLSQETFSDLWKL 15  
RESULT 15  
AAY45227  
ID AAY45227 standard; peptide; 17 AA.  
XX  
AC AAY45227;  
DT 06-JAN-2000 (first entry)  
XX  
DE p53 peptide 9-25.  
XX  
KW Immunisation; immunogenicity enhancer; rabies virus strain ERA;  
KW immunodominant T-helper cell determinant; nucleoprotein; antibody;  
KW post-translational modification; p53; cancer; diagnosis.  
XX  
OS Synthetic.  
XX  
PN WO9946574-A2.  
XX  
PD 16-SEP-1999.  
XX  
PF 11-MAR-1999; 99WO-US04653.  
XX  
PR 11-MAR-1998; 98US-0077512.  
XX  
PA (WIST-) WISTAR INST.  
XX  
PI Otvos L, Ertl H, Thurin M, Hoffman R;  
XX  
DR WPI; 1999-561693/47.  
XX  
PT Methods of detecting post-translational modification level of p53,  
PT useful for diagnosis of cancer -  
XX  
PS Disclosure; Page 45; 59pp; English.  
XX  
CC The present invention describes a polypeptide comprising a portion of a  
CC p53 comprising a post-translationally modified amino acid residue where  
CC the modification is a phosphorylation, glycosylation or prenylation, and  
CC an immunogenicity enhancer. The polypeptide is used to detect anti-p53  
CC autoantibodies in a human patient. The antibody can be used to determine  
CC the post-translational modification state of a p53 protein. These are  
CC used especially in the diagnosis of cancer. The present sequence  
CC represents a p53 peptide used in the exemplification of the present  
CC invention.  
XX  
SQ Sequence 17 AA;  
Query Match 73.3%; Score 77; DB 20; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.6e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 PPLSQETFSDLWKL 14  
DB 4 PPLSQETFSDLWKL 17

Search completed: February 12, 2003, 11:13:44  
Job time : 47.5 secs

---

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 12, 2003, 11:12:02 ; Search time 37.2083 Seconds  
(without alignments)  
105.216 Million cell updates/sec

Title: us-09-403-440a-2

Perfect score: 105

Sequence: 1 PPLSQETFSDLWLKLPENG 19

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 9297

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL.21.\*  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phage.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_vertibrate.\*  
14: sp\_unclassified.\*  
15: sp\_virus.\*  
16: sp\_bacteriaph.\*  
17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	77	73.3	25	4 Q9NP68	Q9np68 homo sapien
2	45	42.9	22	13 Q9W6D7	Q9w6d7 gallus gall
3	43	41.4	24	13 Q90Z19	Q90z19 gallus gall
4	33	31.4	24	15 Q85618	Q85618 avian leuko
5	32	30.5	19	5 P83003	P83003 entamoeba h
6	32	30.5	25	2 Q9S0U6	Q9s0u6 shigella so
7	31	29.5	16	6 Q9BG88	Q9bg88 sorex arane
8	31	29.5	24	5 Q94377	Q94377 caenorhabdi
9	30	28.6	14	6 Q77538	Q77538 bos taurus
10	30	28.6	23	4 Q9HCW9	Q9hcw9 homo sapien
11	30	28.6	24	5 Q94368	Q94368 caenorhabdi
12	29	27.6	17	8 Q9XNQ1	Q9xng1 boophilus m
13	29	27.6	24	5 Q95V74	Q95v74 mytilus gal
14	28.5	27.1	24	3 P87182	P87182 trichoderma
15	28	26.7	20	10 Q9LQK5	Q9lqk5 citrus sine
16	28	26.7	20	12 Q912B4	Q912b4 human eryth

## ALIGNMENTS

### RESULT 1

Q9NP68 PRELIMINARY; PRT; 25 AA.  
AC Q9NP68;  
DT 01-OCT-2000 (T-EMBLrel. 15, Created)  
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)  
DT 01-JUN-2001 (T-EMBLrel. 17, Last annotation update)  
DE Tumor suppressor p53 (Fragment).  
GN TP53.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Thompson-Hehir J., Davies M.P.A., Green J.A., Halliwell N.,  
RA Joyce K.A., Salisbury J., Sibson D.R., Vergote I., Walker C.;  
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF209136; AAF36362.1; -  
DR EMBL; AF209128; AAF36354.1; -  
DR EMBL; AF209129; AAF36355.1; -  
DR EMBL; AF209130; AAF36356.1; -  
DR EMBL; AF209131; AAF36357.1; -  
DR EMBL; AF209132; AAF36358.1; -  
DR EMBL; AF209133; AAF36359.1; -  
DR EMBL; AF209134; AAF36360.1; -  
DR EMBL; AF209135; AAF36361.1; -  
DR InterPro; IPR002117; P53.  
DR Pfam; PF00870; P53; 1  
FT NON TER 25  
SQ SEQUENCE 25 AA; 2890 MW; D7FA272EBFAB9798 CRC64;

Query Match 73.3%; Score 77; DB 4; Length 25;

Best Local Similarity 100.0%; Pred. No. 1.8e-05;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWLK 14

Db 12 PPLSQETFSDLWLK 25

```

RESULT 2
Q9W6D7 PRELIMINARY; PRT; 22 AA.
ID AC Q9W6D7;
AC Q9W6D7;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hydroxyindole-o-methyltransferase isoform A (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9067015; PubMed=9851690;
RA Grechez-Cassiau A., Bernard M., Ladjali K., Rodriguez I.R., Voisin P.;
RT "Structural analysis of the chicken hydroxyindole-O-methyltransferase
gene."
RL Eur. J. Biochem. 258:44-52(1998).
DR EMBL; AF116455; AAD23444.1; -.
DR MethyItransferase; Transferase.
KW NON_TER 1
FT NON_TER 1
SQ SEQUENCE 22 AA; 2783 MW; 35726EABF1E450C8 CRC64;

Query Match 42.9%; Score 45; DB 13; Length 22;
Best Local Similarity 58.3%; Pred. No. 2.5;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 4 QSTFSDWLKLL 15
Db 8 SQHGFADLWELM 19

RESULT 3
Q90ZJ9 PRELIMINARY; PRT; 24 AA.
ID AC Q90ZJ9;
AC Q90ZJ9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE C-myc oncogene, aa 44-62 from c-myc/LL3 (ADV provirus)
DE (Fragment)
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84144799; PubMed=6322173;
RA Westaway D., Payne G., Varmus H.E.;
RT "Proviral deletions and oncogene base-substitutions in insertionally
mutagenized c-myc alleles may contribute to the progression of avian
bursal tumors."
RL Proc. Natl. Acad. Sci. U.S.A. 81:843-847(1984).
DR EMBL; K01440; AAA48964.1; -.
DR InterPro; IPR002418; TF_Myc.
DR Pfam; PF01056; Myc_N_term; 1.
FT NON_TER 1
FT NON_TER 24
SQ SEQUENCE 24 AA; 2679 MW; 93F59F2D3B24E527 CRC64;

Query Match 31.4%; Score 33; DB 13; Length 24;
Best Local Similarity 47.4%; Pred. No. 2.4e+02;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 2;

Qy 4 QSTFSDWLKLL 15
Db 8 SQHGFADLWELM 19

RESULT 4
Q85618 PRELIMINARY; PRT; 24 AA.
ID AC Q85618;
AC Q85618;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE RAV-2 proviral DNA, c-myc (Aa 44-67), allele LL3 (Fragment).
OS Avian leukosis virus.
OC Viruses; Retrovirdae; Retroviridae; Alpharetrovirus.
NCBI_TaxID=11864;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84144799; PubMed=6322173;
RA Westaway D., Payne G., Varmus H.E.;
RT "Proviral deletions and oncogene base-substitutions in insertionally
mutagenized c-myc alleles may contribute to the progression of avian
bursal tumors."
RL Proc. Natl. Acad. Sci. U.S.A. 81:843-847(1984).
DR EMBL; K01439; AAA51600.1; -.
DR InterPro; IPR002418; TF_Myc.
DR Pfam; PF01056; Myc_N_term; 1.
FT NON_TER 1
FT NON_TER 24
SQ SEQUENCE 24 AA; 2679 MW; 93F59F2D3B24E527 CRC64;

Query Match 31.4%; Score 33; DB 15; Length 24;
Best Local Similarity 47.4%; Pred. No. 2.4e+02;
Matches 9; Conservative 1; Mismatches 3; Indels 6; Gaps 2;

Qy 1 PPLSOETFSDLWK---LLP 16
Db 2 PPAPSE---DIWKKFELLP 17

RESULT 5
P83003 PRELIMINARY; PRT; 19 AA.
ID AC P83003;
AC P83003;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE Calreticulin-like protein (Fragment).
OS Entamoeba histolytica.
OC Eukaryota; Entamoebidae; Entamoeba.
NCBI_TaxID=5759;
RN [1]
RP SEQUENCE.
RC STRAIN=HM-1:IMMS;
RA Gonzalez E., Mendoza G., Ramos F., Garcia G., Moran P., Valadez A.,
RA Zaragoza M.E., Melendro E.I., Ximenez C.;
RT "Calreticulin-like molecule in trophozoites of Histolytica HM1-IMMS."
RL Submitted (JUN-2001) to the SWISS-PROT data bank.
CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
CC -!- DEVELOPMENTAL STAGE: IN TROPHOZOITES.
CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
DR InterPro; IPR001580; Calreticulin.
DR PROSITE; PS00803; CALRETICULIN_1; PARTIAL.
DR PROSITE; PS00804; CALRETICULIN_2; PARTIAL.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; PARTIAL.
DR Endoplasmic reticulum; Calcium-binding.
FT NON_TER 19
FT NON_TER 19
SQ SEQUENCE 19 AA; 2488 MW; FC90BCAEFE1BA764 CRC64;

Query Match 30.5%; Score 32; DB 5; Length 19;
Best Local Similarity 45.5%; Pred. No. 2.8e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 5 QETFSDLWKL 15
Db 5 EETFGWKXI 15

```

```

RESULT 6
Q9S0U6 PRELIMINARY; PRT; 25 AA.
AC Q9S0U6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ORF10S (Fragment).
OS Shigella sonnei.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Shigella.
OC NCBI_TaxID=624;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HW383;
RA Chida T., Okamura N., Ohtani K., Yoshida Y., Arakawa E., Watanabe H.;
RT "The complete DNA sequence of the O antigen gene region of Plesiomonas
RT shigelloides serotype O17 which is identical to Shigella sonnei form
RT I antigen.";
RN Microbiol. Immunol. 44:161-172(2000).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=HW383;
RX MEDLINE=99036814; PubMed=9817819;
RA Hough H.H., Venkatesan M.M.;
RT "Genetic analysis of Shigella sonnei form I antigen: identification of
RT a novel IS630 as an essential element for the form I antigen
RT expression";
RL Microb. Pathog. 25:165-173(1998).
DR EMBL; AB028134; BAA85070.1; -.
FT NON_TER 25
SQ SEQUENCE 25 AA; 2726 MW; A6CC5D24211CDAAD CRC64;

Query Match 30.5%; Score 32; DB 2; Length 25;
Best Local Similarity 42.9%; Pred. No. 3.7e+02;
Matches 6; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 2 PLSQETFSDLWKL 15
DB 4 PPSAEFFGTFWLVL 17

RESULT 7
Q9BGG8 PRELIMINARY; PRT; 16 AA.
AC Q9BGG8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Thyroid hormone receptor alpha (Fragment).
GN THRA1.
OS Sorex araneus (European common shrew) (European shrew).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Insectivora; Soricidae; Soricinae; Sorex.
OX NCBI_TaxID=42254;
RN [1]
RP SEQUENCE FROM N.A.
RA Larkin D., Serov O., Zhdanova N.;
RT "Mapping of five genes from human chromosome 17 to chromosome 17 of
RT the common shrew (Sorex araneus).";
RL Acta Theriol. (Warsz) 45:143-146(2000).
DR EMBL; AF314827; AAK13419.1; -.
KW Receptor.
FT NON_TER 1
SQ SEQUENCE 16 AA; 1951 MW; 775186E3FE5F2E2 CRC64;

Query Match 29.5%; Score 31; DB 6; Length 16;
Best Local Similarity 60.0%; Pred. No. 3.4e+02;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

RESULT 8
Q94377 PRELIMINARY; PRT; 24 AA.
AC Q94377;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE PPI-like Ser/Thr protein phosphatase (fragment).
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Zeke T., Gergely P., Dombradi V.;
RT "The catalytic subunits of Ser/Thr protein phosphatases from
RT Caenorhabditis elegans: A biochemical and molecular biological
RT survey.";
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: A PHOSPHOPROTEIN + H(2)O = A PROTEIN +
CC PHOSPHATE.
CC -!- SIMILARITY: BELONGS TO THE PPP FAMILY OF PHOSPHATASES.
DR EMBL; Z77740; CAB01299.1; -.
DR HSP; P08129; IPRJ.
DR InterPro; IPR004844; S/T_phosphatse.
DR PRODOM; PD000252; S/T_phosphatse; 1.
KW Hydrolase; Iron; Manganese.
FT NON_TER 1
FT NON_TER 24
SQ SEQUENCE 24 AA; 2816 MW; 2BF73DBB5F20359 CRC64;

Query Match 29.5%; Score 31; DB 5; Length 24;
Best Local Similarity 41.7%; Pred. No. 5.2e+02;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 8 PSDLWKLPPENG 19
DB 2 YSLLRIFDKNG 13

RESULT 9
Q77538 PRELIMINARY; PRT; 14 AA.
AC Q77538; Q9TQV9;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Growth hormone receptor (Fragment).
GN GHR.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Jiang H., Lucy M.C.;
RT "Identification of 5' untranslated variants of bovine growth hormone
RT receptor mRNA.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRED HOLSTEIN;
RX MEDLINE=99175163; PubMed=10075683;
RA Jiang H., Okamura C.S., Lucy M.C.;
RT "Isolation and characterization of a novel promoter for the bovine
RT growth hormone receptor gene.";
RL J. Biol. Chem. 274:7893-7900(1999).

```

```

RN [3]
RP SEQUENCE FROM N.A.
RA Jiang H., Lucy M.C.;
RT "Identification of 5' untranslated variants of bovine growth hormone
  receptor mRNA."; (1997) to the EMBL/GenBank/DBJ databases.
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RN SEQUENCE FROM N.A.
RA Jiang H., Lucy M.C.;
RT "Bovine GH receptor 5' UTR variants.";
  Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF036297; AAC33315.2; -
DR EMBL; AF085281; AAD2521.1; -
DR EMBL; AF036290; AAC33308.1; -
DR EMBL; AF036291; AAC33309.1; -
DR EMBL; AF036292; AAC33310.1; -
DR EMBL; AF036293; AAC33311.1; -
DR EMBL; AF036294; AAC33312.1; -
DR EMBL; AF036295; AAC33313.1; -
DR EMBL; AF036296; AAC33314.1; -
DR EMBL; AF326349; AAK97345.1; -
KW Receptor.
FT NON TER 14 14
SQ SEQUENCE 14 AA; 1544 MW; 5A45D458FF3A9E27 CRC64;

  Query Match 28.6%; Score 30; DB 6; Length 14;
  Best Local Similarity 83.3%; Pred. No. 4.2e+02;
  Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLWKLL 15
   |||:|
Db 2 DLWQLL 7

RESULT 10
Q9HCW9 PRELIMINARY; PRT; 23 AA.
AC Q9HCW9;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE Growth hormone receptor (Fragment).
GN GHR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RA Orlovsky I.V., Sverdlova P.S., Rubtsov P.M.;
RT "Microsatellites within the human growth hormone receptor gene.";
  Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ295613; CAC06615.1; -
KW Receptor.
FT NON TER 23 23
SQ SEQUENCE 23 AA; 2426 MW; 9AD833A0F1DD699E CRC64;

  Query Match 28.6%; Score 30; DB 4; Length 23;
  Best Local Similarity 83.3%; Pred. No. 7.2e+02;
  Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLWKLL 15
   |||:|
Db 2 DLWQLL 7

RESULT 11
Q94368 PRELIMINARY; PRT; 24 AA.
AC Q94368;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

```

```

DE PPI-like Ser/Thr protein phosphatase (Fragment).
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RN SEQUENCE FROM N.A.
RA Zeke T., Gergely P., Dombradi V.;
RT "The catalytic subunits of Ser/Thr protein phosphatases from
  Caenorhabditis elegans: A biochemical and molecular biological
  survey.";
  Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: A PHOSPHOPROTEIN + H(2)O = A PROTEIN +
  PHOSPHATE.
CC -1- SIMILARITY: BELONGS TO THE PPP FAMILY OF PHOSPHATASES.
DR EMBL; Z77728; CAB01287.1; -.
DR HSSP; P08129; IFJM.
DR InterPro; IPR004844; S/T_phosphatse.
DR ProDom; PD000252; S/T_phosphatse; 1.
KW Hydrolase; Iron; Manganese.
FT NON TER 1 1
FT NON TER 24 24
SQ SEQUENCE 24 AA; 2781 MW; 353E423EA763AA75 CRC64;

  Query Match 28.6%; Score 30; DB 5; Length 24;
  Best Local Similarity 58.3%; Pred. No. 7.5e+02;
  Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 8 FSDLWKLLPENG 19
   |||:|
Db 2 YSDELLALLELNG 13

RESULT 12
Q9XNQ1 PRELIMINARY; PRT; 17 AA.
AC Q9XNQ1;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE Cytochrome oxidase subunit 2 (Fragment).
GN COLI.
OS Boophilus microplus (Cattle tick).
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Parasitiformes; Ixodida; Ixodidae; Boophilus.
OX NCBI_TaxID=6941;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=N;
RX MEDLINE=99297341; PubMed=10368952;
RA Campbell N.J.H., Barker S.C.;
RT "The novel mitochondrial gene arrangement of the cattle tick,
  Boophilus microplus: fivefold tandem repetition of a coding region.";
  Mol. Biol. Evol. 16:732-740(1999).
RL EMBL; AF110614; AAD28397.1; -.
KW Mitochondrion.
FT NON TER 17 17
SQ SEQUENCE 17 AA; 1988 MW; 319F2D4D7DA11F3 CRC64;

  Query Match 27.6%; Score 29; DB 8; Length 17;
  Best Local Similarity 75.0%; Pred. No. 7.6e+02;
  Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 SQETFSDL 11
   |||:|
Db 5 SOLTFSDM 12

RESULT 13
Q95V74 PRELIMINARY; PRT; 24 AA.
ID Q95V74
AC Q95V74;

```

DT 01-DEC-2001 (TReMBLrel. 19, Created)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 DE Elongation factor 1 alpha (Fragment).  
 OS Mytilus galloprovincialis (Mediterranean mussel).  
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;  
 OC Mytiloidea; Mytilidae; Mytilus.  
 OX NCBI\_TaxID=29158;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Pierre N., Daguin C., Borsa P., Jollivet D., Viard F., Bonhomme F.,  
 RA David P.;  
 RT "Intgression patterns in the Mytilus edulis / Mytilus  
 RT galloprovincialis mosaic hybrid zone along the Atlantic coasts of  
 RT France.";  
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF424742; AAL24803.1; -  
 FT NON\_TER 1  
 FT NON\_TER 24  
 SQ SEQUENCE 24 AA; 2875 MW; 1D0DEAD3FBD13DCB CRC64;

Query Match 27.6%; Score 29; DB 5; Length 24;  
 Best Local Similarity 38.5%; Pred. No. 1.1e+03;  
 Matches 5; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Oy 1 PPLSQETFSDLWK 13  
 Db 4 PPYSEARFMEIOK 16

## RESULT 14

ID P87182 PRELIMINARY; PRT; 24 AA.  
 AC P87182;  
 DT 01-JUL-1997 (TReMBLrel. 04, Created)  
 DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 DE Carbamoyl phosphate synthetase, small subunit (arg2).  
 OS Trichoderma virens.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Hypocreales; Hypocreaceae; Hypocrea.  
 OX NCBI\_TaxID=29875;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Baek J.-M., Kenerley C.M.;  
 RT "The arg2 gene of Trichoderma virens: Cloning and development of a  
 RT homologous transformation system.";  
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF001029; AAB58298.1; -  
 SQ SEQUENCE 24 AA; 2782 MW; 8FPD15C27EAD244C CRC64;

Query Match 27.1%; Score 28.5; DB 3; Length 24;  
 Best Local Similarity 53.8%; Pred. No. 1.3e+03;  
 Matches 7; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

Oy 4 SQETFSQ-LWKLL 15  
 Db 10 SDYLSDLWRL 22

## RESULT 15

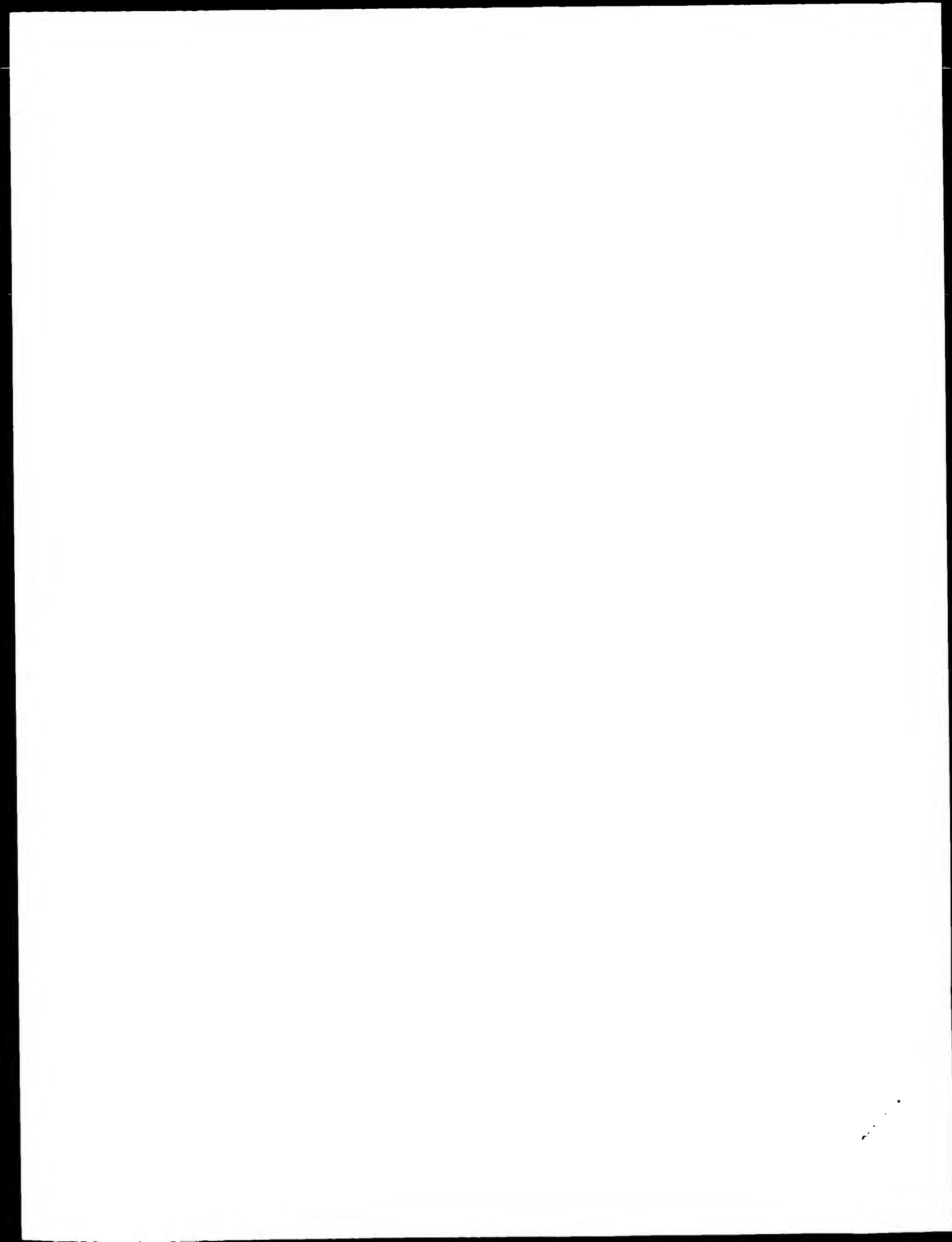
O9LKK5  
 ID Q9LKK5 PRELIMINARY; PRT; 20 AA.  
 AC Q9LKK5;  
 DT 01-OCT-2000 (TReMBLrel. 15, Created)  
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)  
 DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)  
 DE Transcription factor AP1 (Fragment).  
 OS Citrus sinensis (Sweet orange).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Sapindales; Rutaceae; Citrus.  
 OX NCBI\_TaxID=2711;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Liu C., Xu C., Lin B.;  
 RT "Molecular cloning of APETALA1 (AP1) gene from orange (Citrus  
 RT sinensis).";  
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF263991; AAF74291.1; -  
 FT NON\_TER 1  
 FT NON\_TER 20  
 FT NON\_TER 20  
 SQ SEQUENCE 20 AA; 2493 MW; 3F1D0C6F8F8F5C1EAS CRC64;

Query Match 26.7%; Score 28; DB 10; Length 20;  
 Best Local Similarity 54.5%; Pred. No. 1.3e+03;  
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Oy 3 LSQETFSDLWK 13  
 Db 9 LTHESISDLQK 19

Search completed: February 12, 2003, 11:14:59  
 Job time : 38.2083 secs





GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 12, 2003, 11:11:31 ; Search time 10.2917 Seconds  
(without alignments)  
76.572 Million cell updates/sec

Title: US-09-403-440A-2

Perfect score: 105

Sequence: 1 PPLSQETFSDLWKLLPENG 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 1520

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28.5	27.1	24	1 Y3KD NEUCR	P22702 neurospora
2	27	25.7	20	1 LECB_IRIHO	P36231 iris hollan
3	26	24.8	20	1 CRIC_SPIOL	P30806 spinacia ol
4	24	22.9	10	1 HTF_HELZE	P16353 heliothis z
5	24	22.9	20	1 CP35 PAPSP	P80056 papio sp. (
6	24	22.9	23	1 TL17 SPIOL	P81778 spinacia ol
7	24	22.9	23	1 XYC1 ACIGB	P46365 acinetobact
8	23	21.9	10	1 AKHX_LOCM1	P81626 locusta mig
9	22.5	21.4	25	1 LPCE_YEAST	P08521 saccharomyc
10	22	21.0	13	1 NP1_LYMST	P80178 lymnaea sta
11	22	21.0	13	1 NP2_LYMST	P80179 lymnaea sta
12	22	21.0	13	1 NP4_LYMST	P80181 lymnaea sta
13	22	21.0	13	1 NP5_LYMST	P80182 lymnaea sta
14	22	21.0	16	1 IBA4_PIG	P24854 sus scrofa
15	22	21.0	24	1 DMS6_PHYBI	P81490 phyllomedus
16	21.5	20.5	12	1 UR2_SCVCA	P35490 scyllorhinu
17	21	20.0	8	1 HTF2_PERAM	P04549 periplaneta
18	21	20.0	10	1 HTF2_CARMO	P11385 carausius m
19	21	20.0	15	1 URE1_WORMO	P17337 morganella
20	21	20.0	17	1 ACY6_SOYNO	P15986 glycine max
21	21	20.0	18	1 CPAX_BOVIN	P22779 bos taurus
22	21	20.0	21	1 NDK_CANAL	P09466 candida alb
23	20	19.0	8	1 AKH_TABAT	P14595 tabanus atr
24	20	19.0	8	1 HTF1_PERAM	P04548 periplaneta
25	20	19.0	10	1 HTF_TABAT	P14596 tabanus atr
26	20	19.0	13	1 NP3_LYMST	P80180 lymnaea sta
27	20	19.0	17	1 PH4_PERAM	P82697 periplaneta
28	20	19.0	18	1 PCG6_PACGO	P82419 pachycondyl
29	20	19.0	19	1 AL22_HORSE	P81217 equus cabal
30	20	19.0	19	1 IRBP_CAVPO	P12666 cavia porce
31	20	19.0	19	1 PCG7_PACGO	P82420 pachycondyl
32	20	19.0	20	1 PSF7_MAIZE	P13193 zea mays (m
33	20	19.0	22	1 CR32_LITCE	P56239 litoria cae

34 20 19.0 22 1 CR33\_LITCE P56240 litoria cae  
35 20 19.0 23 1 IRBP2\_PIG P24853 sus scrofa  
36 20 19.0 23 1 IRBP2\_RABIT P12664 oryctolagus  
37 20 19.0 23 1 UDF\_LACCA P19662 lactobacill  
38 20 19.0 25 1 FLAA\_TREPH P21983 treponema p  
39 20 19.0 25 1 PCW1\_PACGO P82423 pachycondyl  
40 20 19.0 25 1 PCW2\_PACGO P82424 pachycondyl  
41 19 18.1 8 1 AKHG\_GRYBI P14086 gryllus bim  
42 19 18.1 8 1 CLP\_THICU P80488 thiobacillu  
43 19 18.1 8 1 HTF\_TENMO P25419 tenebrio mo  
44 19 18.1 10 1 HTF\_NAUCI P10939 nauphoeta c  
45 19 18.1 10 1 URA7\_HUMAN P34990 homo sapien

## ALIGNMENTS

RESULT 1  
Y3KD NEUCR  
ID Y3KD NEUCR STANDARD; PRT; 24 AA.  
AC P22702;  
DT 01-AUG-1991 (Rel. 19, Created)  
DT 01-AUG-1991 (Rel. 19, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Hypothetical 2.8 kDa protein in ARG-2 5'region.  
OS Neurospora crassa.  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
OC Sordariales; Sordariaceae; Neurospora.  
OX NCBI\_TaxID=5141;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=90293033; PubMed=2141606;  
RA Orbach M.J., Sachs M.S., Yanofsky C.;  
RT "The Neurospora crassa arg-2 locus. Structure and expression of the  
RT gene encoding the small subunit of arginine-specific carbamoyl  
RT phosphate synthetase.";  
RL J. Biol. Chem. 265:10981-10987(1990).  
CC -!- FUNCTION: MAY HAVE A REGULATORY ROLE IN THE PRODUCTION OF  
CC ARGinine-SPECIFIC CARBAMOYL PHOSPHATE SYNTHETASE.  
CC -!- SIMILARITY: TO YEAST CPAI LEADER PEPTIDE (AC P08521).  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/  
CC or send an email to license@isb-sib.ch).  
CC -----  
CC EMBL; J05512; AAA33610.1; -  
DR PIR; B42224; B42224.  
KW Hypothetical protein.  
SQ SEQUENCE 24 AA; 2779 MW; 8FF33F527EAD244C CRC64;  
Query Match 27.1%; Score 28.5; DB 1; Length 24;  
Best Local Similarity 53.8%; Pred. No. 2.8e+02;  
Matches 7; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

Qy 4 SQETFS-DLWKLL 15  
||: ||: ||:  
Db 10 SQDYLSDHLWRL 22

## RESULT 2

LECB\_IRIHO  
ID LECB\_IRIHO STANDARD; PRT; 20 AA.  
AC P36231;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 01-JUN-1994 (Rel. 29, Last annotation update)  
DE N-acetyl-D-galactosamine-binding lectin subunit B (A-disaccharide-  
DE binding lectin subunit B) (Fragment).  
OS Iris hollandica (Dutch iris).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Iridaceae;  
 OC Iris.  
 OX NCBI\_TaxID=35876;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=CV. GOLDEN HARVEST, and CV. PROF. BLAAUW; TISSUE=Bulb;  
 RX MEDLINE=94171801; PubMed=8125993;  
 RA MO H., van Damme E.J.M., Peumans W.J., Goldstein I.J.;  
 RT "Isolation and characterization of an  
 RT N-acetyl-D-galactosamine-binding lectin from Dutch Iris bulbs which  
 RT recognizes the blood group A disaccharide (GalNAc alpha 1-3Gal).";  
 RL J. Biol. Chem. 269:7656-7673 (1994).  
 CC -1- FUNCTION: GAL / GALNAc-SPECIFIC LECTIN. AGGLUTINATES BOTH NATIVE  
 CC AND TRYPSIN-TREATED RABBIT ERYTHROCYTES BUT NOT HUMAN ERYTHROCYTES  
 CC IRRESPECTIVE OF BLOOD GROUP TYPE.  
 CC -1- SUBUNIT: DISULFIDE-LINKED HETERODIMER OF A AND B CHAINS.  
 KW Lectin.  
 FT NON TER 20 20  
 SQ SEQUENCE 20 AA; 2246 MW; DE08DA025FD17D56 CRC64;  
 Query Match 25.7%; Score 27; DB 1; Length 20;  
 Best Local Similarity 83.3%; Pred. No. 3.9e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 PLSOET 7 25.7%  
 DB 6 PLSOET 11 83.3%  
 RESULT 3  
 CRIC SPICOL  
 ID CRIC SPICOL STANDARD; PRT; 20 AA.  
 AC P30806;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Calreticulin (Fragment).  
 OS Spinacia oleracea (Spinach).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.  
 OX NCBI\_TaxID=3562;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Leaf;  
 RX MEDLINE=93176159; PubMed=8439313;  
 RA Menegazzi P., Guzzo F., Baldan B., Mariani P., Treves S.;  
 RT "Purification of calreticulin-like protein(s) from spinach leaves.";  
 RL Biochem. Biophys. Res. Commun. 190:1130-1135 (1993).  
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM.  
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.  
 CC -1- PTM: GLYCOSYLATED.  
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
 DR PIR; PC1241; PC1241.  
 DR PIR; PC1240; PC1240.  
 DR InterPro; IPR001580; Calreticulin.  
 DR PROSITE; PS00803; CALRETICULIN\_1; PARTIAL.  
 DR PROSITE; PS00804; CALRETICULIN\_2; PARTIAL.  
 DR PROSITE; PS00805; CALRETICULIN\_REPEAT; PARTIAL.  
 KW Endoplasmic reticulum; Calcium-binding; Glycoprotein.  
 FT NON TER 20 20  
 SQ SEQUENCE 20 AA; 2645 MW; 00FAB4C9DEEDCB0F CRC64;  
 Query Match 24.8%; Score 26; DB 1; Length 20;  
 Best Local Similarity 44.4%; Pred. No. 5.5e+02;  
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
 QY 5 QETFSDLWK 13 24.8%  
 DB 6 EERFEGWE 13 44.4%

RESULT 4  
 HTF HELZE  
 ID HTF HELZE STANDARD; PRT; 10 AA.  
 AC P16353;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 01-FEB-1994 (Rel. 28, Last annotation update)  
 DE Hyperrethaloaemic hormone (Hez-HRTH).  
 OS Heliothis zea (Corn earworm) (Bollworm).  
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
 OC Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata;  
 OC Diptera; Noctuidae; Noctuidae; Heliothinae; Helicoverpa.  
 OX NCBI\_TaxID=7113;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Corpora cardiaca;  
 RX MEDLINE=88326324; PubMed=3415690;  
 RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Bird T.G.,  
 RA Tseng C.M., Zhang Y.S., Hayes D.K.;  
 RT "Isolation and primary structure of a neurotrophic hormone from  
 RT Heliothis zea with hyperrethaloemic and adipokinetic activities.";  
 RL Biochem. Biophys. Res. Commun. 155:344-350 (1988).  
 CC -1- FUNCTION: HYPERRETREHALOEMIC FACTORS ARE NEUROPEPTIDES THAT  
 CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS  
 CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).  
 CC -1- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.  
 DR PIR; A31571; A31571.  
 DR InterPro; IPR002047; AKH.  
 DR PROSITE; PS00256; AKH; 1.  
 KW Neuropeptide; Amidation.  
 FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD RES 10 10 AMIDATION.  
 SQ SEQUENCE 10 AA; 1096 MW; 8E70367865A5B9D1 CRC64;  
 Query Match 22.9%; Score 24; DB 1; Length 10;  
 Best Local Similarity 62.5%; Pred. No. 5.3e+02;  
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 5 QETFSDLW 12 22.9%  
 DB 1 QLTFSGW 8 62.5%

RESULT 5  
 CP35\_PAPSP  
 ID CP35\_PAPSP STANDARD; PRT; 20 AA.  
 AC P80056;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-MAY-1992 (Rel. 22, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Cytochrome P450 3A5 (EC 1.14.14.1) (CYFIIAS) (P450 FA) (6-beta-  
 DE testosterone hydroxylase) (Fragment).  
 OS Papio sp. (Baboon).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;  
 OC Cercopitheciinae; Papio.  
 OX NCBI\_TaxID=61183;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Liver;  
 RX MEDLINE=92174920; PubMed=1541278;  
 RA Dalet-Beluche I., Boulenc X., Fabre G., Maurel P., Bonfils C.;  
 RT "Purification of two cytochrome P450 isozymes related to CYP2A and  
 RT CYP3A gene families from monkey (baboon, Papio papio) liver  
 RT microsomes. Cross reactivity with human forms.";  
 RL Eur. J. Biochem. 204:641-648 (1992).  
 CC -1- FUNCTION: 6-BETA-TESTOSTERONE HYDROXYLASE.  
 CC -1- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +  
 CC oxidized flavoprotein + H(2)O.  
 CC -1- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.  
 CC -1- INDUCTION: BY PHENOBARBITAL.  
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.  
 DR PIR; S21176; S21176.

DR InterPro; IPR001128; Cytochrome P450.  
 DR PROSITE; PS00086; CYTOCHROME P450; PARTIAL.  
 KW Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;  
 KW Microsome; Endoplasmic reticulum.  
 FT NON\_TER 20 20  
 SQ SEQUENCE 20 AA; 2226 MW; 3FE8B6B62BC0F36 CRC64;

Query Match 22.9%; Score 24; DB 1; Length 20;  
 Best Local Similarity 46.7%; Pred. No. 1.1e+03;  
 Matches 7; Conservative 1; Mismatches 3; Indels 4; Gaps 1;

QY 1 PPLSQTFSDLWKL 15  
 | | | | |  
 Db 5 PDLAVET---WLL 15

RESULT 6  
 TL17\_SPIOL  
 ID TL17\_SPIOL STANDARD; PRT; 23 AA.  
 AC P81778;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Thylakoid lumenal 17.4 kDa protein (P17.4) (Fragment).  
 OS Spinacia oleracea (Spinach).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.  
 OX NCBI\_TaxID=3562;  
 RN [1]  
 RP SEQUENCE, AND REVISIONS TO 13 AND 15.  
 RA Schubert M., Peterson U., Funk C., Schroeder W.P., Kieselbach T.;  
 RT "The chloroplast lumen from Arabidopsis thaliana";  
 RL Submitted (JUL-2001) to the SWISS-PROT data bank.  
 RN [2]  
 RP SEQUENCE OF 1-16.  
 RC TISSUE=Leaf;  
 RX MEDLINE=98175931; PubMed=9506969;  
 RA Kieselbach T., Hagman A., Andersson B., Schroeder W.P.;  
 RT "The thylakoid lumen of chloroplasts - isolation and  
 characterization.";  
 RL J. Biol. Chem. 273:6710-6716 (1998).  
 CC -1- SUBCELLULAR LOCATION: Chloroplast; within the thylakoid lumen.  
 KW Chloroplast; Thylakoid.  
 FT NON\_TER 23 23  
 SQ SEQUENCE 23 AA; 2571 MW; 022C92717AE9AF2D CRC64;

Query Match 22.9%; Score 24; DB 1; Length 23;  
 Best Local Similarity 66.7%; Pred. No. 1.3e+03;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PPLSQE 6  
 | | | | |  
 Db 6 PPLSND 11

RESULT 7  
 XYC1\_ACIGB  
 ID XYC1\_ACIGB STANDARD; PRT; 23 AA.  
 AC P46365;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Benzaldehyde dehydrogenase [NAD+] I (EC 1.2.1.28) (Fragment).  
 OS Acinetobacter genomosp. 11.  
 OC Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae;  
 OC Acinetobacter.  
 OX NCBI\_TaxID=106649;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=ATCC 11171 / NCIB 8250 / CIP 63.46 / B94;  
 RX MEDLINE=91113163; PubMed=1989592;  
 RA Chalmers R.M., Keen J.N., Fawson C.A.;

RT "Comparison of benzyl alcohol dehydrogenases and benzaldehyde  
 RT dehydrogenases from the benzyl alcohol and mandelate pathways in  
 RT Acinetobacter calcoaceticus and from the TOL-plasmid-encoded toluene  
 RT pathway in Pseudomonas putida. N-terminal amino acid sequences, amino  
 RT acid compositions and immunological cross-reactions.";  
 RL Biochem. J. 273:99-107 (1991).  
 CC -1- CATALYTIC ACTIVITY: Benzaldehyde + NAD(+) + H(2)O = benzoate +  
 CC NADH.  
 CC -1- SUBUNIT: HOMOTETRAMER.  
 CC -1- SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.  
 DR InterPro; IPR002086; Aldehyde dehydr.  
 DR PROSITE; PS00070; ALDEHYDE DEHYDR\_CYS; PARTIAL.  
 DR PROSITE; PS00687; ALDEHYDE DEHYDR\_GLU; PARTIAL.  
 KW Aromatic hydrocarbons catabolism; Oxidoreductase; NAD.  
 FT NON\_TER 23 23  
 SQ SEQUENCE 23 AA; 2750 MW; 50496D4930DF9E40 CRC64;

Query Match 22.9%; Score 24; DB 1; Length 23;  
 Best Local Similarity 23.1%; Pred. No. 1.3e+03;  
 Matches 3; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWK 13  
 | | | | |  
 Db 1 PNQTKIIIEQIWK 13

RESULT 8  
 AKHX\_LOCMI  
 ID AKHX\_LOCMI STANDARD; PRT; 10 AA.  
 AC P81626;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Peptide hormone.  
 OS Locusta migratoria (Migratory locust).  
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
 OC Insecta; Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;  
 OC Acridomorpha; Acridoidea; Acrididae; Oedipodinae; Locusta.  
 OX NCBI\_TaxID=7004;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Corpora cardiaca;  
 RA Siegest K.J.;  
 RL Submitted (DEC-1998) to the SWISS-PROT data bank.  
 CC -1- FUNCTION: PROBABLY INVOLVED IN THE REGULATION OF LOCUST  
 CC INTERMEDIARY METABOLISM, BEHAVIOR AND/OR DEVELOPMENT.  
 CC -1- SIMILARITY: SOME SIMILARITY TO THE AKH / HRTH / RPCH FAMILY.  
 DR InterPro; IPR002047; AKH.  
 DR PROSITE; PS00256; AKH; 1.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 1 1  
 FT MOD\_RES 10 10 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 10 10 AMIDATION.  
 SQ SEQUENCE 10 AA; 1222 MW; 81BFF67AB415B9D1 CRC64;

Query Match 21.9%; Score 23; DB 1; Length 10;  
 Best Local Similarity 62.5%; Pred. No. 7.6e+02;  
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 QETFSDLW 12  
 | | | | |  
 Db 1 QVTFSDRW 8

RESULT 9  
 LPCP\_YEAST  
 ID LPCP\_YEAST STANDARD; PRT; 25 AA.  
 AC P08521;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-AUG-1988 (Rel. 08, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE CPAL leader peptide.  
 GN YOR302W.  
 OS Saccharomyces cerevisiae (Baker's yeast).

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
 NCBI\_TaxID=4932;  
 [1]  
 SEQUENCE FROM N.A.  
 RX MEDLINE=87215944; PubMed=3555844;  
 RA Werner M., Feller A., Messenguy F., Pierard A.;  
 RT "The leader peptide of yeast gene CPA1 is essential for the  
 translational repression of its expression.";  
 RL Cell 49:805-813(1987).  
 RN [2]  
 SEQUENCE FROM N.A.  
 RP MEDLINE=85101411; PubMed=3881260;  
 RX Werner M., Feller A., Pierard A.;  
 RA "Nucleotide sequence of yeast gene CP A1 encoding the small subunit  
 of arginine-pathway carbamoyl-phosphate synthetase. Homology of the  
 deduced amino acid sequence to other glutamine amidotransferases.";  
 RL Eur. J. Biochem. 146:371-381(1985).  
 RN [3]  
 SEQUENCE FROM N.A.  
 RP STRAIN=S288C / FY1679;  
 RX MEDLINE=97298310; PubMed=9153758;  
 RA Poiry R., Cziepluch C., Tobiasch E., Pujol A., Kordes E.,  
 JAuniaux J.-C.;  
 RT "Sequence and analysis of a 36.2 kb fragment from the right arm of  
 yeast chromosome XV reveals 19 open reading frames including SNF2 (5'  
 end), CPA1, SLY4, a putative transport ATPase, a putative ribosomal  
 protein and an SNF2 homologue.";  
 RL Yeast 13:479-482(1997).  
 CC -!- SIMILARITY: TO A HYPOTHETICAL PROTEIN IN ARG2 5' REGION FROM  
 CC NEUROSPORA CRASSA.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; M16690; AAA34526.1; -;  
 DR EMBL; X01764; CAA25904.1; -;  
 DR EMBL; Z75210; CAA99620.1; -;  
 DR PIR; A26965; A26965.  
 DR PIR; S25434; S25434.  
 DR SGD; S0005828; YOR302W.  
 KW Leader peptide.  
 SQ SEQUENCE 25 AA; 2979 MW; 01D494C8AFEA4AA CRC64;  
 Query Match 21.4%; Score 22.5; DB 1; Length 25;  
 Best Local Similarity 50.0%; Pred. No. 2.4e+03;  
 Matches 5; Conservative 2; Mismatches 2; Indels 1; Gaps 1;  
 QY 5 QETFS-D-LWK 13  
 Db 12 QDYISDHIWK 21  
 RESULT 10  
 NP1\_LYMST  
 ID NP1\_LYMST STANDARD; PRT; 13 AA.  
 AC P80178;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 01-JUL-1993 (Rel. 26, Last annotation update)  
 DE Lyman-DP-amide 1.  
 OS Lymanaea stagnalis (Great pond snail).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;  
 OC Lymnaeidae; Lymnaea.  
 OX NCBI\_TaxID=6523;  
 RN [1]  
 RN SEQUENCE.  
 RP TISSUE=Ganglion;  
 RC

RX MEDLINE=93238777; PubMed=8477756;  
 RA Johnsen A.H., Rehfeld J.F.;  
 RT "Lymnaeidae, a new family of neuropeptides from the pond snail,  
 Lymnaea stagnalis. Clue to cholecystokinin immunoreactivity in  
 invertebrates?";  
 RL Eur. J. Biochem. 213:875-879(1993).  
 CC -!- SIMILARITY: RELATED TO THE CHOLECYSTOKININ (CKK) FAMILY.  
 DR PIR; S32471; S32471.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 13 13  
 SQ SEQUENCE 13 AA; 1519 MW; 9CA07BA3F5D5B455 CRC64;  
 Query Match 21.0%; Score 22; DB 1; Length 13;  
 Best Local Similarity 50.0%; Pred. No. 1.4e+03;  
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 QY 3 LSQETFS-D 10  
 Db 5 TSNSAFSD 12  
 RESULT 11  
 NP2\_LYMST  
 ID NP2\_LYMST STANDARD; PRT; 13 AA.  
 AC P80179;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 01-JUL-1993 (Rel. 26, Last annotation update)  
 DE Lyman-DP-amide 2.  
 OS Lymanaea stagnalis (Great pond snail).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;  
 OC Lymnaeidae; Lymnaea.  
 OX NCBI\_TaxID=6523;  
 RN [1]  
 RN SEQUENCE.  
 RP TISSUE=Ganglion;  
 RC MEDLINE=93238777; PubMed=8477756;  
 RA Johnsen A.H., Rehfeld J.F.;  
 RT "Lymnaeidae, a new family of neuropeptides from the pond snail,  
 Lymnaea stagnalis. Clue to cholecystokinin immunoreactivity in  
 invertebrates?";  
 RL Eur. J. Biochem. 213:875-879(1993).  
 CC -!- SIMILARITY: RELATED TO THE CHOLECYSTOKININ (CKK) FAMILY.  
 DR PIR; S32472; S32472.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 13 13  
 FT UNSURE 8 8  
 SQ SEQUENCE 13 AA; 1492 MW; 9CA07BA3F5D5A5A5 CRC64;  
 Query Match 21.0%; Score 22; DB 1; Length 13;  
 Best Local Similarity 50.0%; Pred. No. 1.4e+03;  
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 QY 3 LSQETFS-D 10  
 Db 5 ISSSAFSD 12  
 RESULT 12  
 NP4\_LYMST  
 ID NP4\_LYMST STANDARD; PRT; 13 AA.  
 AC P80181;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 01-JUL-1993 (Rel. 26, Last annotation update)  
 DE Lyman-DP-amide 4.  
 OS Lymanaea stagnalis (Great pond snail).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;  
 OC Lymnaeidae; Lymnaea.  
 OX NCBI\_TaxID=6523;  
 RN [1]  
 RN SEQUENCE.  
 RP TISSUE=Ganglion;  
 RC

```

RX MEDLINE=93238777; PubMed=8477756;
RA Johnsen A.H., Rehfeld J.F.;
RT "LymnaeaFamides, a new family of neuropeptides from the pond snail,
RT Lymnaea stagnalis. Clue to cholecystokinin immunoreactivity in
RT invertebrates?";
RL Eur. J. Biochem. 213:875-879(1993).
CC -|- SIMILARITY: RELATED TO THE CHOLECYSTOKININ (CCK) FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 13 13 AMIDATION.
SQ SEQUENCE 13 AA; 1503 MW; 9CA07BBB56D5B455 CRC64;

Query Match 21.0%; Score 22; DB 1; Length 13;
Best Local Similarity 50.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 LSQETFS 10
   :|||
Db 5 ISNSAFSD 12

RESULT 13
NP5_LYMST STANDARD; PRT; 13 AA.
AC P80182;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE Lymnaea-DP-amide 5.
OS Lymnaea stagnalis (Great pond snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
OC Lymnaeidae; Lymnaea.
OX NCBI_TaxID=6523;
RN [1]
RP SEQUENCE.
RC TISSUE=Ganglion;
RA MEDLINE=93238777; PubMed=8477756;
RX Johnsen A.H., Rehfeld J.F.;
RT "LymnaeFamides, a new family of neuropeptides from the pond snail,
RT Lymnaea stagnalis. Clue to cholecystokinin immunoreactivity in
RT invertebrates?";
RL Eur. J. Biochem. 213:875-879(1993).
CC -|- SIMILARITY: RELATED TO THE CHOLECYSTOKININ (CCK) FAMILY.
DR PIR; S32475; S32475.
KW Neuropeptide; Amidation.
FT MOD_RES 13 13 AMIDATION.
SQ SEQUENCE 13 AA; 1476 MW; 9CA07BBB56D5A5A5 CRC64;

Query Match 21.0%; Score 22; DB 1; Length 13;
Best Local Similarity 50.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 LSQETFS 10
   :|||
Db 5 ISNSAFSD 12

RESULT 14
IBP4_PIG STANDARD; PRT; 16 AA.
ID IBP4_PIG
AC P24854;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Insulin-like growth factor binding protein 4 (IGFBP-4) (IBP-4)
DE (IGF-binding protein 4) (Fragment).
DN IGFBP4.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE.
RA MEDLINE=92109718; PubMed=1722398;

```

```

RA Coleman M.E., Pan Y.-C.E., Esherton T.D.;
RT "Identification and NH2-terminal amino acid sequence of three
RT insulin-like growth factor-binding proteins in porcine serum.";
RL Biochem. Biophys. Res. Commun. 181:1131-1136(1991).
CC -|- FUNCTION: IGF-BINDING PROTEINS PROLONG THE HALF-LIFE OF THE IGFs
CC AND HAVE BEEN SHOWN TO EITHER INHIBIT OR STIMULATE THE GROWTH
CC PROMOTING EFFECTS OF THE IGFs ON CELL CULTURE. THEY ALTER THE
CC INTERACTION OF IGFs WITH THEIR CELL SURFACE RECEPTORS.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- SIMILARITY: CONTAINS 1 THYROGLOBULIN TYPE-I DOMAIN.
CC -|- SIMILARITY: BELONGS TO THE INSULIN-LIKE GROWTH FACTOR BINDING
CC PROTEIN FAMILY.
DR PIR; JH0517; JH0517.
DR InterPro; IPR000867; Insl_gro_fac.pr.
DR InterPro; IPR000716; Thyroglobulin 1.
DR PROSITE; PS00222; IGF BINDING; PARTIAL.
DR PROSITE; PS00484; THYROGLOBULIN_1; PARTIAL.
KW Growth factor binding.
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1799 MW; 40988840096655E2 CRC64;

```

```

Query Match 21.0%; Score 22; DB 1; Length 16;
Best Local Similarity 66.7%; Pred. No. 1.8e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 PPLSQE 6
   |||
Db 7 PPPSEE 12

```

```

RESULT 15
DMS6_PHYBI STANDARD; PRT; 24 AA.
ID DMS6_PHYBI
AC P81490;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Dermaseptin BVI (Dermaseptin B6).
OS Phyllomedusa bicolor (Two-colored leaf frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Phyllomedusinae; Phyllomedusa.
OX NCBI_TaxID=8393;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin;
RA MEDLINE=98278974; PubMed=9614066;
RX Charpentier S., Amiche M., Mester J., Vouille V., Le Caer J.-P.,
RA Nicolas P., Delfour A.;
RT "Structure, synthesis, and molecular cloning of dermaseptins B, a
RT family of skin peptide antibiotics.";
RL J. Biol. Chem. 273:14690-14697(1998).
CC -|- FUNCTION: POSSESSES A POTENT ANTIMICROBIAL ACTIVITY AGAINST
CC GRAM-POSITIVE AND GRAM-NEGATIVE BACTERIA. PROBABLY ACTS BY
CC DISTURBING MEMBRANE FUNCTIONS WITH ITS AMPHIPATHIC STRUCTURE.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- SIMILARITY: BELONGS TO THE DERMASEPTIN FAMILY.
KW Antibiotic; Multigene family; Amphibian skin; Amidation.
FT MOD_RES 24 24 AMIDATION (POTENTIAL).
SQ SEQUENCE 24 AA; 2665 MW; E5987D7F50E08F4F CRC64;

```

```

Query Match 21.0%; Score 22; DB 1; Length 24;
Best Local Similarity 50.0%; Pred. No. 2.7e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```

```

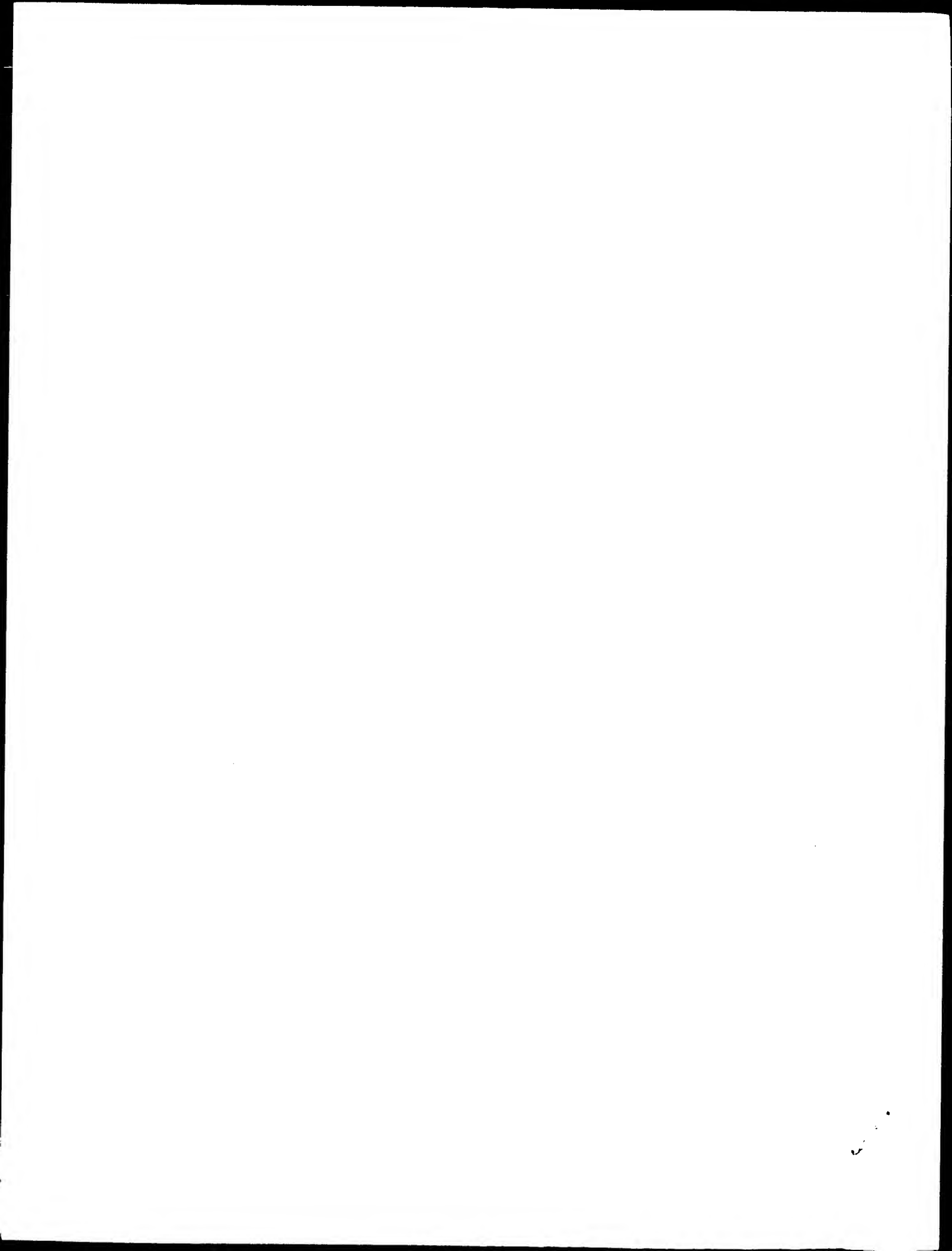
QY 11 LMKLLPEN 18
   |||
Db 2 LMKDILKN 9

```

```

Search completed: February 12, 2003, 11:14:05
Job time : 10.2917 secs

```



GenCore version 5.1.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 12, 2003, 11:12:22 ; Search time 20.5833 Seconds  
(without alignments)  
88.739 Million cell updates/sec

Title: US-09-403-440A-2

Perfect score: 105

Sequence: 1 PPLSQFTFSDLWKLLPENG 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 4984

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

PIR 73:\*

1: PIR1:\*

2: PIR2:\*

3: PIR3:\*

4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	32.4	19	2	B61409
2	33	31.4	24	2	I50387
3	30	28.6	24	2	T42442
4	28.5	27.1	24	2	B42224
5	27	25.7	23	2	D25865
6	26	24.8	18	2	A59396
7	26	24.8	20	2	D40728
8	26	24.8	20	2	D42842
9	26	24.8	20	2	PC1240
10	26	24.8	20	2	A61506
11	26	24.8	23	2	PH1334
12	25	23.8	14	2	A35105
13	25	23.8	15	2	PA0110
14	25	23.8	20	2	A60372
15	25	23.8	20	2	A53592
16	25	23.8	25	2	A34921
17	24.5	23.3	20	2	PH1326
18	24	22.9	10	2	A31571
19	24	22.9	11	2	S41747
20	24	22.9	20	2	S21176
21	24	22.9	20	2	PC2347
22	24	22.9	20	2	JN0252
23	24	22.9	22	2	F23734
24	24	22.9	23	2	S13238
25	24	22.9	24	2	T42259
26	24	22.9	25	2	B53415
27	23.5	22.4	24	2	S35641
28	23	21.9	8	2	S11545
29	23	21.9	9	2	A24244

30 23 21.9 15 2 S20410 protein kinase (EC  
31 23 21.9 23 2 S65379 cytochrome-c oxida  
32 23 21.9 24 2 T42257 phosphoprotein pho  
33 22.5 21.4 25 2 S25434 gene CPA1 leader p  
34 22 21.0 5 2 S70615 endo-1,4-beta-xyla  
35 22 21.0 8 2 S16324 hypothetical prote  
36 22 21.0 13 2 S32471 lymnaDFamide 1 - g  
37 22 21.0 13 2 S32472 lymnaDFamide 2 - g  
38 22 21.0 13 2 S32474 lymnaDFamide 4 - g  
39 22 21.0 13 2 S32475 lymnaDFamide 5 - g  
40 22 21.0 14 2 B44854 L-2,4-diaminobuty  
41 22 21.0 16 2 JH0517 insulin-like growt  
42 22 21.0 17 2 S59481 hydroxyproline-ric  
43 22 21.0 20 2 A60812 plasma proteinase  
44 22 21.0 20 2 A56894 intracrySTALLINE c  
45 22 21.0 21 2 S68023 nucleoside-diphosp

## ALIGNMENTS

### RESULT 1

B61409 genome polyprotein (clone L3/S2) - Skalica virus (fragment)  
C;Species: Skalica virus

C;Date: 19-Mar-1997 #sequence\_revision 19-Dec-1997 #text\_change 17-Nov-2000  
C;Accession: B61409

R;Guirakhoo, F.; Heinz, F.X.; Mandl, C.W.; Holzmann, H.; Kunz, C.; Gresikova, M.  
J. Gen. Virol. 72, 333-338, 1991

A;Title: The relationship between the flaviviruses Skalica and Langat as revealed by mon

A;Reference number: A61409; MUID:91132129; PMID:1847173

A;Accession: B61409

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: genomic RNA

A;Residues: 1-19 <GUI>

C;Superfamily: yellow fever virus genome polyprotein

Query Match 32.4%; Score 34; DB 2; Length 19;  
Best Local Similarity 41.7%; Pred. No. 81;  
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 PPLSQFTFSDLW 12  
DB 2 PPVYRTGTDCW 13  
||:|:|:|:|

### RESULT 2

I50387 c-myc protein - chicken (fragment)

C;Species: Gallus gallus (chicken)

C;Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 21-Jul-2000

C;Accession: I50387

R;Westaway, D.; Payne, G.; Varmus, H.E.

Proc. Natl. Acad. Sci. U.S.A. 81, 843-847, 1984

A;Title: Proviral deletions and oncogene base-substitutions in insertional mutagenized

A;Reference number: I50387; MUID:84144799; PMID:6322173

A;Accession: I50387

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-24 <WES>

A;Cross-references: GB:K01440; NID:g212357; PIDN:AAA48964.1; PID:g212358

Query Match 31.4%; Score 33; DB 2; Length 24;  
Best Local Similarity 47.4%; Pred. No. 1.5e+02;  
Matches 9; Conservative 1; Mismatches 3; Indels 6; Gaps 2;

QY 1 PPLSQFTFSDLWK--LLP 16

DB 2 PPAPSE--DIWKKFELLP 17

### RESULT 3

T42442

protein phosphatase - Caenorhabditis elegans (fragment)  
 C:Species: Caenorhabditis elegans  
 C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 02-Jun-2000  
 C:Accession: T42442  
 R;Zeke, T.; Gergely, P.; Dombradi, V.  
 A:Submitted to the EMBL Data Library, July 1996  
 A:Description: The catalytic subunits of Ser/Thr protein phosphatases from Caenorhabditis elegans  
 A:Reference number: Z22025  
 A:Accession: T42442  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-24 <ZEK>  
 A:Cross-references: EMBL:Z77728; PIDN:CA801287.1  
 C:Superfamily: phosphoprotein phosphatase; phosphoesterase core homology; phosphoprotein

Query Match 28.6%; Score 30; DB 2; Length 24;  
 Best Local Similarity 58.3%; Pred. No. 4.2e+02;  
 Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
 QY 8 FSDLWKLPLNG 19  
 :||| |||  
 DB 2 YSLLALLELNG 13

RESULT 4  
 B42224  
 hypothetical protein (arg-2 5' region) - Neurospora crassa  
 C:Species: Neurospora crassa  
 C:Date: 19-Jun-1992 #sequence\_revision 19-Jun-1992 #text\_change 21-Jul-2000  
 C:Accession: B42224  
 R;Orbach, M.J.; Sachs, M.S.; Yanofsky, C.  
 J. Biol. Chem. 265, 10981-10987, 1990  
 A:Title: The Neurospora crassa arg-2 locus. Structure and expression of the gene encoding the arginine deiminase  
 A:Reference number: A42224; MUID:90293033; PMID:2141606  
 A:Accession: B42224  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-24 <ORB>  
 A:Cross-references: GB:J05512; NID:g168864; PIDN:AAA33610.1; PID:g168866

Query Match 27.1%; Score 28.5; DB 2; Length 24;  
 Best Local Similarity 53.8%; Pred. No. 7.1e+02;  
 Matches 7; Conservative 2; Mismatches 3; Indels 1; Gaps 1;  
 QY 4 SQETPSD-LWKL 15  
 :||| |||  
 DB 10 SQDYLSDLWRL 22

RESULT 5  
 D25865  
 gamma-crystallin IV - common carp (fragment)  
 C:Species: Cyprinus carpio (common carp)  
 C:Date: 02-Jun-1988 #sequence\_revision 02-Jun-1988 #text\_change 21-Nov-1997  
 C:Accession: D25865  
 R;Chou, S.H.; Chen, S.W.; Lo, T.B.  
 FEBS Lett. 209, 107-110, 1986  
 A:Title: The amino-terminal sequences of four major carp gamma-crystallin polypeptides  
 A:Reference number: A91369; MUID:87105907; PMID:3803569  
 A:Accession: D25865  
 A:Molecule type: protein  
 A:Residues: 1-23 <CHI>  
 A:Note: the residues 3-ile, 15-Asn, 17-Asp, 18-Cys, and 20-His were also found  
 C:Superfamily: beta-crystallin  
 C:Keywords: duplication

Query Match 25.7%; Score 27; DB 2; Length 23;  
 Best Local Similarity 75.0%; Pred. No. 1.1e+03;  
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 3 LSQETPSD 10  
 :||| |||  
 DB 14 LSYETMSD 21

## RESULT 6

A59396

Tha P 1 - Thaumetopoea pityocampa (fragment)

C:Species: Thaumetopoea pityocampa

C:Date: 03-Jun-2002 #sequence\_revision 03-Jun-2002 #text\_change 03-Jun-2002

C:Accession: A59396

R;Moneo, I.

A:Submitted to the Protein Sequence Database, September 2001

A:Description: Isolation and characterization of a major allergen of the pine processionary moth

A:Reference number: A59396

A:Accession: A59396

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-18 &lt;MON&gt;

A:Experimental source: I5

A:Note: IGE-binding protein, major allergen

Query Match 24.8%; Score 26; DB 2; Length 18;  
 Best Local Similarity 38.5%; Pred. No. 1.2e+03;  
 Matches 5; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 6 ETFSDLWKLLEN 18

||| |||

DB 2 ETYSKDYTDVNV 14

## RESULT 7

A60728

cytochrome P450 3A, troleanomycin-induced - sheep (fragment)

N:Contains: oxidoreductase (EC 1.-.-.-)

C:Species: Ovis sp. (sheep)

C:Date: 14-May-1993 #sequence\_revision 14-May-1993 #text\_change 05-Mar-1999

C:Accession: A60728

R;Pineau, T.; Galtier, P.; Bonfils, C.; Derancourt, J.; Maurel, P.

Biochem. Pharmacol. 39, 901-909, 1990

A:Title: Purification of a sheep liver cytochrome P-450 from the P450IIIa gene subfamily

A:Reference number: A60728; MUID:90179800; PMID:2310415

A:Accession: A60728

A:Molecule type: protein

A:Residues: 1-20 &lt;PIN&gt;

A:Comment: This cytochrome P450 isozyme is a member of the P450IIIa family but is not found in sheep

C:Genetics:

A:Gene: CYP3A

C:Superfamily: human cytochrome P450 CYP3A5; cytochrome P450 homology

C:Keywords: electron transfer; endoplasmic reticulum; heme; monooxygenase; oxidoreductase

Query Match 24.8%; Score 26; DB 2; Length 20;  
 Best Local Similarity 46.7%; Pred. No. 1.4e+03;  
 Matches 7; Conservative 1; Mismatches 3; Indels 4; Gaps 1;

QY 1 PPLSQETPSDLWKL 15

||| |||

DB 5 PSFSKET----WVLL 15

## RESULT 8

D42842

antifungal 2S storage albumin large chain - radish (fragment)

C:Species: Raphanus sativus (radish)

C:Date: 27-Apr-1993 #sequence\_revision 18-Nov-1994 #text\_change 12-Apr-1995

C:Accession: D42842

R;Terras, F.R.; Schoofs, H.M.; De Bolle, M.F.; Van Leuven, F.; Rees, S.B.; Vanderleyden,

J. Biol. Chem. 267, 15301-15309, 1992

A:Title: Analysis of two novel classes of plant antifungal proteins from radish (Raphanus

A:Reference number: A42842; MUID:92348373; PMID:1639777

A:Accession: D42842

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-20 &lt;TER&gt;

A:Experimental source: seed

A:Note: sequence extracted from NCBI backbone (NCBI:109925)



C;Superfamily: wheat alpha-amylase inhibitor

Query Match 24.8%; Score 26; DB 2; Length 20;  
Best Local Similarity 45.5%; Pred. No. 1.4e+03;  
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 PPLSQETFSDL 11  
||| | : :  
Db 8 PPLQQCCNNL 18

# RESULT 9

PC1240  
Calcium-binding protein, 53K - spinach (fragment)  
C;Species: Spinacia oleracea (spinach)  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 23-Aug-1997  
C;Accession: PC1240; PC1241  
R;Menegazzi, P.; Guzzo, F.; Balzan, B.; Mariani, P.; Treves, S.  
Biochem. Biophys. Res. Commun. 190, 1130-1135, 1993  
A;Title: Purification of calreticulin-like protein(s) from spinach leaves.  
A;Reference number: PC1240; MUID:93176159; PMID:8439313  
A;Accession: PC1240  
A;Molecule type: protein  
A;Residues: 1-20 <MEN>  
A;Experimental source: leaf  
A;Note: 53K form  
A;Accession: PC1241  
A;Molecule type: protein  
A;Residues: 1-20 <ME2>  
A;Experimental source: leaf  
A;Note: 55K form  
C;Superfamily: calreticulin  
C;Keywords: calcium binding; metal binding

Query Match 24.8%; Score 26; DB 2; Length 20;  
Best Local Similarity 44.4%; Pred. No. 1.4e+03;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 QETFSDLWK 13  
: | | | :  
Db 5 EERFEDGWE 13

# RESULT 10

alpha-1-antitrypsin - golden hamster (fragment)  
C;Species: Mesocricetus auratus (golden hamster)  
C;Date: 15-Oct-1994 #sequence\_revision 15-Oct-1994 #text\_change 11-May-2000  
C;Accession: A61506  
R;Amemiya, S.; Yamamoto, K.; Sinohara, H.  
Comp. Biochem. Physiol. B 100, 293-296, 1991  
A;Title: Purification, characterization, and acute phase response of plasma alpha-1-antitrypsin from golden hamster.  
A;Reference number: A61506; MUID:92191572; PMID:1724745  
A;Accession: A61506  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-20 <AME>

Query Match 24.8%; Score 26; DB 2; Length 20;  
Best Local Similarity 60.0%; Pred. No. 1.4e+03;  
Matches 6; Conservative 1; Mismatches 1; Indels 2; Gaps 1;

QY 4 SQETFSDLWK 13  
: | | | :  
Db 3 AQET--DAWK 10

# RESULT 11

PHI334  
Ig heavy chain DJ region (clone C280-120) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
C;Accession: PHI334

R;Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.  
J. Exp. Med. 176, 1577-1581, 1992  
A;Title: Predominance of fetal type DJH joining in young children with B precursor lymphoma.  
A;Reference number: PHI302; MUID:93094761; PMID:1460419  
A;Accession: PHI334

A;Molecule type: DNA  
A;Residues: 1-23 <WAS>  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin

Query Match 24.8%; Score 26; DB 2; Length 23;  
Best Local Similarity 33.3%; Pred. No. 1.8e+03;  
Matches 4; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLW 12  
||| | : | :  
Db 8 PPVYVYVMDVM 19

# RESULT 12

A35105  
hypothetical protein - Neurospora crassa mitochondrion (fragment)  
C;Species: mitochondrion Neurospora crassa  
C;Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 07-Dec-1999  
C;Accession: A35105  
R;Saville, B.J.; Collins, R.A.  
Cell 61, 685-696, 1990

A;Title: A site-specific self-cleavage reaction performed by a novel RNA in neurospora crassa.  
A;Reference number: A35105; MUID:90263093; PMID:2160856  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: DNA  
A;Residues: 1-14 <SAV>  
C;Genetics:  
A;Genome: mitochondrion  
A;Genetic code: SGC3  
C;Keywords: mitochondrion

Query Match 23.8%; Score 25; DB 2; Length 14;  
Best Local Similarity 54.5%; Pred. No. 1.3e+03;  
Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 9 SDLWKLLPENG 19  
||| | : | :  
Db 2 SFLWTLQLKG 12

# RESULT 13

PA0110  
translation elongation factor eEF-1 beta' chain - Arabidopsis thaliana (fragment)  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 07-Apr-1995 #sequence\_revision 26-May-1995 #text\_change 26-Apr-1996  
C;Accession: PA0110  
R;Kamo, M.; Kawakami, T.; Tsugita, A.  
submitted to JIPID, March 1995  
A;Reference number: PA0109  
A;Accession: PA0110  
A;Molecule type: protein  
A;Residues: 1-15 <KAW>

Query Match 23.8%; Score 25; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 TFSDL 11  
||| | : | :  
Db 3 TFSDL 7

# RESULT 14

A60372  
pollen allergen Poa-pi - Kentucky bluegrass (fragment)  
C;Species: Poa pratensis (Kentucky bluegrass)

C;Date: 11-Feb-1993 #sequence\_revision 11-Feb-1993 #text\_change 09-Jun-2000  
 C;Accession: A60372; A33086  
 R;Ekramoddoullah, A.K.M.  
 Int. Arch. Allergy Appl. Immunol. 93, 371-377, 1990  
 A;Title: Two-dimensional gel electrophoretic analyses of Kentucky bluegrass and rye grass  
 A;Reference number: A60372; PMID:91317571; PMID:2101126  
 A;Accession: A60372  
 A;Molecule type: protein  
 A;Residues: 1-20 <BR>  
 C;Superfamily: expansin  
 C;Keywords: hydroxyproline; pollen  
 F;5,8/Modified site: hydroxyproline (Pro) #status experimental

Query Match 23.8%; Score 25; DB 2; Length 20;  
 Best Local Similarity 36.4%; Pred. No. 2e+03;  
 Matches 4; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 2 PLSQETFSDLW 12  
 | | | | |  
 DB 8 PXITATYGDKW 18

RESULT 15  
 A53592  
 H+-exporting ATPase (EC 3.6.3.6) 24k chain - Thermus aquaticus (fragment)  
 C;Species: Thermus aquaticus  
 C;Date: 01-Dec-1995 #sequence\_revision 01-Dec-1995 #text\_change 03-Jun-2002  
 C;Accession: A53592  
 R;Yokoyama, K.; Akabane, Y.; Ishii, N.; Yoshida, M.  
 J. Biol. Chem. 269, 12248-12253, 1994  
 A;Title: Isolation of prokaryotic V-OV-1-ATPase from a thermophilic eubacterium Thermus  
 A;Reference number: A53592; PMID:94216345; PMID:8163530  
 A;Accession: A53592  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-20 <YOK>  
 C;Keywords: hydrolase

Query Match 23.8%; Score 25; DB 2; Length 20;  
 Best Local Similarity 46.2%; Pred. No. 2e+03;  
 Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 3 LSQETFSDLWKLL 15  
 | | | | |  
 DB 7 LSQVEAEIQALL 19

Search completed: February 12, 2003, 11:15:31  
 Job time : 21.5833 secs

GenCore version 5.1.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 12, 2003, 10:43:13 ; Search time 30 Seconds  
(without alignments)  
18.635 Million cell updates/sec

Title: US-09-403-440A-2

Perfect score: 105

Sequence: 1 PPLSQTFTSLWKLLPENG 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 127244

Minimum DB seq length: 0  
Maximum DB seq length: 19

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*
- 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*
- 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*
- 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*
- 5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pcp:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	90	85.7	19	4	US-09-081-975-13
2	77	73.3	15	1	US-08-277-660A-1
3	77	73.3	15	1	US-08-277-660A-4
4	77	73.3	15	1	US-08-424-957-1
5	77	73.3	15	1	US-08-424-957-20
6	77	73.3	15	4	US-09-035-686-1
7	77	73.3	15	4	US-09-035-686-20
8	74	70.5	15	1	US-08-277-660A-5
9	74	70.5	15	1	US-08-424-957-21
10	74	70.5	15	4	US-09-035-686-21
11	74	70.5	15	4	US-09-081-975-23
12	65	61.9	15	3	US-09-280-047-6
13	65	61.9	15	4	US-08-208-573B-6
14	65	61.9	15	5	PCT-US95-02856-6
15	60	57.1	18	4	US-09-081-975-22
16	59	56.2	11	1	US-08-277-660A-9
17	59	56.2	11	1	US-08-424-957-17
18	59	56.2	11	4	US-09-035-686-17
19	59	56.2	13	4	US-09-236-415-5
20	57	54.3	11	1	US-08-424-957-45
21	57	54.3	11	1	US-08-424-957-46
22	57	54.3	11	4	US-09-035-686-45
23	57	54.3	11	4	US-09-035-686-46
24	57	54.3	14	4	US-09-400-653A-7
25	57	54.3	14	4	US-09-248-061B-7
26	56	53.3	11	1	US-08-277-660A-10
27	56	53.3	11	1	US-08-277-660A-15

28 56 53.3 11 1 US-08-424-957-23 Sequence 23, Appl  
29 56 53.3 11 1 US-08-424-957-28 Sequence 28, Appl  
30 56 53.3 11 1 US-08-424-957-40 Sequence 40, Appl  
31 56 53.3 11 4 US-09-035-686-23 Sequence 23, Appl  
32 56 53.3 11 4 US-09-035-686-28 Sequence 28, Appl  
33 56 53.3 11 4 US-09-035-686-40 Sequence 40, Appl  
34 55 52.4 10 1 US-08-277-660A-7 Sequence 7, Appl  
35 55 52.4 10 1 US-08-424-957-11 Sequence 11, Appl  
36 55 52.4 10 4 US-09-035-686-11 Sequence 11, Appl  
37 55 52.4 11 1 US-08-277-660A-20 Sequence 20, Appl  
38 55 52.4 11 1 US-08-424-957-33 Sequence 33, Appl  
39 55 52.4 11 1 US-08-424-957-34 Sequence 34, Appl  
40 55 52.4 11 1 US-08-424-957-35 Sequence 35, Appl  
41 55 52.4 11 1 US-08-424-957-36 Sequence 36, Appl  
42 55 52.4 11 1 US-08-424-957-42 Sequence 42, Appl  
43 55 52.4 11 4 US-09-035-686-33 Sequence 33, Appl  
44 55 52.4 11 4 US-09-035-686-34 Sequence 34, Appl  
45 55 52.4 11 4 US-09-035-686-35 Sequence 35, Appl

## ALIGNMENTS

RESULT 1  
US-09-081-975-13  
; Sequence 13, Application US/09081975  
; Patent No. 6451979  
; GENERAL INFORMATION:  
; APPLICANT: Kaelin, William  
; APPLICANT: Jost, Christine  
; TITLE OF INVENTION: METHODS OF TREATMENT USING  
; TITLE OF INVENTION: NBS-1, ANTIBODIES AND PROTEINS THEREO, AND USES OF THE  
; TITLE OF INVENTION: ANTIBODIES  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Nixon Peabody LLP  
; STREET: 101 Federal Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/081,975  
; FILING DATE: 12-MAY-1998  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/046,207  
; FILING DATE: 12-MAY-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Eisenstein, Ronald I  
; REGISTRATION NUMBER: 30,628  
; REFERENCE/DOCKET NUMBER: 47400  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-345-6054  
; TELEFAX: 617-345-1300  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 19 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-09-081-975-13

Query Match 85.7%; Score 90; DB 4; Length 19;  
Best Local Similarity 88.9%; Pred. No. 4.2e-08;  
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
QY 1 PPLSQETFSDLWKLLPEN 18
    |||||:|||||
Db 1 PPLSQETFSDLWKLLPEN 18

RESULT 2
US-08-277-660A-1
; Sequence 1, Application US/08277660A
; Patent No. 5702908
; GENERAL INFORMATION:
; APPLICANT: Pickesley, Steven M.
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 20-JUL-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Dregler, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-60244/WHd
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-277-660A-4

Query Match 73.3%; Score 77; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.8e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLL 14
    |||||
Db 2 PPLSQETFSDLWKLL 15
    |||||

RESULT 4
US-08-424-957-1
; Sequence 1, Application US/08424957
; Patent No. 5770377
; GENERAL INFORMATION:
; APPLICANT: Pickesley, Steven M.
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 19-APR-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/277,660
; FILING DATE: 20-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dregler, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-61228/WHd
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:

QY 5 QETFSDLWKLLPEN 18
    |||||
Db 1 QETFSDLWKLLPEN 14

RESULT 3
US-08-277-660A-4
; Sequence 4, Application US/08277660A
; Patent No. 5702908
; GENERAL INFORMATION:
; APPLICANT: Pickesley, Steven M.
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
```

```

; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
US-08-424-957-1

```

Query Match 73.3%; Score 77; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.8e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels

Qy 5 QETFSDLWKLLPEN 18  
Db 1 QETFSDLWKLLPEN 14

## RESULTS

US-08-424-957-20  
; Sequence 20, Application US/08424957  
: Patent No. 5770377

/ Patent No. 57770377  
 / GENERAL INFORMATION:  
 / APPLICANT: Pickaley, Steven M.  
 / APPLICANT: Lane, David P.  
 / TITLE OF INVENTION: Interruption of Binding of WDM2 and P53  
 / TITLE OF INVENTION: Protein and Therapeutic Application Thereof  
 / NUMBER OF SEQUENCES: 50  
 / CORRESPONDENCE ADDRESS:  
 / ADDRESS: Flehr, Hobbach, Test, Albritton & Herbert  
 / STREET: Four Embarcadero Center, Suite 3400  
 / CITY: San Francisco  
 / STATE: California  
 / COUNTRY: United States  
 / ZIP: 94111-4187

Query Match 73.3%; Score 77; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. NO. 3.8e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels

Qy 1 PPLSQETFSDLWKL 14  
|||  
Db 2 PPLSOETFSDLWKL 15

RES. IT. 6

RESUMÉ 6  
US-09-035-686-1  
; Sequence 1, Application US/09035686  
; Patent No. 6153391

```

/ GENERAL INFORMATION:
/ APPLICANT: Pickseley, Steven M.
/ APPLICANT: Lane, David P.
/ TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
/ TITLE OF INVENTION: Protein and Therapeutic Application Thereof
/ NUMBER OF SEQUENCES: 50
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
/ STREET: Four Embarcadero Center, Suite 3400
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: United States
/ ZIP: 94111-4187
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent'n Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/035,686
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/424,957
/ FILING DATE: 19-APR-1995
/ APPLICATION NUMBER: US 08/277,660
/ FILING DATE: 20-JUL-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Dreger, Walter H.
/ REGISTRATION NUMBER: 24,190
/ REFERENCE/DOCKET NUMBER: A-61228/WH/D
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 781-1989
/ TELEFAX: (415) 398-3249
/ TELEX: 910 277299
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 15 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: unknown
/
/ US-09-035-686-1

```

Query Match	73.3%;	Score 77;	DB 4;	Length 15;
Best Local Similarity	100.0%;	Pred. NO. 3.8e-06;		
Matches 14;	Conservative	0;	Mismatches 0;	Indels 0;
				Gaps 0;

Qy 5 QETFSDLWKLLEN 18  
| | | | | | | | | |  
Db 1 OETFSDLWKLLEN 14

## RESULT, T 7

US-09-035-686-20  
Sequence 20, Application US/09035686  
Patent No. 6153391  
GENERAL INFORMATION:  
APPLICANT: Picketsley, Steven M.  
APPLICANT: Lane, David P.  
TITLE OF INVENTION: Interruption of Binding of MDM2 and p53  
TITLE OF INVENTION: Protein and Therapeutic Application Thereof  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert  
STREET: Four Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: United States  
ZIP: 94111-4187  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS



```
/ APPLICANT: Lane, David P.
/ TITLE OF INVENTION: Interruption of Binding of MDM2 and p53
/ TITLE OF INVENTION: Protein and Therapeutic Application Thereof
/ NUMBER OF SEQUENCES: 50
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
/ STREET: Four Embarcadero Center, Suite 3400
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: United States
/ ZIP: 94111-4187
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/035,686
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/424,957
/ FILING DATE: 19-APR-1995
/ APPLICATION NUMBER: US 08/277,660
/ FILING DATE: 20-JUL-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Dreger, Walter H.
/ REGISTRATION NUMBER: 24,190
/ REFERENCE/DOCKET NUMBER: A-61228/WHd
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 781-1989
/ TELEFAX: (415) 398-3249
/ TELEX: 910 277299
/ INFORMATION FOR SEQ ID NO: 21:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 15 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: unknown
/ US-09-035-686-21

Query Match 70.5%; Score 74; DB 4; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.2e-05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PLSQETFSDLWLKLP 16
Db 1 PLSQETFSGLWLKLP 15

RESULT 11
US-09-081-975-23
/ Sequence 23, Application US/09081975
/ Patent No. 6451979
/ GENERAL INFORMATION:
/ APPLICANT: Kaelin, William
/ APPLICANT: Jost, Christine
/ TITLE OF INVENTION: METHODS OF TREATMENT USING
/ TITLE OF INVENTION: NBS-1, ANTIBODIES AND PROTEINS THEREO, AND USES OF THE
/ TITLE OF INVENTION: ANTIBODIES
/ NUMBER OF SEQUENCES: 27
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Nixon Peabody LLP
/ STREET: 101 Federal Street
/ CITY: Boston
/ STATE: MA
/ COUNTRY: USA
/ ZIP: 02110
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: Windows
/ SOFTWARE: FastSeq for Windows Version 2.0b
```

```
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/081,975
/ FILING DATE: 12-MAY-1998
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 60/046,207
/ FILING DATE: 12-MAY-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Eisenstein, Ronald I
/ REGISTRATION NUMBER: 30,628
/ REFERENCE/DOCKET NUMBER: 47400
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 617-345-6054
/ TELEFAX: 617-345-1300
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 23:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 16 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-09-081-975-23

Query Match 70.5%; Score 74; DB 4; Length 16;
Best Local Similarity 81.2%; Pred. No. 1.2e-05;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PLSQETFSDLWLKLP 17
Db 1 PLSQETFEDLWSLLPD 16

RESULT 12
US-09-280-047-6
/ Sequence 6, Application US/09280047
/ Patent No. 6068462
/ GENERAL INFORMATION:
/ APPLICANT: GOUJELI, SAID A.
/ TITLE OF INVENTION: QUANTITATION OF INDIVIDUAL PROTEIN
/ TITLE OF INVENTION: KINASE ACTIVITY
/ NUMBER OF SEQUENCES: 10
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Ross & Stevens, S.C.
/ STREET: One South Pinckney Street, P.O. Box 2599
/ CITY: Madison
/ STATE: Wisconsin
/ COUNTRY: U.S.A.
/ ZIP: 53701-2599
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/280,047
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/208,573
/ FILING DATE: 04-MAR-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: SARA, CHARLES S.
/ REGISTRATION NUMBER: 30,492
/ REFERENCE/DOCKET NUMBER: 34506.006
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (608) 257-5353
/ TELEFAX: (608) 257-9175
/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 15 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
```

US-09-280-047-6

Query Match 61.9%; Score 65; DB 3; Length 15;  
Best Local Similarity 84.6%; Pred. No. 0.00031;  
Matches 11; Conservative 1; Mismatches 1; Indels

Qy	1	PPLSQETFS	DWLK	13
		:	:	:
Db	2	PPLSQEAFAD	LWK	14

RESULT 13

US-08-208-573B-6  
Sequence 6, Application US/08208573B  
Patent No. 6348310  
GENERAL INFORMATION:  
APPLICANT: GOUJELI, SAID A.  
TITLE OF INVENTION: QUANTITATION OF INDIVIDUAL PROTEIN  
KINASE ACTIVITY  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Ross & Stevens, S.C.  
STREET: One South Pinckney Street, P.O. Box 2599  
CITY: Madison  
STATE: Wisconsin  
COUNTRY: U.S.A.  
ZIP: 53701-2599  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/208,573B

Query Match 61.9%; Score 65; DB 4; Length 15;  
Best Local Similarity 84.6%; Pred. No. 0.00031;  
Matches 11; Conservative 1; Mismatches 1; Indels

Qy 1 PPLSQETFSDLWK 13  
||| :|||  
Db 2 PPLSQEAFADLWK 14

## RESULT 14

```

; PCRT-US95-02856-6
; Sequence 6, Application PC/TUS9502856
; GENERAL INFORMATION:
; APPLICANT: Goueli, Said A
; TITLE OF INVENTION: QUANTITATION OF INDIVIDUAL PROTEIN
; TITLE OF INVENTION: KINASE ACTIVITY
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSES: DeWitt Ross & Stevens, S.C.
; STREET: 8000 Excelsior Drive, Suite 401
; CITY: Madison

```

```

: STATE: WI
: COUNTRY: USA
: ZIP: 53717-1914
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC Compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US95/02856
: FILING DATE:
:

```

```
Query Match      61.9%; Score 65; DB 5; Length 15;
Best Local Similarity 84.6%; Pred. No. 0.00031;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

Qy 1 PPLSQETFSDLWK 13  
 ||||| :|||  
 Db 2 PPLSQEAFADLWK 14

RESULT 15

US-09-081-975-22  
; Sequence 22, Application US/09081975  
; Patent No. 6451979  
; GENERAL INFORMATION:  
; APPLICANT: Kaelin, William  
; APPLICANT: Jost, Christine  
; TITLE OF INVENTION: METHODS OF TREATMENT USING  
; TITLE OF INVENTION: NBS-1, ANTIBODIES AND PROTEINS THERETO, AND USES OF THE  
; TITLE OF INVENTION: ANTIBODIES  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Nixon Peabody LLP  
; STREET: 101 Federal Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/081,975  
; FILING DATE: 12-MAY-1998  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/046,207  
; FILING DATE: 12-MAY-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Eisenstein, Ronald I  
; REGISTRATION NUMBER: 30,628  
; REFERENCE/DOCKET NUMBER: 47400  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-345-6054  
; TELEFAX: 617-345-1300

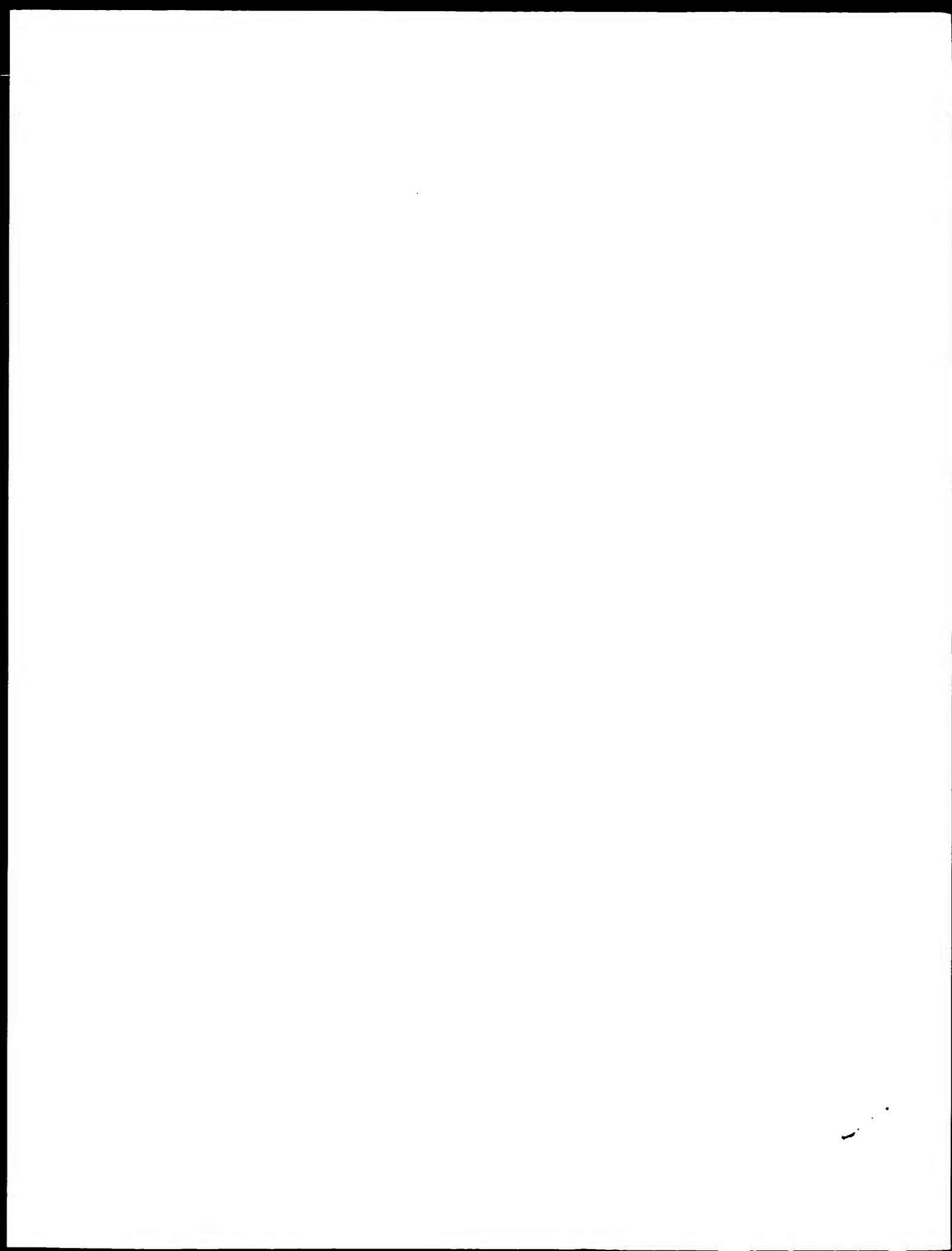


TELE:  
; INFORMATION FOR SEQ ID NO: 22:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-09-081-975-22

Query Match 57.1%; Score 60; DB 4; Length 18;  
Best Local Similarity 76.9%; Pred. No. 0.0024;  
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 2 PLSQETFSDLWKL 14  
| | | | | | | | | |  
Db 3 PLSQESFEDLWKM 15

Search completed: February 12, 2003, 10:46:27  
Job time : 30 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 12, 2003, 10:44:28 ; Search time 56 Seconds  
(without alignments)  
28.428 Million cell updates/sec

Title: US-09-403-440A-2

Perfect score: 105

Sequence: 1 PLSQETFSDLWKLLPEN 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425801 seqs, 83787487 residues

Total number of hits satisfying chosen parameters: 152190

Minimum DB seq length: 0

Maximum DB seq length: 19

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending Patents AA New.\*  
1: /cgn2\_6/prodata1/paa/PCT\_NEW\_COMB.pcp.\*  
2: /cgn2\_6/prodata1/paa/US06\_NEW\_COMB.pcp.\*  
3: /cgn2\_6/prodata1/paa/US07\_NEW\_COMB.pcp.\*  
4: /cgn2\_6/prodata1/paa/US08\_NEW\_COMB.pcp.\*  
5: /cgn2\_6/prodata1/paa/US09\_NEW\_COMB.pcp.\*  
6: /cgn2\_6/prodata1/paa/US10\_NEW\_COMB.pcp.\*  
7: /cgn2\_6/prodata1/paa/US60\_NEW\_COMB.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	92	87.6	19	7	US-60-438-805-9
2	81	77.1	15	6	US-10-211-088-141
3	70	66.7	13	5	US-09-701-080C-22
4	70	66.7	13	5	US-09-701-080C-27
5	59	56.2	11	5	US-09-189-702A-286
6	41	39.0	14	6	US-10-049-428-6
7	40	38.1	7	5	US-09-701-080C-12
8	35	33.3	14	6	US-10-049-428-7
9	31.5	30.0	14	6	US-10-268-332-53
10	31.5	30.0	16	6	US-10-225-567A-1177
11	31	29.5	9	5	US-09-189-702A-7
12	31	29.5	12	5	US-09-281-717A-31
13	31	29.5	12	5	US-09-281-717A-33
14	31	29.5	12	5	US-09-281-717A-35
15	31	29.5	12	5	US-09-830-693B-6
16	31	29.5	12	5	US-09-830-693B-8
17	30	28.6	16	6	US-10-348-131-49
18	29	27.6	15	6	US-10-169-026-3
19	29	27.6	16	6	US-10-225-567A-942
20	29	27.6	17	1	PCT-US02-28371-70
21	29	27.6	17	6	US-10-236-878-70
22	29	27.6	18	5	US-09-552-802B-30
23	28.5	27.1	18	5	US-09-632-036E-11
24	28	26.7	7	6	US-10-174-717A-36
25	28	26.7	16	7	US-60-427-045-297
26	28	26.7	18	6	US-10-283-599-219

```

27 26.7 18 6 US-10-232-410-9 Sequence 9, Appli
28 25.7 9 5 US-09-641-528-25751 Sequence 25751, A
29 25.7 9 5 US-09-641-528-29042 Sequence 29042, A
30 25.7 9 5 US-09-641-528A-25751 Sequence 25751, A
31 25.7 9 5 US-09-641-528A-29042 Sequence 29042, A
32 25.7 9 6 US-10-029-206A-67 Sequence 67, Appl
33 25.7 9 6 US-10-301-644-18 Sequence 18, Appl
34 25.7 9 6 US-10-028-075B-67 Sequence 67, Appl
35 25.7 10 5 US-09-641-528-463 Sequence 463, App
36 25.7 10 5 US-09-641-528-1442 Sequence 1442, App
37 25.7 10 5 US-09-641-528-12880 Sequence 12880, A
38 25.7 10 5 US-09-641-528-15661 Sequence 15661, A
39 25.7 10 5 US-09-641-528-25791 Sequence 25791, A
40 25.7 10 5 US-09-641-528-29085 Sequence 29085, A
41 25.7 10 5 US-09-641-528A-463 Sequence 463, App
42 25.7 10 5 US-09-641-528A-1442 Sequence 1442, App
43 25.7 10 5 US-09-641-528A-12880 Sequence 12880, A
44 25.7 10 5 US-09-641-528A-15661 Sequence 15661, A
45 25.7 10 5 US-09-641-528A-25791 Sequence 25791, A

```

## ALIGNMENTS

```

RESULT 1
US-60-438-805-9
; Sequence 9, Application US/60438805
; GENERAL INFORMATION:
; APPLICANT: KODADEK, THOMAS
; TITLE OF INVENTION: MIXED ELEMENT CAPTURE AGENTS
; FILE REFERENCE: UTSD:93SUSP1
; CURRENT APPLICATION NUMBER: US/60/438,805
; CURRENT FILING DATE: 2003-01-09
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 9
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-60-438-805-9

```

```

Query Match 87.6%; Score 92; DB 7; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.5e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLSQETFSDLWKLLPEN 18
Db 1 PLSQETFSDLWKLLPEN 17

RESULT 2
US-10-211-088-141
; Sequence 141, Application US/10211088
; GENERAL INFORMATION:
; APPLICANT: Bright, Gary R.
; APPLICANT: Premkumar, D. David
; TITLE OF INVENTION: Novel Fusion Proteins And Assays For Molecular Binding
; FILE REFERENCE: 01-1022-US
; CURRENT APPLICATION NUMBER: US/10/211,088
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/309,395
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/341,589
; PRIOR FILING DATE: 2001-12-13
; NUMBER OF SEQ ID NOS: 366
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 141
; LENGTH: 15
; TYPE: PRT

```

```

; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Binding domain
US-10-211-088-141

Query Match      77.1%; Score 81; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLL 15
Db 1 PPLSQETFSDLWKLL 15

RESULT 3
US-09-701-080C-22
; Sequence 22, Application US/09701080C
; GENERAL INFORMATION:
; APPLICANT: INSTITUTE OF MOLECULAR AND CELL BIOLOGY
; TITLE OF INVENTION: POLYPEPTIDES FROM CREB BINDING PROTEIN AND RELATED PROTEIN P300
; FILE REFERENCE: N73477C GCW
; CURRENT APPLICATION NUMBER: US/09/701,080C
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: GB 9811303.8
; PRIOR FILING DATE: 1998-05-26
; PRIOR APPLICATION NUMBER: GB 9900157.0
; PRIOR FILING DATE: 1999-01-05
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: derived from p53
US-09-701-080C-22

Query Match      66.7%; Score 70; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.6e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SQETFSDLWKLLP 16
Db 1 SQETFSDLWKLLP 13

RESULT 4
US-09-701-080C-27
; Sequence 27, Application US/09701080C
; GENERAL INFORMATION:
; APPLICANT: INSTITUTE OF MOLECULAR AND CELL BIOLOGY
; TITLE OF INVENTION: POLYPEPTIDES FROM CREB BINDING PROTEIN AND RELATED PROTEIN P300
; FILE REFERENCE: N73477C GCW
; CURRENT APPLICATION NUMBER: US/09/701,080C
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: GB 9811303.8
; PRIOR FILING DATE: 1998-05-26
; PRIOR APPLICATION NUMBER: GB 9900157.0
; PRIOR FILING DATE: 1999-01-05
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: derived from p53
US-09-701-080C-27

Query Match      66.7%; Score 70; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.6e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SQETFSDLWKLLP 16
Db 1 SQETFSDLWKLLP 13

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 4 SQETFSDLWKLLP 16
Db 1 SQETFSDLWKLLP 13

RESULT 5
US-09-189-702A-286
; Sequence 286, Application US/09189702A
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Kast, W. Martin
; APPLICANT: Southwood, Scott
; APPLICANT: Epimmune, Inc.
; TITLE OF INVENTION: HLA Binding Peptides and Their Uses
; FILE REFERENCE: 39963-20019.20
; CURRENT APPLICATION NUMBER: US/09/189,702A
; CURRENT FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 286
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: p53.14 peptide 34.0324
US-09-189-702A-286

Query Match      56.2%; Score 59; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0046;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LSQETFSDLWK 13
Db 1 LSQETFSDLWK 11

RESULT 6
US-10-049-428-6
; Sequence 6, Application US/10049428
; GENERAL INFORMATION:
; APPLICANT: Charles, Ian G.
; APPLICANT: Xu, Weiming
; APPLICANT: Liu, Lizhi
; TITLE OF INVENTION: Unducible Screen for Drug Discovery
; FILE REFERENCE: HO-P02380USO
; CURRENT APPLICATION NUMBER: US/10/049,428
; CURRENT FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: GB 9918077
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: GB 0016171.1
; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 14
; TYPE: PRT
; ORGANISM: HUMAN
; OTHER INFORMATION:
US-10-049-428-6

Query Match      39.0%; Score 41; DB 6; Length 14;
Best Local Similarity 69.2%; Pred. No. 4.3;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWK 13
Db 2 PPLSQEAFALLKK 14

```

RESULT 7  
 US-09-701-080C-12  
 ; Sequence 12, Application US/09701080C  
 ; GENERAL INFORMATION:  
 ; APPLICANT: INSTITUTE OF MOLECULAR AND CELL BIOLOGY  
 ; TITLE OF INVENTION: POLYPEPTIDES FROM CREB BINDING PROTEIN AND RELATED PROTEIN P300  
 ; FILE REFERENCE: N73477C GCW  
 ; CURRENT APPLICATION NUMBER: US/09/701,080C  
 ; CURRENT FILING DATE: 2001-02-27  
 ; PRIOR FILING DATE: 1998-05-26  
 ; PRIOR FILING DATE: 1998-05-26  
 ; PRIOR FILING DATE: 1999-01-05  
 ; NUMBER OF SEQ ID NOS: 36  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 12  
 ; LENGTH: 7  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: derived from p53  
 US-09-701-080C-12

Query Match 38.1%; Score 40; DB 5; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 8 FSDWLK 14  
 Db 1 FSDWLK 7

RESULT 8  
 US-10-049-428-7  
 ; Sequence 7, Application US/10049428  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Charles, Ian G.  
 ; APPLICANT: Xu, Weiming  
 ; APPLICANT: Liu, Lizhi  
 ; TITLE OF INVENTION: Undruggable Screen for Drug Discovery  
 ; FILE REFERENCE: HO-P02380US0  
 ; CURRENT APPLICATION NUMBER: US/10/049,428  
 ; CURRENT FILING DATE: 2000-07-28  
 ; PRIOR FILING DATE: 1999-07-30  
 ; PRIOR FILING DATE: 1999-07-30  
 ; PRIOR FILING DATE: 2000-06-30  
 ; NUMBER OF SEQ ID NOS: 7  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 7  
 ; LENGTH: 14  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Mutagen  
 US-10-049-428-7

Query Match 33.3%; Score 35; DB 6; Length 14;  
 Best Local Similarity 53.8%; Pred. No. 38;  
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 PPLSQETFSDLWK 13  
 Db 2 PPLSEQAFALLKK 14

RESULT 9  
 US-10-268-332-53  
 ; Sequence 53, Application US/10268332  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bristol-Myers Squibb Company  
 ; TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRTMY3, EXPRESSED HIGHLY

; TITLE OF INVENTION: IMMUNE- AND COLON- RELATED TISSUES  
 ; FILE REFERENCE: D0042A CIP  
 ; CURRENT APPLICATION NUMBER: US/10/268,332  
 ; CURRENT FILING DATE: 2002-10-10  
 ; PRIOR FILING DATE: 2000-09-27  
 ; PRIOR FILING DATE: 2000-09-27  
 ; PRIOR FILING DATE: 2001-01-16  
 ; PRIOR FILING DATE: 2001-01-16  
 ; PRIOR FILING DATE: 2001-07-13  
 ; PRIOR FILING DATE: 2001-07-13  
 ; PRIOR FILING DATE: 2001-08-17  
 ; PRIOR FILING DATE: 2001-08-17  
 ; PRIOR FILING DATE: 2001-09-26  
 ; NUMBER OF SEQ ID NOS: 66  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 53  
 ; LENGTH: 14  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-268-332-53

Query Match 30.0%; Score 31.5; DB 6; Length 14;  
 Best Local Similarity 77.8%; Pred. No. 1.4e+02;  
 Matches 7; Conservative 1; Mismatches 0; Indels 1; Gaps 1;  
 QY 6 ETFSDELWK 13  
 Db 5 ESFDELWK 13

RESULT 10  
 US-10-225-567A-1177  
 ; Sequence 1177, Application US/10225567A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: LifeSpan Biosciences  
 ; APPLICANT: Brown, Joseph P.  
 ; APPLICANT: Burmer, Glenna C.  
 ; APPLICANT: Roush, Christine L.  
 ; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS  
 ; FILE REFERENCE: 1920-4-4  
 ; CURRENT APPLICATION NUMBER: US/10/225,567A  
 ; CURRENT FILING DATE: 2001-12-19  
 ; PRIOR FILING DATE: 2001-12-19  
 ; PRIOR FILING DATE: 2000-12-19  
 ; NUMBER OF SEQ ID NOS: 2292  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 1177  
 ; LENGTH: 16  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-225-567A-1177

Query Match 30.0%; Score 31.5; DB 6; Length 16;  
 Best Local Similarity 53.3%; Pred. No. 1.6e+02;  
 Matches 8; Conservative 2; Mismatches 2; Indels 3; Gaps 1;  
 QY 4 SQETFSDELWKLPEN 18  
 Db 5 SQENHNS---RILPEN 16

RESULT 11  
 US-09-189-702A-7  
 ; Sequence 7, Application US/09189702A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Sette, Alessandro  
 ; APPLICANT: Sidney, John  
 ; APPLICANT: Kast, W. Martin  
 ; APPLICANT: Southwood, Scott  
 ; APPLICANT: Epimmune, Inc.  
 ; TITLE OF INVENTION: HLA Binding Peptides and Their Uses  
 ; FILE REFERENCE: 39963-20019.20

```

; CURRENT APPLICATION NUMBER: US/09/189,702A
; CURRENT FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: p53.24V9 peptide 1323.02
US-09-189-702A-7

Query Match      29.5%; Score 31; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 KLLPEN 18
Db 1 KLLPEN 6

```

```

RESULT 12
US-09-281-717A-31
; Sequence 31, Application US/09281717A
; GENERAL INFORMATION:
; APPLICANT: Baxter, John
; APPLICANT: Darimont, Beatrice
; APPLICANT: Feng, Weijun
; APPLICANT: Fletcher, Robert
; APPLICANT: Kushner, Peter
; APPLICANT: West, Brian
; APPLICANT: Yamamoto, Keith
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING NUCLEAR RECEPTOR
; FILE REFERENCE: 9811-008-999
; CURRENT APPLICATION NUMBER: US/09/281,717A
; CURRENT FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: US 60/079,956
; PRIOR FILING DATE: 1998-03-30
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 31
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: MUTAGEN
; LOCATION: (5)..(5)
; OTHER INFORMATION: Leu --> Arg (L454R)
; FEATURE:
; NAME/KEY: MUTAGEN
; LOCATION: (7)..(7)
; OTHER INFORMATION: Leu --> Arg (L456R)
; FEATURE:
; NAME/KEY: MUTAGEN
; LOCATION: (8)..(8)
; OTHER INFORMATION: Glu --> Lys (E457K)
US-09-281-717A-31

Query Match      29.5%; Score 31; DB 5; Length 12;
Best Local Similarity 60.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 PPLSQETFS 10
Db 3 PPLFLEVFED 12

```

```

RESULT 13
US-09-281-717A-33

```

```

; Sequence 33, Application US/09281717A
; GENERAL INFORMATION:
; APPLICANT: Baxter, John
; APPLICANT: Darimont, Beatrice
; APPLICANT: Feng, Weijun
; APPLICANT: Fletcher, Robert
; APPLICANT: Kushner, Peter
; APPLICANT: West, Brian
; APPLICANT: Wagner, Richard
; APPLICANT: Yamamoto, Keith
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING NUCLEAR RECEPTOR
; FILE REFERENCE: 9811-008-999
; CURRENT APPLICATION NUMBER: US/09/281,717A
; CURRENT FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: US 60/079,956
; PRIOR FILING DATE: 1998-03-30
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 33
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-281-717A-33

```

```

Query Match      29.5%; Score 31; DB 5; Length 12;
Best Local Similarity 60.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

```

Qy 1 PPLSQETFS 10
Db 3 PPLFLEVFED 12

```

```

RESULT 14
US-09-281-717A-35
; Sequence 35, Application US/09281717A
; GENERAL INFORMATION:
; APPLICANT: Baxter, John
; APPLICANT: Darimont, Beatrice
; APPLICANT: Feng, Weijun
; APPLICANT: Fletcher, Robert
; APPLICANT: Kushner, Peter
; APPLICANT: West, Brian
; APPLICANT: Wagner, Richard
; APPLICANT: Yamamoto, Keith
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING NUCLEAR RECEPTOR
; FILE REFERENCE: 9811-008-999
; CURRENT APPLICATION NUMBER: US/09/281,717A
; CURRENT FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: US 60/079,956
; PRIOR FILING DATE: 1998-03-30
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 35
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-281-717A-35

```

```

Query Match      29.5%; Score 31; DB 5; Length 12;
Best Local Similarity 60.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 PPLSQETFS 10
Db 3 PPLFLEVFED 12

```

```

RESULT 15
US-09-830-693B-6
; Sequence 6, Application US/09830693B

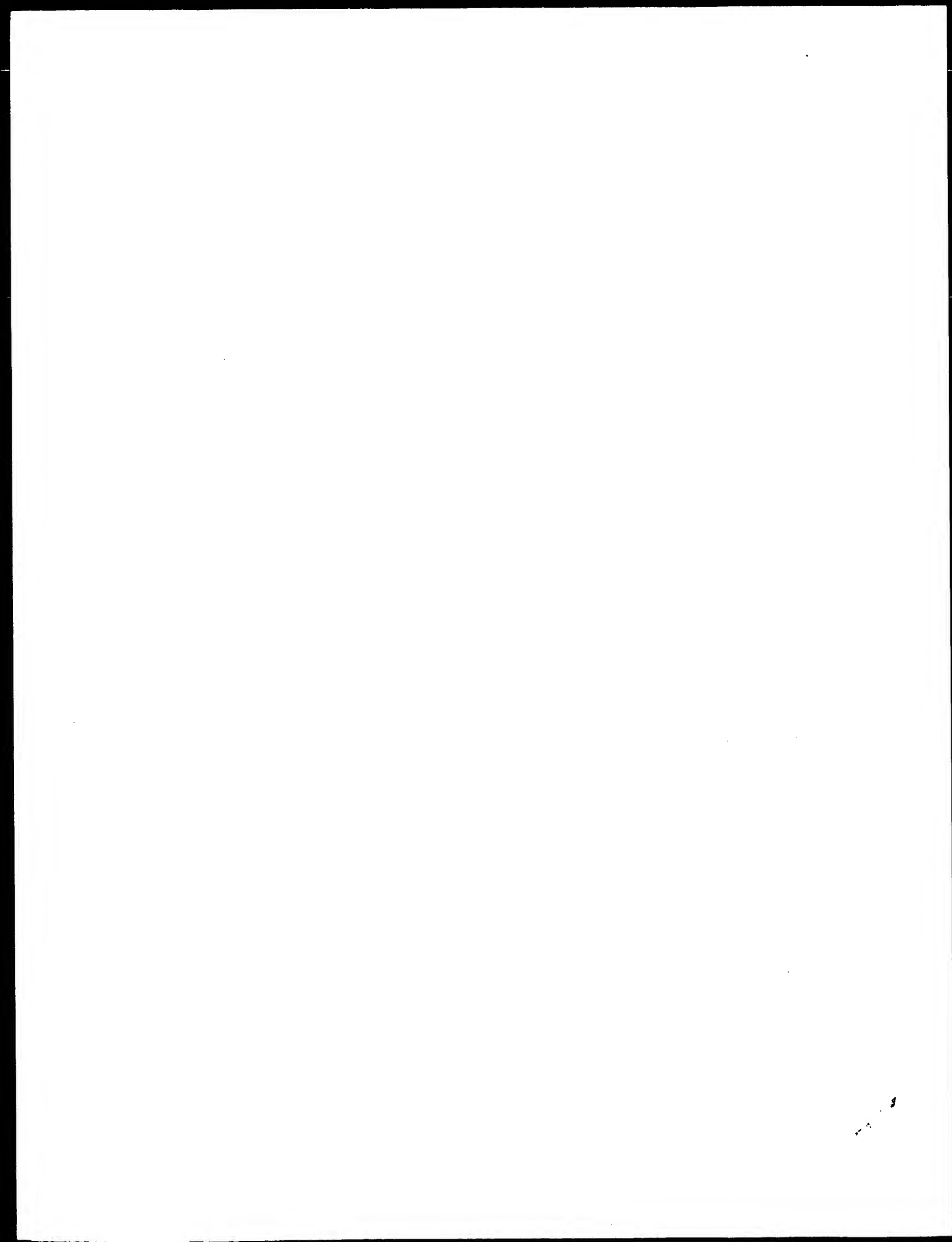
```

GENERAL INFORMATION:  
; APPLICANT: Shiau, Andrew  
; APPLICANT: Kushner, Peter  
; APPLICANT: Agard, David  
; APPLICANT: Greene, Geoffrey  
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING NUCLEAR RECEPTOR  
; TITLE OF INVENTION: ACTIVITY  
; FILE REFERENCE: 9811-013-999  
; CURRENT APPLICATION NUMBER: US/09/830,693B  
; CURRENT FILING DATE: 2002-01-29  
; PRIOR APPLICATION NUMBER: PCT/US99/06937  
; PRIOR FILING DATE: 1999-03-30  
; PRIOR APPLICATION NUMBER: US 60/079,956  
; PRIOR FILING DATE: 1998-03-30  
; PRIOR APPLICATION NUMBER: US 60/113,146  
; PRIOR FILING DATE: 1998-12-16  
; PRIOR APPLICATION NUMBER: US 60/113,014  
; PRIOR FILING DATE: 1998-12-16  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-830-693B-6

Query Match 29.5%; Score 31; DB 5; Length 12;  
Best Local Similarity 60.0%; Pred. No. 1.4e+02;  
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 PPLSQTFSD 10  
Db 3 PPLFLEVFD 12

Search completed: February 12, 2003, 10:49:50  
Job time : 56 secs





GenCore version 5.1.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 12, 2003, 10:45:03 ; Search time 11 Seconds  
(without alignments)  
44.130 Million cell updates/sec

Title: US-09-403-440A-2

Perfect score: 105

Sequence: 1 PPLSQETFSDLWKLLPEN 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 140259 seqs, 25548876 residues

Total number of hits satisfying chosen parameters: 36726

Minimum DB seq length: 0

Maximum DB seq length: 19

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Databases :

Published Applications AA:\*

- 1: /cgn2\_6/prodata/1/pubpaa/US08 NEW PUB.pdb.\*
- 2: /cgn2\_6/prodata/1/pubpaa/US08 NEW PUB.pdb.\*
- 3: /cgn2\_6/prodata/1/pubpaa/US06 NEW PUB.pdb.\*
- 4: /cgn2\_6/prodata/1/pubpaa/US06 PUBCOMB.pdb.\*
- 5: /cgn2\_6/prodata/1/pubpaa/US07 NEW PUB.pdb.\*
- 6: /cgn2\_6/prodata/1/pubpaa/US07 PUBCOMB.pdb.\*
- 7: /cgn2\_6/prodata/1/pubpaa/US08 PUBCOMB.pdb.\*
- 8: /cgn2\_6/prodata/1/pubpaa/US08 PUBCOMB.pdb.\*
- 9: /cgn2\_6/prodata/1/pubpaa/US09 NEW PUB.pdb.\*
- 10: /cgn2\_6/prodata/1/pubpaa/US09 PUBCOMB.pdb.\*
- 11: /cgn2\_6/prodata/1/pubpaa/US10 NEW PUB.pdb.\*
- 12: /cgn2\_6/prodata/1/pubpaa/US10 PUBCOMB.pdb.\*
- 13: /cgn2\_6/prodata/1/pubpaa/US60 NEW PUB.pdb.\*
- 14: /cgn2\_6/prodata/1/pubpaa/US60 PUBCOMB.pdb.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	99	94.3	18	10	US-09-214-371-74
2	92	87.6	19	10	US-09-732-384-7
3	90	85.7	19	12	US-10-155-059-13
4	89	84.8	19	10	US-09-214-371-1
5	77	73.3	15	10	US-09-732-384-5
6	74	70.5	16	12	US-10-155-059-23
7	66	62.9	12	10	US-09-214-371-17
8	65	61.9	15	10	US-09-950-692-6
9	60	57.1	18	12	US-10-155-059-22
10	59	56.2	16	10	US-09-214-371-39
11	57	54.3	14	9	US-10-024-123-7
12	55	52.4	12	10	US-09-214-371-7
13	54	51.4	12	10	US-09-214-371-24
14	54	51.4	16	10	US-09-214-371-41
15	53	50.5	16	10	US-09-214-371-40
16	49	46.7	12	10	US-09-214-371-25
17	49	46.7	12	10	US-09-214-371-26
18	48	45.7	14	10	US-09-214-371-33
19	48	45.7	14	10	US-09-214-371-34

Sequence 17, Appl  
Sequence 3, Appl  
Sequence 21, Appl  
Sequence 20, Appl  
Sequence 24, Appl  
Sequence 83, Appl  
Sequence 4, Appl  
Sequence 1, Appl  
Sequence 37, Appl  
Sequence 38, Appl  
Sequence 35, Appl  
Sequence 36, Appl  
Sequence 2, Appl  
Sequence 66, Appl  
Sequence 110, Appl  
Sequence 13, Appl  
Sequence 22, Appl  
Sequence 46, Appl  
Sequence 47, Appl  
Sequence 52, Appl  
Sequence 69, Appl  
Sequence 31, Appl  
Sequence 33, Appl  
Sequence 35, Appl  
Sequence 18, Appl  
Sequence 5, Appl

Sequence 17, Appl  
Sequence 3, Appl  
Sequence 21, Appl  
Sequence 20, Appl  
Sequence 24, Appl  
Sequence 83, Appl  
Sequence 4, Appl  
Sequence 1, Appl  
Sequence 37, Appl  
Sequence 38, Appl  
Sequence 35, Appl  
Sequence 36, Appl  
Sequence 2, Appl  
Sequence 66, Appl  
Sequence 110, Appl  
Sequence 13, Appl  
Sequence 22, Appl  
Sequence 46, Appl  
Sequence 47, Appl  
Sequence 52, Appl  
Sequence 69, Appl  
Sequence 31, Appl  
Sequence 33, Appl  
Sequence 35, Appl  
Sequence 18, Appl  
Sequence 5, Appl

#### ALIGNMENTS

RESULT 1  
US-09-214-371-74  
; Sequence 74, Application US/09214371B  
; Patent No. US20010018511A1  
; GENERAL INFORMATION:  
; APPLICANT: Lane, David  
; APPLICANT: Bottger, Volker  
; APPLICANT: Bottger, Angelica  
; APPLICANT: Picklesley, Stephen  
; APPLICANT: Chene, Patrick  
; APPLICANT: Hochkeppel, Heinz-Kurt  
; APPLICANT: Garcia-Echeverria, Carlos  
; APPLICANT: Furet, Pascal  
; TITLE OF INVENTION: Inhibitors of the interaction of P53 and MDM2  
; FILE REFERENCE: 4-20937/A/PCT  
; CURRENT APPLICATION NUMBER: US/09/214,371B  
; CURRENT FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: PCT/EP97/03549  
; PRIOR FILING DATE: 1997-07-04  
; NUMBER OF SEQ ID NOS: 83  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 74  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:peptide  
US-09-214-371-74

Query Match 94.3%; Score 99; DB 10; Length 18;  
Best Local Similarity 100.0%; Pred. No. 5,5e-09;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLPEN 18  
Db 1 PPLSQETFSDLWKLLPEN 18

RESULT 2  
US-09-732-384-7  
; Sequence 7, Application US/09732384  
; Patent No. US20020132977A1

```
; GENERAL INFORMATION:
; APPLICANT: Yuan, Zhi-Min
; APPLICANT: Gu, Jijie
; TITLE OF INVENTION: Inhibition of p53 Degradation
; FILE REFERENCE: 21508-044
; CURRENT APPLICATION NUMBER: US/09/732,384
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 60/169,816
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Protein
; OTHER INFORMATION: fragment not in inhibitory p53 polypeptide
;
US-09-732-384-7
Query Match      87.6%; Score 92; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.6e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 PLSQETFSDLWKLLPEN 18
Db      1 PLSQETFSDLWKLLPEN 17

RESULT 3
US-10-155-059-13
; Sequence 13, Application US/10155059
; Patent No. US20020147173A1
; GENERAL INFORMATION:
; APPLICANT: Kaelin, William
; APPLICANT: Jost, Christine
; TITLE OF INVENTION: METHODS OF TREATMENT USING
; NBS-1, ANTIBODIES AND PROTEINS THERETO, AND USES OF THE
; ANTIBODIES
;
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon Peabody LLP
; STREET: 101 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
;
COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
;
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/155,059
; FILING DATE: 24-May-2002
; CLASSIFICATION: <Unknown>
;
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/081,975
; FILING DATE: 12-MAY-1998
; APPLICATION NUMBER: 60/046,207
; FILING DATE: 12-MAY-1997
;
ATTORNEY/AGENT INFORMATION:
; NAME: Eisenstein, Ronald I
; REGISTRATION NUMBER: 30,628
; REFERENCE/DOCKET NUMBER: 47400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-345-6054
; TELEFAX: 617-345-1300
; TELEX: <Unknown>
;
INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
```

```
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-155-059-13
Query Match      85.7%; Score 90; DB 12; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.3e-07;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 PLSQETFSDLWKLLPEN 18
Db      1 PLSQETFSDLWKLLPEN 18

RESULT 4
US-09-214-371-1
; Sequence 1, Application US/09214371B
; Patent No. US20010018511A1
; GENERAL INFORMATION:
; APPLICANT: Lane, David
; APPLICANT: Bottger, Volker
; APPLICANT: Bottger, Angelica
; APPLICANT: Picksley, Stephen
; APPLICANT: Chene, Patrick
; APPLICANT: Hochkeppel, Heinz-Kurt
; APPLICANT: Garcia-Echeverria, Carlos
; APPLICANT: Furet, Pascal
; TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2
; FILE REFERENCE: 4-20937/A/PCT
; CURRENT APPLICATION NUMBER: US/09/214,371B
; CURRENT FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: PCT/EP97/03549
; PRIOR FILING DATE: 1997-07-04
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:peptide
;
US-09-214-371-1
Query Match      84.8%; Score 89; DB 10; Length 19;
Best Local Similarity 94.1%; Pred. No. 1.9e-07;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 PLSQETFSDLWKLLPEN 18
Db      1 PLSQETFSDLWKLLPEN 17

RESULT 5
US-09-732-384-6
; Sequence 6, Application US/09732384
; Patent No. US20020132977A1
; GENERAL INFORMATION:
; APPLICANT: Yuan, Zhi-Min
; APPLICANT: Gu, Jijie
; TITLE OF INVENTION: Inhibition of p53 Degradation
; FILE REFERENCE: 21508-044
; CURRENT APPLICATION NUMBER: US/09/732,384
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 60/169,816
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Protein
```

```
; OTHER INFORMATION: fragment not in inhibitory p53 polypeptide
US-09-732-384-6

Query Match      73.3%; Score 77; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.4e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QETFSDLWKLLPEN 18
Db 1 QETFSDLWKLLPEN 14

RESULT 6
US-10-155-059-23
; Sequence 23, Application US/10155059
; Patent No. US20020147173A1
; GENERAL INFORMATION:
; APPLICANT: Kaelin, William
; Jost, Christine
; TITLE OF INVENTION: METHODS OF TREATMENT USING
; NBS-1, ANTIBODIES AND PROTEINS THEREOF, AND USES OF THE
; ANTIBODIES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon Peabody LLP
; STREET: 101 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/155.059
; FILING DATE: 24-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/081,975
; FILING DATE: 12-MAY-1998
; APPLICATION NUMBER: 60/046,207
; FILING DATE: 12-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Eisenstein, Ronald I
; REGISTRATION NUMBER: 30,628
; REFERENCE/DOCKET NUMBER: 47400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-345-6054
; TELEFAX: 617-345-1300
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-10-155-059-23

Query Match      70.5%; Score 74; DB 12; Length 16;
Best Local Similarity 81.2%; Pred. No. 2.8e-05;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PLSQETFSDLWKLLPE 17
Db 1 PLSQETFSDLWKLLPD 16

RESULT 7
US-09-214-371-17
; Sequence 17, Application US/09214371B
```

```
; Patent No. US20010018511A1
; GENERAL INFORMATION:
; APPLICANT: Lane, David
; APPLICANT: Bottger, Volker
; APPLICANT: Bottger, Angelica
; APPLICANT: Picksley, Stephen
; APPLICANT: Chene, Patrick
; APPLICANT: Hochkeppel, Heinz-Kurt
; APPLICANT: Garcia-Echeverria, Carlos
; APPLICANT: Furet, Pascal
; TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2
; FILE REFERENCE: 4-20937/A/PCT
; CURRENT APPLICATION NUMBER: US/09/214,371B
; CURRENT FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: PCT/EP97/03549
; PRIOR FILING DATE: 1997-07-04
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:peptide
US-09-214-371-17

Query Match      62.9%; Score 66; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00033;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QETFSDLWKLLP 16
Db 1 QETFSDLWKLLP 12

RESULT 8
US-09-950-692-6
; Sequence 6, Application US/09950692
; Patent No. US20020106701A1
; GENERAL INFORMATION:
; APPLICANT: Goueli, Said A
; TITLE OF INVENTION: Quantitation of Individual Protein Kinase Activity
; FILE REFERENCE: kinase
; CURRENT APPLICATION NUMBER: US/09/950,692
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 08/208,573
; PRIOR FILING DATE: 1994-03-04
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: polypeptide
US-09-950-692-6

Query Match      61.9%; Score 65; DB 10; Length 15;
Best Local Similarity 84.6%; Pred. No. 0.0006;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWK 13
Db 2 PPLSQEAFADLWK 14

RESULT 9
US-10-155-059-22
; Sequence 22, Application US/10155059
; Patent No. US20020147173A1
; GENERAL INFORMATION:
; APPLICANT: Kaelin, William
```

;  
; Jost, Christine  
; TITLE OF INVENTION: METHODS OF TREATMENT USING  
; NBS-1, ANTIBODIES AND PROTEINS THERETO, AND USES OF THE  
; ANTIBODIES  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Nixon Peabody LLP  
; STREET: 101 Federal Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/155,059  
; FILING DATE: 24-May-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/081,975  
; FILING DATE: 12-MAY-1998  
; APPLICATION NUMBER: 60/046,207  
; FILING DATE: 12-MAY-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Eisenstein, Ronald I  
; REGISTRATION NUMBER: 30,628  
; REFERENCE/DOCKET NUMBER: 47400  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-345-6054  
; TELEFAX: 617-345-1300  
; TELEX: <Unknown>  
; INFORMATION FOR SEQ ID NO: 22:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:  
US-10-155-059-22

Query Match 57.1%; Score 60; DB 12; Length 18;  
Best Local Similarity 76.9%; Pred. No. 0.0041;  
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 2 PLSQETFSDLWKL 14  
| | | | | | | | | |  
Db 3 PLSQSFEDLWKM 15

RESULT 10  
US-09-214-371-39  
; Sequence 39, Application US/09214371B  
; Patent No. US20010018511A1  
; GENERAL INFORMATION:  
; APPLICANT: Lane, David  
; APPLICANT: Bottger, Volker  
; APPLICANT: Bottger, Angelica  
; APPLICANT: Pinksley, Stephen  
; APPLICANT: Chene, Patrick  
; APPLICANT: Hochkeppel, Heinz-Kurt  
; APPLICANT: Garcia-Echeverria, Carlos  
; APPLICANT: Furet, Pascal  
; TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2  
; FILE REFERENCE: 4-20937/A/PCT  
; CURRENT APPLICATION NUMBER: US/09/214,371B  
; CURRENT FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: PCT/EP97/03549  
; PRIOR FILING DATE: 1997-07-04  
; NUMBER OF SEQ ID NOS: 83  
; SOFTWARE: Patent in Ver. 2.0

; SEQ ID NO 39  
; LENGTH: 16  
; TYPE: PRI  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:peptide  
; NAME/KEY: VARIANT  
; LOCATION: (1)  
; OTHER INFORMATION: X = Biotin-Ser  
; NAME/KEY: VARIANT  
; LOCATION: (16)  
; OTHER INFORMATION: X = Pro-NH2  
US-09-214-371-39

Query Match 56.2%; Score 59; DB 10; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0.0051;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 5 QETFSDLWKLL 15  
| | | | | | | | | |  
Db 5 QETFSDLWKLL 15

RESULT 11  
US-10-024-123-7  
; Sequence 7, Application US/10024123  
; Publication No. US20030022263A1  
; GENERAL INFORMATION:  
; APPLICANT: Keston, Michael  
; APPLICANT: Canman, Christine  
; APPLICANT: Kim, Seong-Tae  
; APPLICANT: Lim, Dae-Sik  
; APPLICANT: St. Jude Children's Research Hospital  
; TITLE OF INVENTION: ATM Kinase Modulation for Screening and  
; FILE REFERENCE: 2427/1f142  
; CURRENT APPLICATION NUMBER: US/10/024,123  
; CURRENT FILING DATE: 2001-12-17  
; PRIOR APPLICATION NUMBER: 09/400,653  
; PRIOR FILING DATE: 1999-09-21  
; PRIOR APPLICATION NUMBER: 09/248,061  
; PRIOR FILING DATE: 1999-02-10  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 7  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-024-123-7

Query Match 54.3%; Score 57; DB 9; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.0089;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 PPLSQETFSDL 11  
| | | | | | | | | |  
Db 4 PPLSQETFSDL 14

RESULT 12  
US-09-214-371-7  
; Sequence 7, Application US/09214371B  
; Patent No. US20010018511A1  
; GENERAL INFORMATION:  
; APPLICANT: Lane, David  
; APPLICANT: Bottger, Volker  
; APPLICANT: Bottger, Angelica  
; APPLICANT: Pinksley, Stephen  
; APPLICANT: Chene, Patrick  
; APPLICANT: Hochkeppel, Heinz-Kurt  
; APPLICANT: Garcia-Echeverria, Carlos  
; APPLICANT: Furet, Pascal  
; TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2

```

; FILE REFERENCE: 4-20937/A/PCT
; CURRENT APPLICATION NUMBER: US/09/214,371B
; CURRENT FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: PCT/EP97/03549
; PRIOR FILING DATE: 1997-07-04
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:peptide
; US-09-214-371-7

```

```

Query Match 52.4%; Score 55; DB 10; Length 12;
Best Local Similarity 83.3%; Pred. No. 0.015;
Matches 10; Conservative 0; Mismatches 0; Indels 2; Gaps 0;

```

```

Qy 5 QETFSDLWKLLP 16
Db 1 QPTFSDYWKLLP 12

```

## RESULT 13

```

US-09-214-371-24
; Sequence 24, Application US/09214371B
; Patent No. US20010018511A1
; GENERAL INFORMATION:
; APPLICANT: Lane, David
; APPLICANT: Bottger, Volker
; APPLICANT: Bottger, Angelica
; APPLICANT: Picksley, Stephen
; APPLICANT: Chene, Patrick
; APPLICANT: Hochkeppel, Heinz-Kurt
; APPLICANT: Garcia-Echeverria, Carlos
; APPLICANT: Furet, Pascal
; TITLE OF INVENTION: Inhibitors of the Interaction of p53 and MDM2
; FILE REFERENCE: 4-20937/A/PCT
; CURRENT APPLICATION NUMBER: US/09/214,371B
; CURRENT FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: PCT/EP97/03549
; PRIOR FILING DATE: 1997-07-04
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)
; OTHER INFORMATION: X = Ac-Gln
; NAME/KEY: VARIANT
; LOCATION: (12)
; OTHER INFORMATION: X = Pro-NH2
; OTHER INFORMATION: Description of Artificial Sequence:peptide
; US-09-214-371-24

```

```

Query Match 51.4%; Score 54; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 6 ETFSDLWKLL 15
Db 2 ETFSDLWKLL 11

```

## RESULT 14

```

US-09-214-371-41
; Sequence 41, Application US/09214371B
; Patent No. US20010018511A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Lane, David
; APPLICANT: Bottger, Volker
; APPLICANT: Bottger, Angelica
; APPLICANT: Picksley, Stephen
; APPLICANT: Chene, Patrick
; APPLICANT: Hochkeppel, Heinz-Kurt
; APPLICANT: Garcia-Echeverria, Carlos
; APPLICANT: Furet, Pascal
; TITLE OF INVENTION: Inhibitors of the Interaction of p53 and MDM2
; FILE REFERENCE: 4-20937/A/PCT
; CURRENT APPLICATION NUMBER: US/09/214,371B
; CURRENT FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: PCT/EP97/03549
; PRIOR FILING DATE: 1997-07-04
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:peptide
; NAME/KEY: VARIANT
; LOCATION: (1)
; OTHER INFORMATION: Biotin-Ser
; NAME/KEY: VARIANT
; LOCATION: (16)
; OTHER INFORMATION: X = Pro-NH2
; US-09-214-371-41

```

```

Query Match 51.4%; Score 54; DB 10; Length 16;
Best Local Similarity 90.9%; Pred. No. 0.029;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 5 QETFSDLWKLL 15
Db 5 QETFSDYWKLL 15

```

## RESULT 15

```

US-09-214-371-40
; Sequence 40, Application US/09214371B
; Patent No. US20010018511A1
; GENERAL INFORMATION:
; APPLICANT: Lane, David
; APPLICANT: Bottger, Volker
; APPLICANT: Bottger, Angelica
; APPLICANT: Picksley, Stephen
; APPLICANT: Chene, Patrick
; APPLICANT: Hochkeppel, Heinz-Kurt
; APPLICANT: Garcia-Echeverria, Carlos
; APPLICANT: Furet, Pascal
; TITLE OF INVENTION: Inhibitors of the Interaction of p53 and MDM2
; FILE REFERENCE: 4-20937/A/PCT
; CURRENT APPLICATION NUMBER: US/09/214,371B
; CURRENT FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: PCT/EP97/03549
; PRIOR FILING DATE: 1997-07-04
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:peptide
; NAME/KEY: VARIANT
; LOCATION: (1)
; OTHER INFORMATION: X = Biotin-Ser
; NAME/KEY: VARIANT
; LOCATION: (16)
; OTHER INFORMATION: X = Pro-NH2
; US-09-214-371-40

```

Query Match 50.5%; Score 53; DB 10; Length 16;  
Best Local Similarity 90.9%; Pred. No. 0.041;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 QETFSDLWKLL 15  
| | | | | | | | | |  
Db 5 QPTFSDLWKLL 15

Search completed: February 12, 2003, 10:50:08  
Job time : 12 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 12, 2003, 10:36:07 ; Search time 34 Seconds  
(without alignments)  
74.464 Million cell updates/sec

Title: US-09-403-440A-2

Perfect score: 105

Sequence: 1 PPLSQTFSDLWKLLPENG 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 278369

Minimum DB seq length: 0

Maximum DB seq length: 19

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_101002:\*  
1: /SID22/gcgdata/geneseq/geneseq-embl/AA1980.DAT:\*  
2: /SID22/gcgdata/geneseq/geneseq-embl/AA1981.DAT:\*  
3: /SID22/gcgdata/geneseq/geneseq-embl/AA1982.DAT:\*  
4: /SID22/gcgdata/geneseq/geneseq-embl/AA1983.DAT:\*  
5: /SID22/gcgdata/geneseq/geneseq-embl/AA1984.DAT:\*  
6: /SID22/gcgdata/geneseq/geneseq-embl/AA1985.DAT:\*  
7: /SID22/gcgdata/geneseq/geneseq-embl/AA1986.DAT:\*  
8: /SID22/gcgdata/geneseq/geneseq-embl/AA1987.DAT:\*  
9: /SID22/gcgdata/geneseq/geneseq-embl/AA1988.DAT:\*  
10: /SID22/gcgdata/geneseq/geneseq-embl/AA1989.DAT:\*  
11: /SID22/gcgdata/geneseq/geneseq-embl/AA1990.DAT:\*  
12: /SID22/gcgdata/geneseq/geneseq-embl/AA1991.DAT:\*  
13: /SID22/gcgdata/geneseq/geneseq-embl/AA1992.DAT:\*  
14: /SID22/gcgdata/geneseq/geneseq-embl/AA1993.DAT:\*  
15: /SID22/gcgdata/geneseq/geneseq-embl/AA1994.DAT:\*  
16: /SID22/gcgdata/geneseq/geneseq-embl/AA1995.DAT:\*  
17: /SID22/gcgdata/geneseq/geneseq-embl/AA1996.DAT:\*  
18: /SID22/gcgdata/geneseq/geneseq-embl/AA1997.DAT:\*  
19: /SID22/gcgdata/geneseq/geneseq-embl/AA1998.DAT:\*  
20: /SID22/gcgdata/geneseq/geneseq-embl/AA1999.DAT:\*  
21: /SID22/gcgdata/geneseq/geneseq-embl/AA2000.DAT:\*  
22: /SID22/gcgdata/geneseq/geneseq-embl/AA2001.DAT:\*  
23: /SID22/gcgdata/geneseq/geneseq-embl/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	105	100.0	19	AAW82321	p53 homologue TIP
2	105	100.0	19	AAW82319	p53 homologue TIP
3	99	94.3	18	AAW37228	p53 N-terminal pep
4	97	92.4	19	AAW47074	p53/RB interaction
5	81	77.1	15	AA106310	Human p53 peptide
6	77	73.3	15	AAR54909	Immunodominant epi
7	77	73.3	15	AAR54910	Immunodominant epi
8	77	73.3	15	AAR89914	p53 protein bindin
9	77	73.3	15	AAB29157	Peptide #1. Unide
10	77	73.3	15	AAG89500	p53 DR 3a motif bi

11	77	73.3	15	22	AAG89730	p53 DR3 binding pe
12	77	73.3	17	20	AAV45227	Peptide 9-25.
13	74	70.5	15	21	AAB29159	Peptide #3. Unide
14	74	70.5	15	21	AAB29163	Peptide #7. Unide
15	73	69.5	14	23	ABE05528	Biotinylated pepi
16	73	69.5	15	21	AAB29167	Peptide #11. Unid
17	71	67.6	15	21	AAB29161	Peptide #4. Unide
18	71	67.6	15	21	AAB29161	Peptide #5. Unide
19	71	67.6	15	21	AAV99001	HLA class II bindi
20	70	66.7	13	21	AAV57799	TRAM-interaction m
21	69	65.7	15	21	AAB29162	Peptide #6. Unide
22	69	65.7	15	21	AAB29164	Peptide #8. Unide
23	66.5	63.3	16	21	AAB29149	Ligand #1. Uniden
24	66.5	63.3	16	21	AAB29158	Peptide #2. Unide
25	66	62.9	12	19	AAW37181	Human p53 wild-typ
26	66	62.9	12	19	AAW37188	Human oncogenic pr
27	66	62.9	12	21	AAB17075	Mdm/hdm antagonist
28	66	62.9	12	21	AAB17087	Mdm/hdm antagonist
29	66	62.9	12	23	ABE73170	Mdm/hdm antagonist
30	66	62.9	12	23	ABE73182	Mdm/hdm antagonist
31	66	62.9	16	19	AAW37201	Human oncogenic pr
32	65	61.9	15	16	AAE83012	Promega protein ki
33	65	61.9	15	21	AAV58559	Tumour suppressor
34	65	61.9	15	23	ABE09246	Target activatabl
35	62	59.0	15	22	AAG89447	p53 DR supermotif
36	61	58.1	11	23	AAW52269	Miniature protein
37	61	58.1	12	19	AAW37190	Human oncogenic pr
38	61	58.1	12	21	AAB17077	Mdm/hdm antagonist
39	61	58.1	12	21	AAB17089	Mdm/hdm antagonist
40	61	58.1	12	23	ABE73172	Mdm/hdm antagonist
41	61	58.1	12	23	ABE73184	Mdm/hdm antagonist
42	61	58.1	16	19	AAW37203	Human oncogenic pr
43	60	57.1	12	19	AAW37189	Human oncogenic pr
44	60	57.1	12	21	AAB17076	Mdm/hdm antagonist
45	60	57.1	12	21	AAB17088	Mdm/hdm antagonist

#### ALIGNMENTS

#### RESULT 1

AAW82321  
ID AAW82321 standard; Peptide; 19 AA.

XX AC

XX AAW82321;

XX 22-FEB-1999 (first entry)

XX p53 homologue TIP peptide.

DE

XX p53; mdm2; inhibitor; therapy; activator; treatment; cancer; medicament.

XX Synthetic.

XX WO9847919-A1.

XX 29-OCT-1998.

XX 20-APR-1998; 98WO-GB01140.

XX 22-APR-1997; 97GB-0008089.

XX (UYDU-) UNIV DUNDEE.

XX Lane DP;

XX WPI; 1998-609975/51.

XX New substance with a mdm2 binding domain and coupling partner -

XX useful for stabilising in cells without an efficient mdm2-mediated

XX degradation pathway

XX Disclosure; Fig 1; 52pp; English.

XX This sequence is a peptide homologue of a region of p53 which binds  
 CC to mdm2. This peptide is used in the construction of a novel agent  
 CC capable of disrupting the binding of p53 and mdm2 or inhibiting the  
 CC production of mdm2 in a population of cells. This agent is also used in  
 CC the preparation of a therapeutic for activating p53, where the population  
 CC of cells do not overexpress mdm2. Inhibiting mdm2 production and/or  
 CC inhibiting the binding of mdm2 to p53 allows levels of p53 to increase by  
 CC reducing the clearance of p53 by mdm2, and can be used to activate p53  
 CC function. The agents for use in therapeutics for activating p53 can be  
 CC used for the treatment of cancer, viral conditions or other conditions  
 CC associated with non-functional p53.

XX Sequence 19 AA;

Query Match 100.0%; Score 105; DB 19; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 5.7e-10;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLPENG 19  
 Db 1 PPLSQETFSDLWKLLPENG 19  
 |||||

# RESULT 2

AAW82319  
 ID AAW82319 standard; Peptide; 19 AA.

XX AC AAW82319;

XX DT 22-FEB-1999 (first entry)

XX DE p53 homologue TIP peptide.

XX KW p53; mdm2; inhibitor; therapy; activator; treatment; cancer; medicament.

XX OS Synthetic.

XX FN WO9847525-A1.

XX PD 29-OCT-1998.

XX XX 20-APR-1998; 98WO-GB01144.

XX PR 22-APR-1997; 97GB-0008092.

XX XX (UYDU-) UNIV DUNDEE.

XX PA Lane DP;

XX DR WPI; 1998-609932/51.

XX New agents which inhibit interaction of p53 and mdm2 - useful for  
 PT activating p53, e.g. for treating cancers, viral conditions or other  
 PT conditions associated with non functional p53 or mdm2

XX Disclosure; Fig 1; 52pp; English.

XX This sequence is a peptide homologue of a region of p53 which binds  
 CC to mdm2. This peptide is used in the construction of a novel agent  
 CC capable of disrupting the binding of p53 and mdm2 or inhibiting the  
 CC production of mdm2 in a population of cells. This agent is also used in  
 CC the preparation of a therapeutic for activating p53, where the population  
 CC of cells do not overexpress mdm2. Inhibiting mdm2 production and/or  
 CC inhibiting the binding of mdm2 to p53 allows levels of p53 to increase by  
 CC reducing the clearance of p53 by mdm2, and can be used to activate p53  
 CC function. The agents for use in therapeutics for activating p53 can be  
 CC used for the treatment of cancer, viral conditions or other conditions  
 CC associated with non-functional p53.

XX Sequence 19 AA;

Query Match 100.0%; Score 105; DB 19; Length 19;

Best Local Similarity 100.0%; Pred. No. 5.7e-10;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLPENG 19  
 Db 1 PPLSQETFSDLWKLLPENG 19  
 |||||

# RESULT 3

AAW37228  
 ID AAW37228 standard; peptide; 18 AA.

XX AC AAW37228;

XX DT 20-JUL-1998 (first entry)

XX DE p53 N-terminal peptide fragment for Elisa TIP assay.

XX KW MDM2; oncogenic protein; p53; human; inhibition; interaction; cancer;  
 KW tumour; diagnosis; binding; viral infection; Elisa TIP assay.

XX OS Homo sapiens.

XX FN WO9801467-A2.

XX PD 15-JAN-1998.

XX PF 04-JUL-1997; 97WO-EP03549.

XX PR 07-APR-1997; 97GB-0007041.

XX PR 05-JUL-1996; 96GB-0014197.

XX XX (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.

XX PA (NOVS) NOVARTIS AG.

XX PI Boettger A, Boettger V, Chene P, Furet P, Garcia-echeverria C;

XX PI Hochkeppel H, Lane D, Picksley S;

XX DR WPI; 1998-100996/09.

XX Compounds binding to MDM2 protein and inhibit its interaction with

PT p53 - useful in, e.g. diagnosis and treatment of cancer and viral

PT infections and identifying binding agents

XX Disclosure; Page 34; 45pp; English.

XX This represents a p53 N-terminal peptide fragment used in an Elisa TIP  
 CC assay for analysing the interaction between human oncogenic protein MDM2  
 CC and p53. The invention provides peptide derivatives capable of binding to  
 CC the human MDM2. These peptides can specifically inhibit or block the  
 CC binding of MDM2 to the human p53 protein, in vitro or in vivo. Inhibiting  
 CC the interaction between the p53 and MDM2 can induce growth arrest or  
 CC apoptosis in tumour cells comprising a wild-type p53 and non-elevated  
 CC levels of MDM2. The peptides may be used to identify molecules that bind  
 CC to MDM2 and to identify and design inhibitors of MDM2/p53 binding. They  
 CC may also be used to purify binding partners especially MDM2, diagnose  
 CC disease by measuring levels of MDM2 in blood of cancer and leukaemia  
 CC patients and for treatment or prevention of disease involving p53/MDM2  
 CC interactions, especially tumours and viral infections. The peptides can  
 CC be administered nasally, rectally, orally or by injection. By interfering  
 CC with MDM2/p53 interaction, the peptides can activate p53 function and  
 CC accumulation in normal cells. The peptides which mimic the MDM2 binding  
 CC site in p53, have a significantly greater blocking activity compared  
 CC with wild-type p53.

XX Sequence 18 AA;

Query Match 94.3%; Score 99; DB 19; Length 18;

Best Local Similarity 100.0%; Pred. No. 4.9e-09;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLPEN 18  
 |||||







RESULT 9  
 AAB29157  
 ID AAB29157 standard; Peptide; 15 AA.  
 XX AC AAB29157;  
 XX DT 02-FEB-2001 (first entry)  
 XX DE Peptide #1.  
 XX KW Fork head associated; FHA; domain; transcriptional control;  
 XX KW DNA replication; DNA repair; cell cycle control.  
 XX OS Unidentified.  
 XX PN WO200057184-A2.  
 XX PD 28-SEP-2000.  
 XX PF 17-MAR-2000; 2000WO-GB01024.  
 XX PR 19-MAR-1999; 99GB-0006432.  
 XX PR 28-JUN-1999; 99GB-0015075.  
 XX PA (KUDO-) KUDOS PHARM LTD.  
 XX PI Jackson SP, Durocher D;  
 XX PI WPI; 2000-664872/64.  
 XX DR Assays and screening methods based on direct interaction between FHA  
 PT domains and phosphopeptides, useful for characterizing binding and to  
 PT identify binding partners and modulators of FHA domain-phosphopeptide  
 PT binding -  
 XX PS Disclosure; Fig 2; 92pp; English.  
 XX CC The present invention relates to assays and screening methods based on  
 CC a direct interaction between fork head associated (FHA) domains and  
 CC phosphorylated polypeptides, for characterizing the binding of these  
 CC molecules. FHA peptides may be useful for treating medical conditions  
 CC associated with defects in transcriptional control, DNA replication,  
 CC DNA repair, cell cycle control or other cellular processes. The method  
 CC may provide valuable insights into checkpoint signalling, has important  
 CC implications for the functions of other FHA domain-containing  
 CC proteins and provides basis for new lines of therapy. The present  
 CC sequence is a peptide used in the present invention.  
 XX SQ Sequence 15 AA;  
 Query Match 73.3%; Score 77; DB 21; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 PPLSQETFSDLWKL 14  
 Db 1 PPLSQETFSDLWKL 15  
 RESULT 10  
 AAG89500  
 ID AAG89500 standard; Peptide; 15 AA.  
 XX AC AAG89500;  
 XX DT 11-SEP-2001 (first entry)  
 XX DE p53 DR 3a motif binding peptide exemplary sequence #3.  
 XX DE Human; p53; tumour suppressor; human leukocyte antigen; CTL;  
 XX KW cytotoxic T lymphocyte; T cell; immune response; tumour; cancer;  
 KW cytotoxic T lymphocyte; T cell; immune response; tumour; cancer;

KW vaccine; epitope; cytostatic.  
 XX Homo sapiens.  
 OS Synthetic.  
 XX PN WO200141788-A1.  
 XX PD 14-JUN-2001.  
 XX PF 11-DEC-2000; 2000WO-US33629.  
 XX PR 10-DEC-1999; 99US-0458297.  
 XX PA (EPIM-) EPIMMUNE INC.  
 XX PI Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;  
 PI Keogh E;  
 XX WPI; 2001-381493/40.  
 XX DR Epitope-based vaccines comprising P53 epitope having a specified  
 PT sequences, useful for treating and preventing cancer, the epitopic  
 PT peptides is useful as diagnostic agents and for evaluating immune  
 PT response -  
 XX PS Disclosure; Page 113; 138pp; English.  
 XX CC The present invention describes isolated prepared P53 epitopes (I). Also  
 CC described are: (1) a cytotoxic T lymphocyte (CTL) that is cultured  
 CC in vivo and binds to a complex of (I); (2) a peptide (II) comprising (I)  
 CC and a second epitope and has less than 50 contiguous amino acids; (3) a  
 CC vaccine composition comprising (II), a unit dose of a peptide with less  
 CC than 50 contiguous amino acids with 100% identity to the native peptide  
 CC sequence of p53, and a pharmaceutical excipient; (4) an isolated nucleic  
 CC acid encoding (I); and (5) an isolated nucleic acid encoding (II). (I)  
 CC has cytostatic activity and can be used in vaccines. The vaccine  
 CC composition is useful for treating or preventing cancer. (I) and (II)  
 CC are useful as diagnostic agents and for evaluating immune responses.  
 CC Unlike conventional epitopes, immunosuppressive epitopes that may be  
 CC present in whole antigens can be avoided with the use of the vaccine  
 CC composition of (I). The ability to combine selected epitopes and  
 CC further, to modify the composition of the epitopes enhances the  
 CC immunogenicity. The possible pathological side effects caused by  
 CC infectious agents or whole protein antigens, which might have their own  
 CC intrinsic biological activity, are eliminated. AAG89363 to AAG89747  
 CC represent amino acid sequences used in the exemplification of the  
 CC present invention.  
 XX SQ Sequence 15 AA;  
 Query Match 73.3%; Score 77; DB 22; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 PPLSQETFSDLWKL 14  
 Db 2 PPLSQETFSDLWKL 15  
 RESULT 11  
 AAG89730  
 ID AAG89730 standard; Peptide; 15 AA.  
 XX AC AAG89730;  
 XX DT 11-SEP-2001 (first entry)  
 XX DE p53 DR3 binding peptide #1.  
 XX DE Human; p53; tumour suppressor; human leukocyte antigen; HLA; CTL;  
 XX KW cytotoxic T lymphocyte; T cell; immune response; tumour; cancer;  
 KW vaccine; epitope; cytostatic.  
 XX

OS Homo sapiens.  
 OS Synthetic.  
 PN WO200141788-A1.  
 XX  
 PD 14-JUN-2001.  
 XX  
 PF 11-DEC-2000; 2000WO-US33629.  
 XX  
 PR 10-DEC-1999; 99US-0458297.  
 XX  
 PA (EPIM-) EPIMUNE INC.  
 XX  
 PI Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;  
 PI Keogh E;  
 DR WPI; 2001-381493/40.  
 XX  
 XX Epitope-based vaccines comprising p53 epitope having a specified  
 PT sequences, useful for treating and preventing cancer, the epitopic  
 PT peptides is useful as diagnostic agents and for evaluating immune  
 PT response -  
 PS Example 5; Page 131; 138pp; English.  
 XX  
 CC The present invention describes isolated prepared p53 epitopes (I). Also  
 CC described are: (1) a cytotoxic T lymphocyte (CTL) that is cultured  
 CC in vivo and binds to a complex of (I); (2) a peptide (II) comprising  
 CC a vaccine composition and has less than 50 contiguous amino acids; (3) a  
 CC vaccine composition comprising (II), a unit dose of a peptide with less  
 CC than 50 contiguous amino acids with 100% identity to the native peptide  
 CC sequence of p53, and a pharmaceutical excipient; (4) an isolated nucleic  
 CC acid encoding (I); and (5) an isolated nucleic acid encoding (II). (I)  
 CC has cytostatic activity and can be used in vaccines. The vaccine  
 CC composition is useful for treating or preventing cancer. (I) and (II)  
 CC are useful as diagnostic agents and for evaluating immune responses.  
 CC Unlike conventional epitopes, immunosuppressive epitopes that may be  
 CC present in whole antigens can be avoided with the use of the vaccine  
 CC composition of (I). The ability to combine selected epitopes and  
 CC further, to modify the composition of the epitopes enhances the  
 CC immunogenicity. The possible pathological side effects caused by  
 CC infectious agents or whole protein antigens, which might have their own  
 CC intrinsic biological activity, are eliminated. AAG89363 to AAG89747  
 CC represent amino acid sequences used in the exemplification of the  
 CC present invention.  
 XX  
 SQ Sequence 15 AA;  
 Query Match 73.3%; Score 77; DB 22; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 PPLSQETFSDLWKL 14  
 Db 2 PPLSQETFSDLWKL 15  
 RESULT 12  
 AAY45227  
 XX AAY45227 standard; peptide; 17 AA.  
 XX  
 AC AAY45227;  
 DT 06-JAN-2000 (first entry)  
 XX  
 DE p53 peptide 9-25.  
 XX  
 KW Immunisation; immunogenicity enhancer; rabies virus strain ERA;  
 KW immunodominant T-helper cell determinant; nucleoprotein; antibody;  
 KW post-translational modification; p53; cancer; diagnosis.  
 XX  
 OS Synthetic.  
 XX

PN WO9946574-A2.  
 XX  
 PD 16-SEP-1999.  
 XX  
 PF 11-MAR-1999; 99WO-US04653.  
 XX  
 PR 11-MAR-1998; 98US-0077512.  
 XX  
 PA (WIST-) WISTAR INST.  
 XX  
 PI Otvos L, Ertl H, Thurin M, Hoffman R;  
 PI WPI; 1999-561693/47.  
 DR  
 DR Methods of detecting post-translational modification level of p53,  
 PT useful for diagnosis of cancer -  
 PT  
 PT Disclosure; Page 45; 59pp; English.  
 PS  
 XX The present invention describes a polypeptide comprising a portion of a  
 CC p53 comprising a post-translationally modified amino acid residue where  
 CC the modification is a phosphorylation, glycosylation or prenylation, and  
 CC an immunogenicity enhancer. The polypeptide is used to detect anti-p53  
 CC autoantibodies in a human patient. The antibody can be used to determine  
 CC the post-translational modification state of a p53 protein. These are  
 CC used especially in the diagnosis of cancer. The present sequence  
 CC represents a p53 peptide used in the exemplification of the present  
 CC invention.  
 XX  
 SQ Sequence 17 AA;  
 Query Match 73.3%; Score 77; DB 20; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 PPLSQETFSDLWKL 14  
 Db 4 PPLSQETFSDLWKL 17  
 RESULT 13  
 AAB29159  
 ID AAB29159 standard; Peptide; 15 AA.  
 XX  
 AC AAB29159;  
 XX  
 DT 02-FEB-2001 (first entry)  
 XX  
 DE Peptide #3.  
 XX  
 KW Fork head associated; FHA; domain; transcriptional control;  
 KW DNA replication; DNA repair; cell cycle control.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200057184-A2.  
 XX  
 PD 28-SEP-2000.  
 XX  
 PF 17-MAR-2000; 2000WO-GB01024.  
 XX  
 PR 19-MAR-1999; 99GB-0006432.  
 PR 28-JUN-1999; 99GB-0015075.  
 XX  
 PA (KUDO-) KUDOS PHARM LTD.  
 XX  
 PI Jackson SP, Durocher D;  
 XX  
 DR WPI; 2000-664872/64.  
 XX  
 PT Assays and screening methods based on direct interaction between FHA  
 PT domains and phosphopeptides, useful for characterizing binding and to  
 PT identify binding partners and modulators of FHA domain-phosphopeptide

```

PT binding -
XX
PS Disclosure; Fig 2; 92pp; English.
XX
CC The present invention relates to assays and screening methods based on
CC a direct interaction between fork head associated (FHA) domains and
CC phosphorylated polypeptides, for characterizing the binding of these
CC molecules. FHA peptides may be useful for treating medical conditions
CC associated with defects in transcriptional control, DNA replication,
CC DNA repair, cell cycle control or other cellular processes. The method
CC may provide valuable insights into checkpoint signalling, has important
CC implications for the functions of other FHA domain-containing
CC proteins and provides basis for new lines of therapy. The present
CC sequence is a peptide used in the present invention.
XX
SQ Sequence 15 AA;
  Query Match 70.5%; Score 74; DB 21; Length 15;
  Best Local Similarity 92.9%; Pred. No. 4.2e-05;
  Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKL 14
  |||:|||||
Db 2 PPLAQETFSDLWKL 15

RESULT 14
AAB29163
ID AAB29163 standard; Peptide; 15 AA.
XX
AC AAB29163;
XX
DT 02-FEB-2001 (first entry)
XX
DE Peptide #7.
XX
KW Fork head associated; FHA; domain; transcriptional control;
KW DNA replication; DNA repair; cell cycle control.
XX
OS Unidentified.
XX
PN WO200057184-A2.
XX
PD 28-SEP-2000.
XX
PF 17-MAR-2000; 2000WO-GB01024.
XX
PR 19-MAR-1999; 99GB-0006432.
PR 28-JUN-1999; 99GB-0015075.
XX
PA (KUDO-) KUDOS PHARM LTD.
XX
PI Jackson SP, Durocher D;
XX
WPI; 2000-664872/64.
XX
PT Assays and screening methods based on direct interaction between FHA
PT domains and phosphopeptides, useful for characterizing binding and to
PT identify binding partners and modulators of FHA domain-phosphopeptide
PT binding -
XX
PS Disclosure; Fig 2; 92pp; English.
XX
CC The present invention relates to assays and screening methods based on
CC a direct interaction between fork head associated (FHA) domains and
CC phosphorylated polypeptides, for characterizing the binding of these
CC molecules. FHA peptides may be useful for treating medical conditions
CC associated with defects in transcriptional control, DNA replication,
CC DNA repair, cell cycle control or other cellular processes. The method
CC may provide valuable insights into checkpoint signalling, has important
CC implications for the functions of other FHA domain-containing
CC proteins and provides basis for new lines of therapy. The present
CC sequence is a peptide used in the present invention.
XX
SQ Sequence 15 AA;
  Query Match 70.5%; Score 74; DB 21; Length 15;
  Best Local Similarity 92.9%; Pred. No. 4.2e-05;
  Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKL 14
  |||:|||||
Db 2 PPLAQETFSDLWKL 15

RESULT 15
ABB05528
ID ABB05528 standard; Peptide; 14 AA.
XX
AC ABB05528;
XX
DT 22-APR-2002 (first entry)
XX
DE Biotinylated peptide SEQ ID NO:13.
XX
KW Ubiquitin dependent proteolysis modulation; cdc4 phospho design motif;
KW CDP motif; cytostatic; nontropic; antiproliferative; cell proliferation;
KW growth; differentiation; cancer; neurodegenerative disorder;
KW spinal degeneration.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 8 /note= "phospho-Thr"
FT
XX
PN WO200183518-A2.
XX
PD 08-NOV-2001.
XX
PF 04-MAY-2001; 2001WO-CA00632.
XX
PR 04-MAY-2000; 2000US-202166P.
PR 24-JAN-2001; 2001US-263774P.
XX
PA (MOUN) MOUNT SINAI HOSPITAL.
XX
PI Nash P, Pawson T, Tang X, Tyers M;
XX
WPI; 2002-164074/21.
XX
DR New Cdc4 Phospho Design motif that targets molecules for ubiquitin
PT dependent proteolysis, is useful for the modulation of cell
PT proliferation i.e. cancer treatment -
XX
PS Example 2; Page 47; 83pp; English.
XX
CC The present invention describes a cdc4 phospho design (CPD) motif, (C),
CC that targets molecules for ubiquitin dependent proteolysis. (C) have
CC cytosolic, nontropic and antiproliferative activity. Also described is
CC a method for the treatment of a disease or condition where affected
CC cells have a defective protein, comprising administering (C) to promote
CC degradation of the target protein in cells by ubiquitin dependent
CC proteolysis. (C) can also be used for modulating the proliferation,
CC growth and/or differentiation of cells. (C) can be used to modulate
CC ubiquitin dependent proteolysis or cell proliferation, growth and or
CC differentiation of cells. (C) is useful in the treatment of cancers and
CC neurodegenerative disorders as well as spinal degeneration. The present
CC sequence represents a biotinylated peptide which is used in an example
CC from the present invention.
XX
SQ Sequence 14 AA;
  Query Match 69.5%; Score 73; DB 23; Length 14;
  Best Local Similarity 100.0%; Pred. No. 5.6e-05;
  Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Oy 1 PPLSQETFSDLWK 13  
| | | | | | | | | |  
Db 2 PPLSQETFSDLWK 14

Search completed: February 12, 2003, 10:43:48  
Job time : 35 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 12, 2003, 10:42:32 ; Search time 28 Seconds  
(without alignments)  
139.818 Million cell updates/sec

Title: US-09-403-440A-2

Perfect score: 105

Sequence: 1 PPLSQETFSDLWKLLPENG 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 5270

Minimum DB seq length: 0

Maximum DB seq length: 19

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SPREMBL 21.\*  
2: sp\_archaea.\*  
3: sp\_bacteria.\*  
4: sp\_fungi.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phage.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_rvirus.\*  
16: sp\_bacteriap.\*  
17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	30.5	19	5 P83003	P83003 entamoeba h
2	31	29.5	16	6 Q9BG58	Q9BG58 sox arane
3	30	28.6	14	6 Q77538	Q77538 bos taurus
4	29	27.6	17	8 Q9XNQ1	Q9XNQ1 boophilus m
5	27	25.7	11	4 Q9UELO	Q9UELO homo sapien
6	26	24.8	14	10 P82326	P82326 pisum sativ
7	26	24.8	17	11 Q9QVS7	Q9QVS7 mus sp. lac
8	26	24.8	18	4 Q9UJZ3	Q9UJZ3 homo sapien
9	25	23.8	16	12 Q83960	Q83960 influenzavi
10	25	23.8	17	2 Q9F0P3	Q9F0P3 paracoccus
11	25	23.8	18	6 P82674	P82674 bos taurus
12	25	23.8	18	12 Q84129	Q84129 influenzavi
13	25	23.8	19	10 Q22064	Q22064 dioscorea t
14	25	23.8	19	12 Q83965	Q83965 influenzavi
15	24	22.9	10	8 Q9MJQ5	Q9MJQ5 podospira c
16	24	22.9	10	11 Q9ESU5	Q9ESU5 mus musculus

17 24 22.9 12 7 077919  
18 24 22.9 14 8 Q9MJQ3  
19 24 22.9 15 13 Q9PS10  
20 24 22.9 16 12 Q83967  
21 24 22.9 16 12 Q84055  
22 24 22.9 17 11 Q9QVS6  
23 23 21.9 8 11 Q9QV15  
24 23 21.9 9 8 Q9TLM7  
25 23 21.9 11 7 Q77895  
26 23 21.9 11 7 Q77896  
27 23 21.9 15 2 Q53580  
28 23 21.9 15 4 Q9UEM3  
29 23 21.9 15 4 Q9UC22  
30 23 21.9 15 8 Q9T2K8  
31 23 21.9 15 10 P83141  
32 23 21.9 16 6 Q9TRD1  
33 23 21.9 17 11 Q9QV58  
34 23 21.9 17 12 Q69074  
35 23 21.9 18 1 Q9UWJ7  
36 23 21.9 19 4 Q9BVX6  
37 23 21.9 19 11 Q9QV38  
38 22 21.0 9 4 Q59533  
39 22 21.0 14 2 Q9RS18  
40 22 21.0 17 15 Q72017  
41 22 21.0 18 13 Q13167  
42 21.5 20.5 19 6 Q19107  
43 21 20.0 7 8 Q95945  
44 21 20.0 9 4 Q9H3Y3  
45 21 20.0 13 11 Q91XP1

## ALIGNMENTS

### RESULT 1

P83003 PRELIMINARY; PRT; 19 AA.  
AC P83003;  
DT 01-OCT-2001 (TRENBLrel. 18, Created)  
DT 01-OCT-2001 (TRENBLrel. 18, Last sequence update)  
DT 01-OCT-2001 (TRENBLrel. 18, Last annotation update)  
DE Calreticulin-like protein (fragment).  
OS Entamoeba histolytica.  
OC Eukaryota; Entamoebidae; Entamoeba.  
OX NCBI\_TaxID=5759;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=HM-1:IMMS;  
RA Gonzalez E., Mendoza G., Ramos F., Garcia G., Moran P., Valadez A.,  
RA Zaragoza M.E., Melendro E.I., Ximenez C.;  
RT "Calreticulin-like molecule in trophozoites of Histolytica HM1-IMMS.";  
RL Submitted (JUN-2001) to the SWISS-PROT data bank.  
CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM (BY SIMILARITY).  
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.  
CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
DR InterPro; IPR001580; Calreticulin.  
DR PROSITE; PS00803; CALRETICULIN\_1; PARTIAL.  
DR PROSITE; PS00804; CALRETICULIN\_2; PARTIAL.  
DR PROSITE; PS00805; CALRETICULIN\_REPEAT; PARTIAL.  
KW Endoplasmic reticulum; Calcium-binding.  
FT NON TER 19  
SQ SEQUENCE 19 AA; 2488 MW; FC90BCAEFE1BA764 CRC64;

Query Match 30.5%; Score 32; DB 5; Length 19;

Best Local Similarity 45.5%; Pred. No. 2.8e+02;

Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 5 QETFSDLWKLL 15

Db 5 EETFENGWKXI 15

```

RESULT 2
Q9BG88 PRELIMINARY; PRT; 16 AA.
AC Q9BG88;
DT 01-JUN-2001 (TREMELrel. 17, Created)
DT 01-JUN-2001 (TREMELrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMELrel. 17, Last annotation update)
DE Thyroid hormone receptor alpha (Fragment).
GN THRA1.
OS Sorex araneus (Eurasian common shrew) (European shrew).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Insectivora; Soricidae; Soricinae; Sorex.
OX NCBI_TaxID=42254;
RN [1];
RP SEQUENCE FROM N.A.
RA Larkin D., Serov O., Zhdanova N.;
RT "Mapping of five genes from human chromosome 17 to chromosome 10 of
RT the common shrew (Sorex araneus).";
RL Acta Theriol. (Warsz) 45:143-146(2000).
DR EMBL; AF314827; AAK13419.1; -.
KW Receptor.
FT NON_TER 1
SQ SEQUENCE 16 AA; 1951 MW; 7751863FE5F52E2 CRC64;

Query Match 29.5%; Score 31; DB 6; Length 16;
Best Local Similarity 60.0%; Pred. No. 3.4e+02;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 PPLSQTFSD 10
   ||| |||
DB 4 PPLFLEVFED 13

RESULT 3
O77538 PRELIMINARY; PRT; 14 AA.
AC O77538; Q9TQV9;
DT 01-NOV-1998 (TREMELrel. 08, Created)
DT 01-MAR-2001 (TREMELrel. 16, Last sequence update)
DT 01-MAR-2002 (TREMELrel. 20, Last annotation update)
DE Growth hormone receptor (Fragment).
GN GHR.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1];
RP SEQUENCE FROM N.A.
RA Jiang H., Lucy M.C.;
RT "Identification of 5' untranslated variants of bovine growth hormone
RT receptor mRNA.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [2];
RP SEQUENCE FROM N.A.
RC STRAIN-BREED HOLSTEIN;
RX MEDLINE=99175163; PubMed=10075683;
RA Jiang H., Okamura C.S., Lucy M.C.;
RT "Isolation and characterization of a novel promoter for the bovine
RT growth hormone receptor gene.";
RL J. Biol. Chem. 274:7893-7900(1999).
RN [3];
RP SEQUENCE FROM N.A.
RA Jiang H., Lucy M.C.;
RT "Identification of 5' untranslated variants of bovine growth hormone
RT receptor mRNA.";
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
RN [4];
RP SEQUENCE FROM N.A.
RA Jiang H., Lucy M.C.;
RT "Bovine GH receptor 5' UTR variants.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF036297; AAC33315.2; -.

RESULT 4
Q9XN01 PRELIMINARY; PRT; 17 AA.
AC Q9XN01;
DT 01-NOV-1999 (TREMELrel. 12, Created)
DT 01-NOV-1999 (TREMELrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMELrel. 12, Last annotation update)
DE Cytochrome oxidase subunit 2 (Fragment).
GN COII.
OS Boophilus microplus (Cattle tick).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Parasitiformes; Ixodida; Ixodidae; Boophilus.
OX NCBI_TaxID=6941;
RN [1];
RP SEQUENCE FROM N.A.
RC STRAIN=N;
RX MEDLINE=99297341; PubMed=10368952;
RA Campbell N.J.H., Barker S.C.;
RT "The novel mitochondrial gene arrangement of the cattle tick,
RT Boophilus microplus: fivefold tandem repetition of a coding region.";
RL Mol. Biol. Evol. 16:732-740(1999).
DR EMBL; AF110614; AAD28397.1; -.
KW Mitochondrion.
FT NON_TER 17
SQ SEQUENCE 17 AA; 1988 MW; 319F2D4DA7DA11F3 CRC64;

Query Match 27.6%; Score 29; DB 8; Length 17;
Best Local Similarity 75.0%; Pred. No. 7.6e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 SQTFSD 11
   ||| |||
DB 5 SQTTFSDM 12

RESULT 5
Q9UELO PRELIMINARY; PRT; 11 AA.
AC Q9UELO;
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMELrel. 17, Last annotation update)
DE FAS antigen (C95 antigen) (Fragment).
GN C95.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1];
RP SEQUENCE FROM N.A.

```



RC TISSUE=BL00D;  
RX MEDLINE=95355401; PubMed=7543095;  
RA Wada N., Matsumura M., Ohba Y., Kobayashi N., Takizawa T.,  
RA Nakanishi Y.;  
RT "Transcription stimulation of the Fas-encoding gene by nuclear factor  
RT for interleukin-6 expression upon influenza virus infection.";  
RL J. Biol. Chem. 270:18007-18012(1995).  
RN [2]  
RN SEQUENCE FROM N.A.  
RP Muschen M., Re D., Brauning A., Wolf J., Hansmann M.L., Diehl V.,  
RA Kuppers R., Rajewsky K.;  
RA "Somatic mutations of the CD95 gene in Hodgkin- and Reed-Sternberg  
RT cells.";  
RT Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RN SEQUENCE FROM N.A.  
RP Muschen M., Re D., Jungnickel B., Diehl V., Rajewsky K., Kuppers R.;  
RA "Somatic mutations of the CD95 gene in human B cells as a side-effect  
RT of the germinal center reaction.";  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; D31968; BAA20850.1; -;  
DR EMBL; AJ279011; CAC35539.1; -;  
DR EMBL; AJ279012; CAC35540.1; -;  
DR EMBL; AJ279013; CAC35541.1; -;  
FT NON\_TER 11  
SQ SEQUENCE 11 AA; 1256 MW; 0802145E2731B370 CRC64;  
Query Match 25.7%; Score 27; DB 4; Length 11;  
Best Local Similarity 66.7%; Pred. No. 1e+03;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
Qy 11 LWKLLP 16  
Db 4 IWTLLP 9

RESULT 6  
P82326 ID P82326 PRELIMINARY; PRT; 14 AA.  
AC P82326;  
DT 01-JUN-2000 (TrEMBLrel. 14, Created)  
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)  
DE Unknown protein from 2D-page of thylakoid lumen (SPOT107) (Fragment).  
OS Pisum sativum (Garden pea).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.  
OX NCBI\_TaxID=3888;  
RN [1]  
RN SEQUENCE, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.  
RP STRAIN=CV. DE GRACE; TISSUE=LEAF;  
RX MEDLINE=20181728; PubMed=10715320;  
RA Peltier J.-B., Friso G., Kalume D.E., Roepstorff P., Nilsson F.,  
RA Adamska I., van Wijk K.J.;  
RT "Proteomics of the chloroplast: systematic identification and  
RT targeting analysis of luminal and peripheral thylakoid proteins.";  
RL Plant Cell 12:319-341(2000).  
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE LUMEN.  
CC -1- DEVELOPMENTAL STAGE: UNFOLDED AND FULLY DEVELOPED LEAVES.  
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
CC PROTEIN IS: 6.0, ITS MW IS: 18.3 KDA.  
KW Chloroplast; Thylakoid membrane.  
FT NON\_TER 14  
SQ SEQUENCE 14 AA; 1580 MW; 314A6CB514E1B237 CRC64;  
Query Match 24.8%; Score 26; DB 10; Length 14;  
Best Local Similarity 83.3%; Pred. No. 1.9e+03;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 PPLSQE 6  
Db 6 PPLSTE 11

RESULT 7  
Q9QVS7 ID Q9QVS7 PRELIMINARY; PRT; 17 AA.  
AC Q9QVS7;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Lactate dehydrogenase-A (Fragment).  
OS Mus sp.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10095;  
RN [1]  
RN SEQUENCE FROM N.A.  
RP MEDLINE=95201434; PubMed=7534515;  
RA Sandulache R., Pretsch W., Chatterjee B., Gimbel W., Graw J.,  
RA Favor J.;  
RT "Molecular analysis of four lactate dehydrogenase-A mutants in the  
RT mouse.";  
RL Mamm. Genome 5:777-780(1994).  
SQ SEQUENCE 17 AA; 1982 MW; E941E0A3F2477D45 CRC64;  
Query Match 24.8%; Score 26; DB 11; Length 17;  
Best Local Similarity 30.8%; Pred. No. 2.3e+03;  
Matches 4; Conservative 2; Mismatches 7; Indels 0; Gaps 0;  
Qy 1 PPLSOETFSDLWK 13  
Db 4 PELGTDAHKEQWK 16

RESULT 8  
Q9UJZ3 ID Q9UJZ3 PRELIMINARY; PRT; 18 AA.  
AC Q9UJZ3;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Oviduct glycoprotein (Fragment).  
GN OGP.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RN SEQUENCE FROM N.A.  
RP Lee K.F., Kwok K.L., Agarwal A., Lee Y.L.;  
RT "Human oviduct glycoprotein promoter sequence";  
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF189710; AAF01085.1; -;  
FT NON\_TER 18  
SQ SEQUENCE 18 AA; 2201 MW; 5E8FD91EA210E516 CRC64;  
Query Match 24.8%; Score 26; DB 4; Length 18;  
Best Local Similarity 80.0%; Pred. No. 2.5e+03;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 11 LWKLL 15  
Db 1 MWKLL 5

RESULT 9  
Q83960 ID Q83960 PRELIMINARY; PRT; 16 AA.  
AC Q83960;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE Influenza A/ann arbor/6/60 (H2n2), non-structural protein (seg 8),  
DE cooh terminus of ns1 (Fragment).

OS Influenzavirus A.  
 OC Viruses; sRNA negative-strand viruses; Orthomyxoviridae;  
 OC Influenza A viruses.  
 RN NCBI\_TaxID=11320;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=83303830; PubMed=6612993;  
 RA Parvin J.D., Young J.F., Palese P.;  
 RT "nonsense mutations affecting the lengths of the ns1 nonstructural  
 RL proteins of influenza A virus isolates.";  
 RL Virology 128:512-517(1983).  
 DR EMBL; K00962; AAA43516.1; -.  
 DR InterPro; IPR000256; Flu\_NS1.  
 DR Pfam; PF00600; Flu\_NS1; 1.  
 FT NON\_TER 1  
 SQ SEQUENCE 16 AA; 1811 MW; 23F434B5AEFFAD93 CRC64;  
 Query Match 23.8%; Score 25; DB 12; Length 16;  
 Best Local Similarity 50.0%; Pred. No. 3.2e+03;  
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 QY 12 WKLLPENG 19  
 Db : : : : :  
 2 WRSSDENG 9  
 RESULT 10  
 Q9F0P3 PRELIMINARY; PRT; 17 AA.  
 AC Q9F0P3  
 DT 01-MAR-2001 (TREMBlrel. 16, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DE Electron transfer flavoprotein subunit A (Fragment).  
 GN ETFA.  
 OS Paracoccus denitrificans.  
 OC Plasmid pLE20.  
 OC Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;  
 OC Paracoccus.  
 OC NCBI\_TaxID=266;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=93388590; PubMed=8376381;  
 RA Bedyk L.A., Escudero K.W., Gill R.E., Griffin K.J., Freyman F.E.;  
 RT "Cloning, sequencing, and expression of the genes encoding subunits of  
 RT Paracoccus denitrificans electron transfer flavoprotein.";  
 RL J. Biol. Chem. 268:20211-20217(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21101849; PubMed=11160087;  
 RA Fales L., Kryszak L., Zeilstra-Ryalls J.;  
 RT "Control of hema Expression in Rhodobacter sphaeroides 2.4.1: Effect  
 RL of a Transposon Insertion in the hbdA Gene.";  
 RL J. Bacteriol. 183:1568-1576(2001).  
 DR EMBL; AF212164; AAG43534.1; -.  
 KW Plasmid.  
 FT NON\_TER 1  
 SQ SEQUENCE 17 AA; 1744 MW; F277ELE18F28DEA2 CRC64;  
 Query Match 23.8%; Score 25; DB 2; Length 17;  
 Best Local Similarity 50.0%; Pred. No. 3.4e+03;  
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 QY 10 DLWKLPE 17  
 Db : : : : :  
 5 DLFSVWE 12  
 RESULT 11  
 P82674 PRELIMINARY; PRT; 18 AA.  
 ID P82674  
 AC P82674  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
 DE Mitochondrial 28S ribosomal protein S5 (MRP-S5) (Fragments).  
 OS Bos taurus (Bovine).  
 OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Bovidae; Bovinae; Bos.  
 RN NCBI\_TaxID=9913;  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=LIVER;  
 RA Koc E.C., Burkhardt W., Blackburn K., Moseley A., Koc H.,  
 RA Sprenull L.L.;  
 RT "Identification of four proteins from the small subunit of the  
 RL mammalian mitochondrial ribosome using a proteomics approach.";  
 RT Submitted (JUL-2000) to the SWISS-PROT data bank.  
 CC 1- SUBCELLULAR LOCATION: MITOCHONDRIAL.  
 CC 1- MASS SPECTROMETRY: MW=974.58; METHOD=ELECTROSPRAY; RANGE=1-8.  
 CC 1- SIMILARITY: BELONGS TO THE SEP FAMILY OF RIBOSOMAL PROTEINS.  
 DR InterPro; IPR000851; Ribosomal\_S5.  
 DR PROSITE; PS00585; RIBOSOMAL\_S5; PARTIAL.  
 KW Ribosomal protein; Mitochondrion.  
 FT NON\_TER 1  
 FT NON\_CONS 8 9  
 FT UNSURE 17 17 OR I.  
 FT NON\_TER 18 18  
 SQ SEQUENCE 18 AA; 2127 MW; 199BC913E7E25FAF CRC64;  
 Query Match 23.8%; Score 25; DB 6; Length 18;  
 Best Local Similarity 57.1%; Pred. No. 3.6e+03;  
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 7 TFSDLWK 13  
 Db : : : : :  
 2 TADELWK 8  
 RESULT 12  
 O84129 PRELIMINARY; PRT; 18 AA.  
 ID O84129  
 AC O84129  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
 DE Influenza A/Swine/Wisconsin/OM/2 (H1N1), non-structural protein (Seg  
 DE 8), COOH terminus of NS1 (Fragment).  
 OS Influenzavirus A.  
 OC Viruses; sRNA negative-strand viruses; Orthomyxoviridae;  
 OC Influenza A viruses.  
 OC NCBI\_TaxID=11320;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=83303830; PubMed=6612993;  
 RA Parvin J.D., Young J.F., Palese P.;  
 RT "nonsense mutations affecting the lengths of the ns1 nonstructural  
 RT proteins of influenza A virus isolates.";  
 RL Virology 128:512-517(1983).  
 DR EMBL; K00959; AAA43541.1; -.  
 DR InterPro; IPR000256; Flu\_NS1.  
 DR Pfam; PF00600; Flu\_NS1; 1.  
 FT NON\_TER 1  
 SQ SEQUENCE 18 AA; 2105 MW; 87174BD420FFEBEF CRC64;  
 Query Match 23.8%; Score 25; DB 12; Length 18;  
 Best Local Similarity 50.0%; Pred. No. 3.6e+03;  
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 QY 12 WKLLPENG 19  
 Db : : : : :  
 2 WRSSDENG 9  
 RESULT 13

```

022064
AC O22064 PRELIMINARY; PRT; 19 AA.
ID O22064;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Phosphoglucose isomerase (EC 5.3.1.9) (Fragment).
GN Pgi.
OS Dioscorea tenuipes.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Dioscoreales; Dioscoreaceae;
OC Dioscorea.
OX NCBI_TaxID=64476;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=DTE1;
RC MEDLINE=98072503; PubMed=9409845;
RA Terauchi R., Terachi T., Miyashita N.;
RT "DNA polymorphism at the Pgi locus of a wild yam, Dioscorea tokoro.";
RL Genetics 147:1899-1914(1997).
DR EMBL; AB006004; BAA23204.1; -.
KW Isomerases.
FT NON_TER 1 1
FT NON_TER 19 19
SQ SEQUENCE 19 AA; 2245 MW; 333500DFC9EAD5P8 CRC64;

Query Match 23.8%; Score 25; DB 10; Length 19;
Best Local Similarity 30.8%; Pred. No. 3.8e+03;
Matches 4; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 2 PLQOETPSDLWKL 14
Db 1 PLGPRQLQNIWLL 13

RESULT 14
Q83965 PRELIMINARY; PRT; 19 AA.
AC Q83965;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Influenza A/Berkeley/1/68 (H2N2), non-structural protein (Seg 8), cooh
DE terminus of ns1 (Fragment).
OS Influenzavirus A.
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses.
OX NCBI_TaxID=11320;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83303830; PubMed=6612993;
RA Parvin J.D., Young J.F., Palese P.;
RT "nonsense mutations affecting the lengths of the ns1 nonstructural
RT proteins of influenza A virus isolates.";
RL Virology 128:512-517(1983).
DR EMBL; K00957; AAA43518.1; -.
DR InterPro; IPR000256; Flu_NS1.
DR Pfam; PF00600; Flu_NS1; I.
FT NON_TER 1 1
FT NON_TER 19 19
SQ SEQUENCE 19 AA; 2235 MW; E10F1743F4263EAE CRC64;

Query Match 23.8%; Score 25; DB 12; Length 19;
Best Local Similarity 50.0%; Pred. No. 3.8e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 12 WKLLPENG 19
Db 2 WRSSSENG 9

RESULT 15
Q9MJQ5 PRELIMINARY; PRT; 10 AA.
ID Q9MJQ5

```

```

Q9MJQ5;
AC Q9MJQ5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Cytochrome b (Fragment).
GN CYTB.
OS Podospora curvicolli.
OG Mitochondrion.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariales; Lasiosphaeriaceae; Podospora.
OX NCBI_TaxID=48157;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=A;
RC MEDLINE=20150243; PubMed=10684923;
RA Saguez C., Lecellier G., Koll F.;
RT "Intronic GIV-VIG endonuclease gene in the mitochondrial genome of
RT Podospora curvicolli: evidence for mobility.";
RL Nucleic Acids Res. 28:1299-1306(2000).
DR EMBL; AJ249984; CAB72447.1; -.
DR InterPro; IPR000179; Cyt b b6.
DR PROSITE; PS00193; CYTOCHROME_B_OO; UNKNOWN_1.
KW Mitochondrion.
FT NON_TER 1 1
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1200 MW; C31A223B437B0772 CRC64;

Query Match 22.9%; Score 24; DB 8; Length 10;
Best Local Similarity 80.0%; Pred. No. 2.8e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 WKLLP 16
Db 6 WYLLP 10

Search completed: February 12, 2003, 10:44:59
Job time : 30 secs

```



GenCore version 5.1.3

Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 12, 2003, 10:36:28 ; Search time 29 Seconds  
(without alignments)  
27.174 Million cell updates/sec

Title: US-09-403-440A-2

Perfect score: 105

Sequence: 1 PPLSQETFSDLWLKLPENG 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 1015

Minimum DB seq length: 0

Maximum DB seq length: 19

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40.4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	22.9	10	1	HTF_HELZE
2	23	21.9	10	1	AKHX_LOCFMI
3	22	21.0	13	1	NP2_LYMST
4	22	21.0	13	1	NP2_LYMST
5	22	21.0	13	1	NP4_LYMST
6	22	21.0	13	1	NP5_LYMST
7	22	21.0	16	1	IBP4_PIG
8	21.5	20.5	12	1	UR2_SCYCA
9	21	20.0	8	1	HTF2_PERAM
10	21	20.0	10	1	HTF2_CARMO
11	21	20.0	15	1	URE1_MORMO
12	21	20.0	17	1	ACT6_SOYBN
13	21	20.0	18	1	CPAX_BOVIN
14	20	19.0	8	1	AKH_TABAT
15	20	19.0	8	1	HTF1_PERAM
16	20	19.0	10	1	HTF1_TABAT
17	20	19.0	13	1	NP3_LYMST
18	20	19.0	17	1	PH4_PERAM
19	20	19.0	18	1	PCG6_PACGO
20	20	19.0	19	1	AL22_HORSE
21	20	19.0	19	1	IRBP_CAVPO
22	20	19.0	19	1	PCG7_PACGO
23	19	18.1	8	1	AKHG_GRYBI
24	19	18.1	8	1	CLP_THICU
25	19	18.1	8	1	HTF_TENMO
26	19	18.1	10	1	HTF_NAUCI
27	19	18.1	10	1	HTF7_HUMAN
28	19	18.1	15	1	CH11_PEA
29	19	18.1	15	1	LEC1_PSOSC
30	19	18.1	15	1	PC20_BRANA
31	19	18.1	16	1	ALL1_CALVO
32	19	18.1	19	1	FIBA_ANTAM
33	19	18.1	19	1	HI70_RAT

34 18.5 17.6 15 1 FKX7\_PINPS P81104 pinus pinas  
 35 18.5 17.6 15 1 HS11\_PINPS P81083 pinus pinas  
 36 18.5 17.6 15 1 RBS\_PHYPA P80657 physcomitre  
 37 18 17.1 8 1 AKH\_LIBAU P25418 libellula a  
 38 18 17.1 8 1 RPCH\_PANBO P08939 pandalus bo  
 39 18 17.1 10 1 SLAP\_BACTG P49325 bacillus th  
 40 18 17.1 11 1 PQOC\_PSEFL P55173 pseudomonas  
 41 18 17.1 11 1 Q2OA\_COMTE P80464 comamonas t  
 42 18 17.1 14 1 NSK2\_SAPBU P41493 sarcophaga  
 43 18 17.1 14 1 UC34\_MAIZE P80640 zea mays (m  
 44 18 17.1 15 1 ARCA\_STRPS P58827 streptococc  
 45 18 17.1 15 1 LEC3\_PSOSC P22583 psophocarpu

## ALIGNMENTS

RESULT 1  
 HTF\_HELZE  
 ID HTF\_HELZE STANDARD; PRT; 10 AA.  
 AC P16353;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 01-FEB-1994 (Rel. 28, Last annotation update)  
 DE Hypertrehalosaemic hormone (HeZ-HRTH).  
 OS Heliothis zea (Corn earworm) (Bollworm).  
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
 OC Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata;  
 OC Ditrysia; Noctuoidea; Noctuidae; Heliothinae; Helicoverpa.  
 OX NCBI\_TaxID=7113;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Corpora cardiaca;  
 RA MEDLINE=88326324; PubMed=3415690;  
 RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Bird T.G.,  
 RA Tseng C.M., Zhang Y.S., Hayes D.K.;  
 RT "Isolation and primary structure of a neurotrophic hormone from  
 RT Heliothis zea with hypertrehalosaemic and adipokinetic activities.";  
 RL Biochem. Biophys. Res. Commun. 155:344-350(1988).  
 CC -!- FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT  
 CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS  
 CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).  
 CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.  
 DR PIR; A31571; A31571.  
 DR InterPro: IPR002047; AKH.  
 DR PROSITE; PS00256; AKH; 1.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 1 1  
 FT MOD\_RES 10 10  
 SQ SEQUENCE 10 AA; 1096 MW; 8E70367865A5B9D1 CRC64;  
 PYRROLIDONE CARBOXYLIC ACID.  
 AMIDATION.

Query Match 22.9%; Score 24; DB 1; Length 10;  
 Best Local Similarity 62.5%; Pred. No. 5.3e+02;  
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 5 QETESDLW 12  
 |||||  
 Db 1 QLTSSGN 8

## RESULT 2

AKHX\_LOCFMI  
 ID AKHX\_LOCFMI STANDARD; PRT; 10 AA.  
 AC P81626;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Peptide hormone.  
 OS Locusta migratoria (Migratory locust).  
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
 OC Insecta; Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;  
 OC Acridomorpha; Acridoidea; Acrididae; Oedipodinae; Locusta.  
 OX NCBI\_TaxID=7004;

```

RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=93238777; PubMed=8477756;
RA Johnson A.H., Rehfeld J.F.;
RT "Lymnaeidae", a new family of neuropeptides from the pond snail,
RT Lymnaea stagnalis. Clue to cholecystokinin immunoreactivity in
RT invertebrates?";
RL Eur. J. Biochem. 213:875-879 (1993).
CC -|- SIMILARITY: RELATED TO THE CHOLECYSTOKININ (CCK) FAMILY.
DR InterPro: IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Neuropeptide; Amidation.
FT MOD RES 1 1
FT MOD RES 10 10
FT MOD RES 13 13
SQ SEQUENCE 10 AA; 1222 MW; 81BFF67AB415B9D1 CRC64;

Query Match 21.9%; Score 23; DB 1; Length 10;
Best Local Similarity 62.5%; Pred. No. 7.6e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 QETFSDLW 12
   :|:|:|
Db 1 QVTFSDW 8

RESULT 3
NP1_LYMST
ID NP1_LYMST STANDARD; PRT; 13 AA.
AC P80178;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE Lymnaeidae; Lymnaea.
OS Lymnaea stagnalis (Great pond snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
OC Lymnaeidae; Lymnaea.
OX NCBI_TaxID=6523;
RN [1]
RP SEQUENCE.
RC TISSUE=Ganglion;
RX MEDLINE=93238777; PubMed=8477756;
RA Johnson A.H., Rehfeld J.F.;
RT "Lymnaeidae", a new family of neuropeptides from the pond snail,
RT Lymnaea stagnalis. Clue to cholecystokinin immunoreactivity in
RT invertebrates?";
RL Eur. J. Biochem. 213:875-879 (1993).
CC -|- SIMILARITY: RELATED TO THE CHOLECYSTOKININ (CCK) FAMILY.
DR InterPro: IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Neuropeptide; Amidation.
FT MOD RES 1 1
FT MOD RES 10 10
FT MOD RES 13 13
SQ SEQUENCE 13 AA; 1519 MW; 9CA07BA3F5D5B455 CRC64;

Query Match 21.0%; Score 22; DB 1; Length 13;
Best Local Similarity 50.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 LSOETFSFD 10
   :|:|:|
Db 5 ISNSAFSD 12

RESULT 4
NP2_LYMST
ID NP2_LYMST STANDARD; PRT; 13 AA.
AC P80179;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE Lymnaeidae; Lymnaea.
OS Lymnaea stagnalis (Great pond snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
OC Lymnaeidae; Lymnaea.
OX NCBI_TaxID=6523;
RN [1]
RP SEQUENCE.
RC TISSUE=Ganglion;
RX MEDLINE=93238777; PubMed=8477756;
RA Johnson A.H., Rehfeld J.F.;
RT "Lymnaeidae", a new family of neuropeptides from the pond snail,
RT Lymnaea stagnalis. Clue to cholecystokinin immunoreactivity in
RT invertebrates?";
RL Eur. J. Biochem. 213:875-879 (1993).
CC -|- SIMILARITY: RELATED TO THE CHOLECYSTOKININ (CCK) FAMILY.
DR InterPro: IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Neuropeptide; Amidation.
FT MOD RES 1 1
FT MOD RES 10 10
FT MOD RES 13 13
SQ SEQUENCE 13 AA; 1519 MW; 9CA07BA3F5D5B455 CRC64;

Query Match 21.0%; Score 22; DB 1; Length 13;
Best Local Similarity 50.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 LSOETFSFD 10
   :|:|:|
Db 5 ISNSAFSD 12

RESULT 5
NP4_LYMST
ID NP4_LYMST STANDARD; PRT; 13 AA.
AC P80181;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE Lymnaeidae; Lymnaea.
OS Lymnaea stagnalis (Great pond snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
OC Lymnaeidae; Lymnaea.
OX NCBI_TaxID=6523;
RN [1]
RP SEQUENCE.
RC TISSUE=Ganglion;
RX MEDLINE=93238777; PubMed=8477756;
RA Johnson A.H., Rehfeld J.F.;
RT "Lymnaeidae", a new family of neuropeptides from the pond snail,
RT Lymnaea stagnalis. Clue to cholecystokinin immunoreactivity in
RT invertebrates?";
RL Eur. J. Biochem. 213:875-879 (1993).
CC -|- SIMILARITY: RELATED TO THE CHOLECYSTOKININ (CCK) FAMILY.
DR InterPro: IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Neuropeptide; Amidation.
FT MOD RES 1 1
FT MOD RES 10 10
FT MOD RES 13 13
SQ SEQUENCE 13 AA; 1503 MW; 9CA07BB56D5B455 CRC64;

Query Match 21.0%; Score 22; DB 1; Length 13;
Best Local Similarity 50.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 LSOETFSFD 10
   :|:|:|
Db 5 ISNSAFSD 12

RESULT 6
NP5_LYMST
ID NP5_LYMST STANDARD; PRT; 13 AA.
AC P80182;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE Lymnaeidae; Lymnaea.
OS Lymnaea stagnalis (Great pond snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
OC Lymnaeidae; Lymnaea.
OX NCBI_TaxID=6523;
RN [1]
RP SEQUENCE.
RC TISSUE=Ganglion;
RX MEDLINE=93238777; PubMed=8477756;
RA Johnson A.H., Rehfeld J.F.;
RT "Lymnaeidae", a new family of neuropeptides from the pond snail,
RT Lymnaea stagnalis. Clue to cholecystokinin immunoreactivity in
RT invertebrates?";
RL Eur. J. Biochem. 213:875-879 (1993).
CC -|- SIMILARITY: RELATED TO THE CHOLECYSTOKININ (CCK) FAMILY.
DR InterPro: IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Neuropeptide; Amidation.
FT MOD RES 1 1
FT MOD RES 10 10
FT MOD RES 13 13
SQ SEQUENCE 13 AA; 1503 MW; 9CA07BB56D5B455 CRC64;

Query Match 21.0%; Score 22; DB 1; Length 13;
Best Local Similarity 50.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 LSOETFSFD 10
   :|:|:|
Db 5 ISNSAFSD 12

```

```

RC ZISSU-Ganglion;
RA MEDLINE=93238777; PubMed=8477756;
RX Johnson A.H., Rehfeld J.F.;
RT "Lymnaea stagnalis, a new family of neurotoxic peptides from the pond snail,
RT Lymnaea stagnalis. Clue to cholecystokinin immunoreactivity in
RT invertebrates?";
RL Eur. J. Biochem. 213:875-879(1993).
CC -1- SIMILARITY: RELATED TO THE CHOLECYSTOKININ (CCK) FAMILY.
DR PIR; S32475; S32475.
KW Neuropeptide; Amidation.
FT MOD RES 13 13
SQ SEQUENCE 13 AA; 1476 MW; 9CA07BBB56D5A5A5 CRC64;

Query Match 21.0%; Score 22; DB 1; Length 13;
Best Local Similarity 50.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 LSQTFSD 10
DB 5 ISSAFSD 12

RESULT 7
IBP4_PIG
ID IBP4_PIG STANDARD; PRT; 16 AA.
AC P24854;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Insulin-like growth factor binding protein 4 (IGFBP-4) (IBP-4)
DE (IGF-binding protein 4) (Fragment).
GN IGFBP4.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE.
RX MEDLINE=92109718; PubMed=1722398;
RA Coleman M.E., Pan Y.-C.E., Ethernon T.D.;
RT "Identification and NH2-terminal amino acid sequence of three
RT insulin-like growth factor-binding proteins in porcine serum.";
RL Biochem. Biophys. Res. Commun. 181:1131-1136(1991).
CC -1- FUNCTION: IGF-BINDING PROTEINS PROLONG THE HALF-LIFE OF THE IGFs
CC AND HAVE BEEN SHOWN TO EITHER INHIBIT OR STIMULATE THE GROWTH
CC PROMOTING EFFECTS OF THE IGFs ON CELL CULTURE. THEY ALTER THE
CC INTERACTION OF IGFs WITH THEIR CELL SURFACE RECEPTORS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: CONTAINS 1 THYROGLOBULIN TYPE-I DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE INSULIN-LIKE GROWTH FACTOR BINDING
CC PROTEIN FAMILY.
DR PIR; JH0517; JH0517.
DR InterPro; IPR000867; Ins_lgro_fac.pr.
DR InterPro; IPR000716; Thyroglobulin.1.
DR PROSITE; PS00222; IGF BINDING; PARTIAL.
DR PROSITE; PS00484; THYROGLOBULIN_1; PARTIAL.
KW Growth factor binding.
FT NON TER 16
SQ SEQUENCE 16 AA; 1799 MW; 40988840096655E2 CRC64;

Query Match 21.0%; Score 22; DB 1; Length 16;
Best Local Similarity 66.7%; Pred. No. 1.8e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PPLSQE 6
DB 7 PPSEE 12

RESULT 8
UR2_SCYCA
ID UR2_SCYCA STANDARD; PRT; 12 AA.
AC P35490;

```

```

DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Urotensin II (U-II) (UII).
OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carchariniiformes;
OC Scyliorhinidae; Scyliorhinus.
OX NCBI_TaxID=7830;
RN [1]
RP SEQUENCE.
RX TISSUE=Spinal cord;
RX MEDLINE=92319231; PubMed=1620290;
RA Conlon J.M., O'Harte F., Smith D.D., Balmert R.J., Hazon N.;
RT "Purification and characterization of urotensin II and parvalbumin
RT from an elasmobranch fish, Scyliorhinus canicula (common dogfish).";
RL Neuroendocrinology 55:230-235(1992).
CC -1- FUNCTION: HAS A SUGGESTED ROLE IN OSMOREGULATION AND AS A
CC CORTICOTROPIN-RELEASING FACTOR. PROBABLY INVOLVED IN SMOOTH
CC MUSCLE STIMULATION.
CC -1- SIMILARITY: BELONGS TO THE UROTENSIN 2 FAMILY.
DR InterPro; IPR001483; Urotensin_II.
DR Pfam; PF02083; Urotensin_II; 1.
DR PROSITE; PS00984; UROTENSIN_II; 1.
KW Hormone.
FT DISULFID 6 11
SQ SEQUENCE 12 AA; 1526 MW; 804729F9D579CEBA CRC64;

Query Match 20.5%; Score 21.5; DB 1; Length 12;
Best Local Similarity 71.4%; Pred. No. 1.6e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 8 FSD-LWK 13
DB 3 FSDCFWK 9

RESULT 9
HTF2_PERAM
ID HTF2_PERAM STANDARD; PRT; 8 AA.
AC P04549;
DT 13-AUG-1997 (Rel. 05, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE Hyperrealaesmic factor II (Neuropeptide M-II) (Periplanetin CC-2)
DE (Pea-CAH-II) (LeD-CC-II) (Hyperrealaesmic neuropeptide II).
OS Periplaneta americana (American cockroach),
OS Leptinotarsa decemlineata (Colorado potato beetle), and
OS Blatta orientalis (Oriental cockroach).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattodea; Blattidae; Periplaneta.
OX NCBI_TaxID=6978, 7539, 6976;
RN [1]
RP SEQUENCE.
RX SPECIES=P.americana;
RX MEDLINE=85046530; PubMed=6548628;
RA Witten J.L., Schaffer M.H., O'Shea M., Cook J.C., Hemling M.E.,
RA Rinehart K.L. Jr.;
RT "Structures of two cockroach neuropeptides assigned by fast atom
RT bombardment mass spectrometry.";
RL Biochem. Biophys. Res. Commun. 124:350-358(1984).
RN [2]
RP SEQUENCE.
RX SPECIES=P.americana;
RX MEDLINE=84298179; PubMed=6591205;
RA Scarborough R.M., Jamieson G.C., Kalish F., Kramer S.J., McEnroe G.A.,
RA Miller C.A., Schooley D.A.;
RT "Isolation and primary structure of two peptides with
RT cardioacceleratory and hyperglycemic activity from the corpora
RT cardiaca of Periplaneta americana.";
RT Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).
RN [3]

```

RP SEQUENCE.  
 RC SPECIES=L.decemlineata; TISSUE=Corpora cardiaca;  
 RX MEDLINE=90160053; PubMed=2576128;  
 RA Gaede G., Kellner R.;  
 RT "The metabolic neuropeptides of the corpus cardiaca from the potato  
 beetle and the American cockroach are identical.";  
 RL Peptides 10:1287-1289(1989).  
 RN [4]  
 RP SEQUENCE.  
 RC SPECIES=B.orientalis; TISSUE=Corpora cardiaca;  
 RX MEDLINE=90253659; PubMed=2340112;  
 RA Gaede G., Rinehart K.L. Jr.;  
 RT "Primary structures of hypertrehalosaemic neuropeptides isolated from  
 the corpora cardiaca of the cockroaches Leucophaea maderae,  
 Gromphadorhina portentosa, Blattella germanica and Blatta orientalis  
 and of the stick insect Extatosoma tiaratum assigned by tandem fast  
 atom bombardment mass spectrometry.";  
 RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).  
 RN [3]  
 CC -!- FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT  
 ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS  
 THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).  
 CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.  
 DR PIR; A05170; A05170.  
 DR PIR; S08996; S08996.  
 DR PIR; B4960; B4960.  
 DR PIR; B49823; B49823.  
 DR InterPro; IPR002047; AKH.  
 DR PROSITE; PS00256; AKH; 1.  
 KW Neuropeptide; Amidation.  
 FT MOD RES 1 1  
 FT MOD RES 8 8  
 FT MOD RES 8 8  
 SQ SEQUENCE 8 AA; 1006 MW; 86745771A9D1A736 CRC64;  
 Query Match 20.0%; Score 21; DB 1; Length 8;  
 Best Local Similarity 50.0%; Pred. No. 1.1e+05;  
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 OY 5 QETFSDLW 12  
 DB 1 QLTFTPNW 8  
 RESULT 10  
 HTF2\_CARMO STANDARD; PRT; 10 AA.  
 AC P11385;  
 DT 01-JUL-1989 (Rel. 11, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Hypertrehalosaemic factor II (HTF-II) (HRTH-II) (Hypertrehalosaemic  
 neuropeptide II).  
 DE Carausius morosus (Indian stick insect), and  
 OS Extatosoma tiaratum (Stick insect).  
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
 OC Insecta; Pterygota; Neoptera; Orthopteroidea; Phasmatodea;  
 OC Heteromellidae; Carausius.  
 OX NCBI\_TaxID=7022, 7024;  
 RN [1]  
 RP SEQUENCE.  
 RC SPECIES=C.morosus; TISSUE=Corpora cardiaca;  
 RX MEDLINE=87157103; PubMed=3828078;  
 RA Gaede G., Rinehart K.L. Jr.;  
 RT "Primary structure of the hypertrehalosaemic factor II from the  
 corpus cardiaca of the Indian stick insect, Carausius morosus,  
 determined by fast atom bombardment mass spectrometry.";  
 RL Biol. Chem. Hoppe-Seyler 368:67-75(1987).  
 RN [2]  
 RP SEQUENCE.  
 RC SPECIES=E.tiaratum; TISSUE=Corpora cardiaca;  
 RX MEDLINE=90253659; PubMed=2340112;  
 RA Gaede G., Rinehart K.L. Jr.;  
 RT "Primary structures of hypertrehalosaemic neuropeptides isolated from  
 the corpora cardiaca of the cockroaches Leucophaea maderae,

RT Gromphadorhina portentosa, Blattella germanica and Blatta orientalis  
 and of the stick insect Extatosoma tiaratum assigned by tandem fast  
 atom bombardment mass spectrometry.";  
 RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).  
 RN [3]  
 CC -!- FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT  
 ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS  
 THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).  
 CC -!- MASS SPECTROMETRY: MW=1308.61; METHOD=FAB.  
 CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.  
 DR PIR; S07157; S07157.  
 DR PIR; S09138; S09138.  
 DR InterPro; IPR002047; AKH.  
 DR PROSITE; PS00256; AKH; 1.  
 KW Neuropeptide; Amidation; Glycoprotein.  
 FT MOD RES 1 1  
 FT MOD RES 8 8  
 FT MOD RES 10 10  
 FT CARBOHYD 1 8  
 FT CARBOHYD 10 10  
 SQ SEQUENCE 10 AA; 1164 MW; 9B9036745771A9D1 CRC64;  
 Query Match 20.0%; Score 21; DB 1; Length 10;  
 Best Local Similarity 50.0%; Pred. No. 1.5e+03;  
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 OY 5 QETFSDLW 12  
 DB 1 QLTFTPNW 8  
 RESULT 11  
 UREL\_MORMO STANDARD; PRT; 15 AA.  
 ID UREL\_MORMO  
 AC P17337;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase) (Urease 63 kDa  
 subunit) (Fragment).  
 DE URE.  
 GN Morganella morganii (Proteus morganii).  
 OS Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Morganella.  
 OX NCBI\_TaxID=582;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=90264298; PubMed=2345135;  
 RA Hu L.-T., Nicholson E.B., Jones B.D., Lynch M.J., Mobley H.L.T.;  
 RT "Morganella morganii urease: purification, characterization, and  
 isolation of gene sequences.";  
 RL J. Bacteriol. 172:3073-3080(1990).  
 CC -!- CATALYTIC ACTIVITY: Urea + H(2)O = CO(2) + 2 NH(3).  
 CC -!- COFACTOR: Binds 2 nickel ions per subunit (Potential).  
 CC -!- SUBUNIT: (ALPHA, BETA, GAMMA) (3) (BY SIMILARITY).  
 CC -!- SIMILARITY: BELONGS TO THE UREASE FAMILY.  
 DR PIR; A35389; A35389.  
 DR InterPro; IPR001924; UreaseA.  
 DR PROSITE; PS00145; UREASE 2; PARTIAL.  
 DR PROSITE; PS01120; UREASE 1; PARTIAL.  
 KW Hydrolase; Metal-binding; Nickel.  
 FT NON\_TER 15 15  
 FT NON\_TER 15 15  
 SQ SEQUENCE 15 AA; 1650 MW; 09E27AA54241687B CRC64;  
 Query Match 20.0%; Score 21; DB 1; Length 15;  
 Best Local Similarity 25.0%; Pred. No. 2.4e+03;  
 Matches 3; Conservative 5; Mismatches 4; Indels 0; Gaps 0;



```

QY 1 PPLSQETSDLW 12
Db 1 FOISRQBYGGULF 12

RESULT 12
ACT6 SOYBN
ID ACT6 SOYBN STANDARD; PRT; 17 AA.
AC P15986;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Actin 6 (Fragment).
GN SAC6.
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Wayne.
RX MEDLINE=91346640; PubMed=2102831;
RA Pearson L., Meagher R.B.;
RT "Diverse soybean actin transcripts contain a large intron in the 5'
RT untranslated leader: structural similarity to vertebrate muscle actin
RT genes.";
RL Plant Mol. Biol. 14:513-526(1990).
CC -!- FUNCTION: ACTINS ARE HIGHLY CONSERVED PROTEINS THAT ARE INVOLVED
CC IN VARIOUS TYPES OF CELL MOTILITY AND ARE UBQUITOUSLY EXPRESSED
CC IN ALL EUKARYOTIC CELLS.
CC -!- FUNCTION: ESSENTIAL COMPONENT OF CELL CYTOSKELETON; PLAYS AN
CC IMPORTANT ROLE IN CYTOPLASMIC STREAMING, CELL SHAPE DETERMINATION,
CC CELL DIVISION, ORGANELLE MOVEMENT AND EXTENSION GROWTH.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- MISCELLANEOUS: THERE ARE AT LEAST 16 ACTIN GENES IN SOYBEAN.
CC -!- SIMILARITY: BELONGS TO THE ACTIN FAMILY.

-----
This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
-----
EMBL; X17119; CAA34979.1; -
DR PIR; S15754; S15754.
DR InterPro; IPR004001; Actin.
DR Pfam; PF00022; actin; 1.
DR PROSITE; PS00406; ACTINS 1; PARTIAL.
DR PROSITE; PS00432; ACTINS 2; PARTIAL.
DR PROSITE; PS01132; ACTINS_ACT LIKE; PARTIAL.
KW Structural protein; Multigene family.
FT NON_TER 17
FT SEQUENCE 17 AA; 1749 MW; 38F4970D4BEFF3C3 CRC64;

Query Match 20.0%; Score 21; DB 1; Length 17;
Best Local Similarity 40.0%; Pred. No. 2.7e+03;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 10 DLWKLPLPENG 19
Db 6 DIQPLVCDNG 15

RESULT 13
ID CPAX BOVIN STANDARD; PRT; 18 AA.
AC P22779;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)

```

```

DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Cytochrome P450 2A (OLF2) (Olfactive) (P52) (EC 1.14.14.1) (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=91027757; PubMed=2121272;
RA Lazard D., Tal N., Rubinstein M., Khen M., Lancet D., Zupko K.;
RT "Identification and biochemical analysis of novel olfactory-specific
RT cytochrome P-450IIA and UDP-glucuronosyl transferase.";
RL Biochemistry 29:7433-7440(1990).
CC -!- FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE
CC MONOOXYGENASES. IN LIVER MICROSOMES THIS ENZYME IS INVOLVED IN AN
CC NADPH-DEPENDENT ELECTRON TRANSPORT PATHWAY. IT OXIDIZES A VARIETY
CC OF STRUCTURALLY UNRELATED COMPOUNDS, INCLUDING STEROIDS, FATTY
CC ACIDS, AND XENOBIOTICS.
CC -!- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
CC oxidized flavoprotein + H(2)O.
CC -!- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
DR PIR; A35704; A35704.
DR InterPro; IPR001128; Cytochrome P450.
DR PROSITE; PS00086; CYTOCHROME P450; PARTIAL.
KW Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
KW Microsome; Endoplasmic reticulum; Olfaction.
FT NON_TER 1
FT VARIANT 6 G -> D.
FT VARIANT 11 A -> E.
FT NON_TER 18
FT SEQUENCE 18 AA; 2058 MW; F80746P76CCD77FF CRC64;

Query Match 20.0%; Score 21; DB 1; Length 18;
Best Local Similarity 36.4%; Pred. No. 2.9e+03;
Matches 4; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 PPLSQETSDL 11
Db 5 FQPGQQAQKEL 15

RESULT 14
ID AKH TABAT STANDARD; PRT; 8 AA.
AC P14595;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE Adipokinetic hormone (AKH) (Dipteran corpora cardiaca factor I)
DE (DCC I).
OS Tabanus atratus (Horse fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Tabanomorpha; Tabanidae; Tabanus.
OX NCBI_TaxID=7207;
RN [1]
RP SEQUENCE.
RX TISSUE=Corpora cardiaca;
RX MEDLINE=90046758; PubMed=2813385;
RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Nachman R.J.,
RA Vogel V.W., Zhang Y.-S., Hayes D.K.;
RT "Primary structure of two neuropeptide hormones with adipokinetic and
RT hypotrehalosemic activity isolated from the corpora cardiaca of horse
RT flies (Diptera).";
RL Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164(1989).
CC -!- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
CC CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
CC DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
CC MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
DR PIR; A33995; A33995.

```

```

DR InterPro; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Neuropeptide; Amidation; Flight.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 949 MW; 86786771A9D1A736 CRC64;

Query Match 19.0%; Score 20; DB 1; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.1e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 QETFSDLW 12
Db 1 QLTFTPGW 8

RESULT 15
HTF1_PERAM
ID HTF1_PERAM STANDARD; PRT; 8 AA.
AC P04548;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE Hypertrehalosaemic factor I (Neuropeptide M-I) (Periplanetin CC-I)
DE (PeA-CAH-I) (Led-CC-I) (Hypertrehalosaemic neuropeptide I).
OS Periplaneta americana (American cockroach),
OS Leptinotarsa decemlineata (Colorado potato beetle), and
OS Blatta orientalis (Oriental cockroach).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattellidae; Blattidae; Periplaneta.
OX NCBI_TaxID=6978, 7539, 6976;
RN [1]
RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=85046530; PubMed=6548628;
RA Witten J.L., Schaffer M.H., O'Shea M., Cook J.C., Hemling M.E.,
RA Rinehart K.L. Jr.;
RT "Structures of two cockroach neuropeptides assigned by fast atom
RT bombardment mass spectrometry."
RL Biochem. Biophys. Res. Commun. 124:350-358 (1984).
RN [2]
RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=84298179; PubMed=6591205;
RA Scarborough R.M., Jamieson G.C., Kalish F., Kramer S.J., McEnroe G.A.,
RA Miller C.A., Schooley D.A.;
RT "Isolation and primary structure of two peptides with
RT cardioacceleratory and hyperglycemic activity from the corpora
RT cardiaca of Periplaneta americana."
RL Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579 (1984).
RN [3]
RP SEQUENCE.
RC SPECIES=L.decemlineata; TISSUE=Corpora cardiaca;
RX MEDLINE=90160053; PubMed=2576128;
RA Gaede G., Rinehart K.L. Jr.;
RT "Primary structures of hypertrehalosaemic neuropeptides isolated from
RT the corpora cardiaca of the cockroaches Leucophaea maderae,
RT Gromphadorhina portentosa, Blattella germanica and Blatta orientalis
RT and of the stick insect Extatosoma tiaratum assigned by tandem fast
RT atom bombardment mass spectrometry."
RL Biol. Chem. Hoppe-Seyler 371:345-354 (1990).
RN [4]
RP SEQUENCE.
RC SPECIES=B.orientalis; TISSUE=Corpora cardiaca;
RX MEDLINE=90253659; PubMed=2340112;
RA Gaede G., Rinehart K.L. Jr.;
RT "Primary structures of hypertrehalosaemic neuropeptides isolated from
RT the corpora cardiaca of the cockroaches Leucophaea maderae,
RT Gromphadorhina portentosa, Blattella germanica and Blatta orientalis
RT and of the stick insect Extatosoma tiaratum assigned by tandem fast
RT atom bombardment mass spectrometry."
RL Biol. Chem. Hoppe-Seyler 371:345-354 (1990).
RN [5]
RP SEQUENCE.
CC -!- FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT
CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).

```

---

```

CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
DR PIR; A05169; A05169.
DR PIR; S08995; S08995.
DR PIR; A49823; A49823.
DR PIR; A44960; A44960.
DR InterPro; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Neuropeptide; Amidation.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 991 MW; 86745775B9C452D6 CRC64;

Query Match 19.0%; Score 20; DB 1; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.1e+05;
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 QETFSDLW 12
Db 1 QVNFSPNW 8

Search completed: February 12, 2003, 10:44:24
Job time : 30 secs

```

### RESULT 3

Wed Feb 12 11:22:41 2003

Db 1 QLTFFSGW 8

RESULT 6

S41747

Chaperonin 10 homolog - potato (fragment)

C;Species: Solanum tuberosum (potato)

C;Date: 19-Mar-1997 #sequence\_revision 29-Aug-1997 #text\_change 07-May-1999

C;Accession: S41747

R;Burt, W.J.B.; Leaver, C.J.

A;Title: Identification of a chaperonin-10 homologue in plant mitochondria.

A;Reference number: S41747; PMID:7906228

A;Accession: S41747

A;Molecule type: protein

A;Residues: 1-11 <BUR>

A;Experimental source: mitochondrion

C;Keywords: mitochondrion; molecular chaperone

Query Match 22.9%; Score 24; DB 2; Length 11;

Best Local Similarity 83.3%; Pred. No. 1.5e+03;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 14 LLPENG 19

Db 2 LLPYTG 7

RESULT 7

S11545

adipokinetic hormone - nestling-sucking blowfly

C;Species: Protophormia terraenovae (nestling-sucking blowfly)

C;Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 31-Oct-1997

C;Accession: S11545

R;Gaede, G.; Wilps, H.; Kellner, R.

Biochem. J. 269, 309-313, 1990

A;Title: Isolation and structure of a novel charged member of the red-pigment-concentrate

A;Reference number: S11545; PMID:2386478

A;Accession: S11545

A;Molecule type: protein

A;Residues: 1-8 <GAE>

C;Superfamily: adipokinetic hormone

C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 21.9%; Score 23; DB 2; Length 8;

Best Local Similarity 62.5%; Pred. No. 2.8e+05;

Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 OETFSPLW 12

Db 1 QLTFFSPDW 8

RESULT 8

A24244

adipokinetic hormone - bollworm

N;Alternate names: Hez-AKH

C;Species: Heliothis zea (bollworm, corn earworm, tomato fruitworm)

C;Date: 31-Mar-1988 #sequence\_revision 23-Mar-1995 #text\_change 31-Oct-1997

C;Accession: A24244

R;Jaaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Holman, G.M.; Wagner, R.M.; Ridgwa

Biochem. Biophys. Res. Commun. 135, 622-628, 1986

A;Title: Isolation and primary structure of a peptide from the corpora cardiaca of Heli

A;Reference number: A24244; PMID:86186794; PMID:3964263

A;Accession: A24244

A;Molecule type: protein

A;Residues: 1-9 <JAF>

C;Superfamily: adipokinetic hormone

C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutami

F;10/Modified site: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutami

Query Match 22.9%; Score 24; DB 2; Length 10;

Best Local Similarity 62.5%; Pred. No. 1.3e+03;

Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 SFLWLLQK 12

RESULT 4

PA0110

translation elongation factor eEF-1 beta' chain - Arabidopsis thaliana (fragment)

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 07-Apr-1995 #sequence\_revision 26-May-1995 #text\_change 26-Apr-1996

C;Accession: PA0110

R;Kamo, M.; Kawakami, T.; Tsugita, A.

submitted to JIPID, March 1995

A;Reference number: PA0109

A;Accession: PA0110

A;Molecule type: protein

A;Residues: 1-15 <KAM>

Query Match 23.8%; Score 25; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.4e+03;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 TFSDL 11

Db 3 TFSDL 7

RESULT 5

A31571

hypertrehalosemic/adipokinetic hormone - bollworm

N;Alternate names: Hez-HrTH

C;Species: Heliothis zea (bollworm, corn earworm, tomato fruitworm)

C;Date: 30-Jun-1989 #sequence\_revision 23-Mar-1995 #text\_change 31-Oct-1997

C;Accession: A31571

R;Jaaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Bird, T.G.; Tseng, C.M.; Zhang, Y.S

Biochem. Biophys. Res. Commun. 155, 344-350, 1988

A;Title: Isolation and primary structure of a neuropeptide hormone from Heliothis zea w

A;Reference number: A31571; PMID:88326324; PMID:3415690

A;Accession: A31571

A;Molecule type: protein

A;Residues: 1-10 <JAF>

C;Superfamily: adipokinetic hormone

C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;10/Modified site: amidated carboxyl end (Asn) #status experimental

Query Match 22.9%; Score 24; DB 2; Length 10;

Best Local Similarity 62.5%; Pred. No. 1.3e+03;

Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 SFLWLLQK 12

RESULT 6

S41747

Chaperonin 10 homolog - potato (fragment)

C;Species: Solanum tuberosum (potato)

C;Date: 19-Mar-1997 #sequence\_revision 29-Aug-1997 #text\_change 07-May-1999

C;Accession: S41747

R;Burt, W.J.B.; Leaver, C.J.

A;Title: Identification of a chaperonin-10 homologue in plant mitochondria.

A;Reference number: S41747; PMID:7906228

A;Accession: S41747

A;Molecule type: protein

A;Residues: 1-11 <BUR>

A;Experimental source: mitochondrion

C;Keywords: mitochondrion; molecular chaperone

Query Match 22.9%; Score 24; DB 2; Length 11;

Best Local Similarity 83.3%; Pred. No. 1.5e+03;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 14 LLPENG 19

Db 2 LLPYTG 7

RESULT 7

S11545

adipokinetic hormone - nestling-sucking blowfly

C;Species: Protophormia terraenovae (nestling-sucking blowfly)

C;Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 31-Oct-1997

C;Accession: S11545

R;Gaede, G.; Wilps, H.; Kellner, R.

Biochem. J. 269, 309-313, 1990

A;Title: Isolation and structure of a novel charged member of the red-pigment-concentrate

A;Reference number: S11545; PMID:2386478

A;Accession: S11545

A;Molecule type: protein

A;Residues: 1-8 <GAE>

C;Superfamily: adipokinetic hormone

C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutami

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 21.9%; Score 23; DB 2; Length 8;

Best Local Similarity 62.5%; Pred. No. 2.8e+05;

Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 OETFSPLW 12

Db 1 QLTFFSPDW 8

RESULT 8

A24244

adipokinetic hormone - bollworm

N;Alternate names: Hez-AKH

C;Species: Heliothis zea (bollworm, corn earworm, tomato fruitworm)

C;Date: 31-Mar-1988 #sequence\_revision 23-Mar-1995 #text\_change 31-Oct-1997

C;Accession: A24244

R;Jaaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Holman, G.M.; Wagner, R.M.; Ridgwa

Biochem. Biophys. Res. Commun. 135, 622-628, 1986

A;Title: Isolation and primary structure of a peptide from the corpora cardiaca of Heli

A;Reference number: A24244; PMID:86186794; PMID:3964263

A;Accession: A24244

A;Molecule type: protein

A;Residues: 1-9 <JAF>

C;Superfamily: adipokinetic hormone

C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutami

F;10/Modified site: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutami

Query Match 22.9%; Score 24; DB 2; Length 10;

Best Local Similarity 62.5%; Pred. No. 1.3e+03;

Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 SFLWLLQK 12

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;9/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 21.9%; Score 23; DB 2; Length 9;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 QETPSDLW 12  
DB 1 QLTFTSSW 8

## RESULT 9

S20410  
Lymnaea stagnalis - spinach chloroplast (fragment)  
N;Alternate names: LHCII protein kinase  
C;Species: chloroplast Spinacia oleracea (spinach)  
C;Date: 19-Mar-1997 #sequence\_revision 11-Jun-1999 #text\_change 11-Jun-1999  
C;Accession: S20410  
R;Gal, A.; Herrmann, R.G.; Lottspeich, F.; Ohad, I.  
FEBS Lett. 298, 33-35, 1992  
A;Title: Phosphorylation of cytochrome b6 by the LHC II kinase associated with the cytochrome b6  
A;Reference number: S20410; MUID:92183823; PMID:1544419  
A;Accession: S20410  
A;Molecule type: protein  
A;Residues: 1-15 <GAL>  
C;Genetics:  
A;Genome: chloroplast  
C;Function:  
A;Description: is responsible for the regulation of energy distribution between photosystems  
A;Note: does not exhibit redox-controlled activation  
C;Keywords: chloroplast; light-harvesting complex; membrane-associated complex; phosphotransferase

Query Match 21.9%; Score 23; DB 2; Length 15;  
Best Local Similarity 40.0%; Pred. No. 2.9e+03;  
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 PPLSQETPSD 10  
DB 5 PDVEXSTLSD 14

## RESULT 10

S70615  
endo-1,4-beta-xylanase (EC 3.2.1.8) - Streptomyces sp. (Chainia sp. NCL 82.5.1) (fragment)  
N;Alternate names: xylanase  
C;Species: Streptomyces sp.  
A;Variety: Chainia sp. NCL 82.5.1  
C;Date: 19-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 07-May-1999  
C;Accession: S70615  
R;Rao, M.; Khadilkar, S.; Bandivadekar, K.R.; Deshpande, V.  
Biochem. J. 316, 771-775, 1996  
A;Title: Structural environment of an essential cysteine residue of xylanase from Chainia  
A;Reference number: S70615; MUID:96265041; PMID:8670151  
A;Accession: S70615  
A;Molecule type: protein  
A;Residues: 1-5 <RAO>  
A;Experimental source: Chainia sp. strain NCL 82.5.1  
A;Note: the source is designated as Chainia sp.  
C;Function:  
A;Description: endohydrolyzation of beta-1,4-xylosidic linkages in xylans  
A;Pathway: fermentation of hemicellulose into ethanol  
C;Keywords: glycosidase; hydrolase

Query Match 21.0%; Score 22; DB 2; Length 5;  
Best Local Similarity 80.0%; Pred. No. 2.8e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 ETSPD 10  
DB 1 ETFXD 5

## RESULT 11

S16324  
hypochemical protein 2 - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 21-Nov-1993 #sequence\_revision 12-May-1995 #text\_change 21-Jul-2000  
C;Accession: S16324  
R;Ruberti, I.; Sessa, G.; Lucchetti, S.; Morelli, G.  
EMBO J. 10, 1787-1791, 1991  
A;Title: A novel class of plant proteins containing a homeodomain with a closely linked  
A;Reference number: S16323; MUID:91266907; PMID:1675603  
A;Accession: S16324  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-8 <RUB>  
A;Cross-references: EMBL:X58821; NID:g16327; PIDN:CAA41624.1; PID:g579259

Query Match 21.0%; Score 22; DB 2; Length 8;  
Best Local Similarity 80.0%; Pred. No. 2.8e+05;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 WKLLP 16  
DB 3 YKLLP 7

## RESULT 12

S32471  
Lymnaea stagnalis - great pond snail  
C;Species: Lymnaea stagnalis (great pond snail)  
C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 20-Aug-1999  
C;Accession: S32471  
R;Johnsen, A.H.; Rehfeld, J.F.  
Eur. J. Biochem. 213, 875-879, 1993  
A;Title: Lymnaea stagnalis, a new family of neuropeptides from the pond snail, Lymnaea stagnalis  
A;Reference number: S32471; MUID:93238777; PMID:8477756  
A;Accession: S32471  
A;Molecule type: protein  
A;Residues: 1-13 <JOH>  
A;Cross-references: PIDN:AAB26362.1; PID:g299829  
A;Experimental source: ganglia  
C;Keywords: amidated carboxyl end; neuropeptide  
F;13/Modified site: amidated carboxyl end (Phe) #status predicted

Query Match 21.0%; Score 22; DB 2; Length 13;  
Best Local Similarity 50.0%; Pred. No. 3.5e+03;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 LSQETPSD 10  
DB 5 ISNSAFSD 12

## RESULT 13

S32472  
Lymnaea stagnalis - great pond snail  
C;Species: Lymnaea stagnalis (great pond snail)  
C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 20-Aug-1999  
C;Accession: S32472  
R;Johnsen, A.H.; Rehfeld, J.F.  
Eur. J. Biochem. 213, 875-879, 1993  
A;Title: Lymnaea stagnalis, a new family of neuropeptides from the pond snail, Lymnaea stagnalis  
A;Reference number: S32471; MUID:93238777; PMID:8477756  
A;Accession: S32472  
A;Molecule type: protein  
A;Residues: 1-13 <JOH>  
A;Cross-references: PIDN:AAB26363.1; PID:g299830  
A;Experimental source: ganglia  
C;Keywords: amidated carboxyl end; neuropeptide  
F;13/Modified site: amidated carboxyl end (Phe) #status predicted

Query Match 21.0%; Score 22; DB 2; Length 13;  
Best Local Similarity 50.0%; Pred. No. 3.5e+03;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Wed Feb 12 11:22:41 2003

Qy 3 LSQETFS 10  
: ||||  
Db 5 ISSSAFSD 12

## RESULT 14

S32474  
Lymnaeidae 4 - great pond snail  
C:Species: Lymnaea stagnalis (great pond snail)  
C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 20-Aug-1999  
C:Accession: S32474  
R:Johnsen, A.H.; Rehfeld, J.F.  
Eur. J. Biochem. 213, 875-879, 1993  
A:Title: Lymnaeidae, a new family of neuroleptids from the pond snail, Lymnaea stagnalis  
A:Reference number: S32471; MUID:93238777; PMID:8477756  
A:Accession: S32474  
A:Molecule type: protein  
A:Residues: 1-13 <JOH>  
A:Cross-references: PIDN:AAB26365.1; PID:g299832  
A:Experimental source: ganglia  
C:Keywords: amidated carboxyl end; neuroleptide  
F:13/Modified site: amidated carboxyl end (Phe) #status predicted

Query Match 21.0%; Score 22; DB 2; Length 13;  
Best Local Similarity 50.0%; Pred. No. 3.5e+03;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 LSQETFS 10  
: ||||  
Db 5 ISSSAFSD 12

## RESULT 15

S32475  
Lymnaeidae 5 - great pond snail  
C:Species: Lymnaea stagnalis (great pond snail)  
C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 20-Aug-1999  
C:Accession: S32475  
R:Johnsen, A.H.; Rehfeld, J.F.  
Eur. J. Biochem. 213, 875-879, 1993  
A:Title: Lymnaeidae, a new family of neuroleptids from the pond snail, Lymnaea stagnalis  
A:Reference number: S32471; MUID:93238777; PMID:8477756  
A:Accession: S32475  
A:Molecule type: protein  
A:Residues: 1-13 <JOH>  
A:Cross-references: PIDN:AAB26366.1; PID:g299833  
A:Experimental source: ganglia  
C:Keywords: amidated carboxyl end; neuroleptide  
F:13/Modified site: amidated carboxyl end (Phe) #status predicted

Query Match 21.0%; Score 22; DB 2; Length 13;  
Best Local Similarity 50.0%; Pred. No. 3.5e+03;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 LSQETFS 10  
: ||||  
Db 5 ISSSAFSD 12

Search completed: February 12, 2003, 10:45:51  
Job time : 47 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 12, 2003, 10:34:07 ; Search time 14 Seconds  
(without alignments)  
39.931 Million cell updates/sec

Title: US-09-403-440A-2

Perfect score: 105

Sequence: 1 PPLSQTFSDLWKLPPENG 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/1/iaa/5A COMB.pcp.\*
- 2: /cgn2\_6/ptodata/1/iaa/5B COMB.pcp.\*
- 3: /cgn2\_6/ptodata/1/iaa/6A COMB.pcp.\*
- 4: /cgn2\_6/ptodata/1/iaa/6B COMB.pcp.\*
- 5: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pcp.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfile1.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	99	94.3	20	4	US-09-081-975-8
2	99	94.3	20	4	US-09-081-975-10
3	99	94.3	20	4	US-09-081-975-11
4	99	94.3	20	4	US-09-081-975-16
5	99	94.3	64	1	US-08-245-500A-1
6	99	94.3	64	1	US-08-390-546-1
7	99	94.3	64	1	US-08-390-479A-1
8	99	94.3	64	1	US-08-557-393-1
9	99	94.3	64	1	US-08-390-516C-1
10	99	94.3	64	1	US-08-390-517A-1
11	99	94.3	64	1	US-08-390-515A-1
12	99	94.3	64	2	US-08-801-718-1
13	99	94.3	64	4	US-09-170-159A-1
14	99	94.3	261	4	US-09-414-436-3
15	99	94.3	363	2	US-08-697-221-17
16	99	94.3	363	2	US-08-697-221-18
17	99	94.3	363	2	US-08-697-221-19
18	99	94.3	363	2	US-08-697-221-20
19	99	94.3	363	2	US-08-697-221-21
20	99	94.3	363	2	US-08-697-221-22
21	99	94.3	363	2	US-08-697-221-23
22	99	94.3	363	2	US-08-697-221-24
23	99	94.3	393	1	US-08-047-041A-25
24	99	94.3	393	1	US-08-047-041A-26
25	99	94.3	393	1	US-08-047-041A-27
26	99	94.3	393	1	US-08-047-041A-28
27	99	94.3	393	1	US-08-347-792-2

28 99 94.3 393 1 US-08-390-516C-6 Sequence 6, Appli  
29 99 94.3 393 1 US-08-390-516C-7 Sequence 7, Appli  
30 99 94.3 393 1 US-08-390-516C-8 Sequence 8, Appli  
31 99 94.3 393 1 US-08-390-516C-9 Sequence 9, Appli  
32 99 94.3 393 1 US-08-431-357-2 Sequence 2, Appli  
33 99 94.3 393 1 US-08-390-515A-6 Sequence 6, Appli  
34 99 94.3 393 1 US-08-390-515A-7 Sequence 7, Appli  
35 99 94.3 393 1 US-08-390-515A-8 Sequence 8, Appli  
36 99 94.3 393 1 US-08-390-515A-9 Sequence 9, Appli  
37 99 94.3 393 2 US-08-795-006A-32 Sequence 32, Appli  
38 99 94.3 393 2 US-08-697-221-2 Sequence 2, Appli  
39 99 94.3 393 2 US-08-697-221-3 Sequence 3, Appli  
40 99 94.3 393 2 US-08-697-221-4 Sequence 4, Appli  
41 99 94.3 393 2 US-08-697-221-11 Sequence 11, Appli  
42 99 94.3 393 2 US-08-697-221-12 Sequence 12, Appli  
43 99 94.3 393 2 US-08-697-221-13 Sequence 13, Appli  
44 99 94.3 393 2 US-08-697-221-14 Sequence 14, Appli  
45 99 94.3 393 2 US-08-697-221-15 Sequence 15, Appli

## ALIGNMENTS

## RESULT 1

US-09-081-975-8  
; Sequence 8, Application US/09081975  
; Patent No. 6451979  
; GENERAL INFORMATION:  
; APPLICANT: Kaelin, William  
; APPLICANT: Jost, Christine  
; TITLE OF INVENTION: METHODS OF TREATMENT USING  
; TITLE OF INVENTION: NBS-1, ANTIBODIES AND PROTEINS THERETO, AND USES OF THE  
; TITLE OF INVENTION: ANTIBODIES  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Nixon Peabody LLP  
; STREET: 101 Federal Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/081,975  
; FILING DATE: 12-MAY-1998  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/046,207  
; FILING DATE: 12-MAY-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Eisenstein, Ronald I  
; REGISTRATION NUMBER: 30,628  
; REFERENCE/DOCKET NUMBER: 47400  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-345-6054  
; TELEFAX: 617-345-1300  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-09-081-975-8

Query Match 94.3%; Score 99; DB 4; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.6e-09;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLEN 18  
Db 2 PPLSQETFSDLWKLLEN 19

## RESULT 2

US-09-081-975-10  
Sequence 10, Application US/09081975  
Patent No. 6451979

## GENERAL INFORMATION:

APPLICANT: Kaelin, William

APPLICANT: Jost, Christine

TITLE OF INVENTION: METHODS OF TREATMENT USING

TITLE OF INVENTION: NBS-1, ANTIBODIES AND PROTEINS THERETO, AND USES OF THE

TITLE OF INVENTION: ANTIBODIES

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:

ADDRESSEE: Nixon Peabody LLP

STREET: 101 Federal Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02110

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows

SOFTWARE: FastSEQ for Windows Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/081,975

FILING DATE: 12-MAY-1998

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/046,207

FILING DATE: 12-MAY-1997

ATTORNEY/AGENT INFORMATION:

NAME: Eisenstein, Ronald I

REGISTRATION NUMBER: 30,628

REFERENCE/DOCKET NUMBER: 47400

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-345-6054

TELEFAX: 617-345-1300

TELEX:

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

US-09-081-975-10

Query Match 94.3%; Score 99; DB 4; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.6e-09;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLEN 18  
Db 2 PPLSQETFSDLWKLLEN 19

## RESULT 3

US-09-081-975-11

Sequence 11, Application US/09081975

Patent No. 6451979

## GENERAL INFORMATION:

APPLICANT: Kaelin, William

APPLICANT: Jost, Christine

TITLE OF INVENTION: METHODS OF TREATMENT USING

TITLE OF INVENTION: NBS-1, ANTIBODIES AND PROTEINS THERETO, AND USES OF THE

TITLE OF INVENTION: ANTIBODIES

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:

ADDRESSEE: Nixon Peabody LLP

STREET: 101 Federal Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02110

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows

SOFTWARE: FastSEQ for Windows Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/081,975

FILING DATE: 12-MAY-1998

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/046,207

FILING DATE: 12-MAY-1997

ATTORNEY/AGENT INFORMATION:

NAME: Eisenstein, Ronald I

REGISTRATION NUMBER: 30,628

REFERENCE/DOCKET NUMBER: 47400

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-345-6054

TELEFAX: 617-345-1300

TELEX:

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

US-09-081-975-11

Query Match 94.3%; Score 99; DB 4; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.6e-09;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLEN 18  
Db 2 PPLSQETFSDLWKLLEN 19

## RESULT 4

US-09-081-975-16

Sequence 16, Application US/09081975

Patent No. 6451979

## GENERAL INFORMATION:

APPLICANT: Kaelin, William

APPLICANT: Jost, Christine

TITLE OF INVENTION: METHODS OF TREATMENT USING

TITLE OF INVENTION: NBS-1, ANTIBODIES AND PROTEINS THERETO, AND USES OF THE

TITLE OF INVENTION: ANTIBODIES

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:

ADDRESSEE: Nixon Peabody LLP

STREET: 101 Federal Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02110

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows

SOFTWARE: FastSEQ for Windows Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/081,975

FILING DATE: 12-MAY-1998

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/046,207

FILING DATE: 12-MAY-1997

ATTORNEY/AGENT INFORMATION:



NAME: Eisenstein, Ronald I  
REGISTRATION NUMBER: 30,628  
REFERENCE/DOCKET NUMBER: 47400  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-345-6054  
TELEFAX: 617-345-1300  
TELEX:  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-081-975-16

Query Match 94.3%; Score 99; DB 4; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.6e-09;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18  
Db 2 PPLSQETFSDLWKLLPEN 19

## RESULT 5

US-08-245-500A-1  
Sequence 1, Application US/08245500A  
Patent No. 5550023

## GENERAL INFORMATION:

APPLICANT: BURRELL, MARILEE  
APPLICANT: HILL, DAVID E.  
APPLICANT: KINZLER, KENNETH W.  
APPLICANT: VOGELSTEIN, BERT  
TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN  
TITLE OF INVENTION: HUMAN TUMORS  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT  
STREET: 1001 G STREET, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20001

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/245,500A  
FILING DATE: 07-APR-1993  
CLASSIFICATION: 435

## ATTORNEY/AGENT INFORMATION:

NAME: KAGAN, SARAH A.  
REGISTRATION NUMBER: 32,141  
REFERENCE/DOCKET NUMBER: 01107.42798  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-508-9100  
TELEFAX: 202-508-9299

## INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:  
LENGTH: 64 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
POSITION IN GENOME:

US-08-245-500A-1  
CHROMOSOME/SEGMENT: 17q

Query Match 94.3%; Score 99; DB 1; Length 64;  
Best Local Similarity 100.0%; Pred. No. 5.9e-09;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18  
Db 12 PPLSQETFSDLWKLLPEN 29

## RESULT 6

US-08-390-546-1  
Sequence 1, Application US/08390546  
Patent No. 5606044

## GENERAL INFORMATION:

APPLICANT: BURRELL, MARILEE  
APPLICANT: HILL, DAVID E.  
APPLICANT: KINZLER, KENNETH W.  
APPLICANT: VOGELSTEIN, BERT  
TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN  
TITLE OF INVENTION: HUMAN TUMORS  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT  
STREET: 1001 G STREET, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20001

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/390,546  
FILING DATE: 07-APR-1993  
CLASSIFICATION: 536

## ATTORNEY/AGENT INFORMATION:

NAME: KAGAN, SARAH A.  
REGISTRATION NUMBER: 32,141  
REFERENCE/DOCKET NUMBER: 01107.42798  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-508-9100  
TELEFAX: 202-508-9299

## INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:  
LENGTH: 64 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: 17q  
US-08-390-546-1

Query Match 94.3%; Score 99; DB 1; Length 64;  
Best Local Similarity 100.0%; Pred. No. 5.9e-09;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18  
Db 12 PPLSQETFSDLWKLLPEN 29

```

RESULT 7
US-08-390-479A-1
; Sequence 1, Application US/08390479A
; Patent No. 5618921
; GENERAL INFORMATION:
; APPLICANT: BURRELL, MARILEE
; APPLICANT: HILL, DAVID E.
; APPLICANT: KINZLER, KENNETH W.
; APPLICANT: VOGELSTEIN, BERT
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; TITLE OF INVENTION: HUMAN TUMORS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER & WITCOFF, LTD.
; STREET: 1001 G STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/390,479A
; FILING DATE: 02-FEB-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.48992
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX: 197430 BMB UT
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 64 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: 17q
;
US-08-390-479A-1
;
Query Match 94.3%; Score 99; DB 1; Length 64;
Best Local Similarity 100.0%; Pred. No. 5.9e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18
Db 12 PPLSQETFSDLWKLLPEN 29

RESULT 8
US-08-557-393-1
; Sequence 1, Application US/08557393
; Patent No. 5702903
; GENERAL INFORMATION:
; APPLICANT: BURRELL, MARILEE
; APPLICANT: HILL, DAVID E.
; APPLICANT: KINZLER, KENNETH W.
; APPLICANT: VOGELSTEIN, BERT
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; TITLE OF INVENTION: HUMAN TUMORS
; NUMBER OF SEQUENCES: 5

```

```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/557,393
; FILING DATE: 13-NOV-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/245,500
; FILING DATE: 18-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.42798
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX: 197430 BMB UT
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 64 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: 17q
;
US-08-557-393-1
;
Query Match 94.3%; Score 99; DB 1; Length 64;
Best Local Similarity 100.0%; Pred. No. 5.9e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18
Db 12 PPLSQETFSDLWKLLPEN 29

RESULT 9
US-08-390-516C-1
; Sequence 1, Application US/08390516C
; Patent No. 5708136
; GENERAL INFORMATION:
; APPLICANT: BURRELL, MARILEE
; APPLICANT: HILL, DAVID E.
; APPLICANT: KINZLER, KENNETH W.
; APPLICANT: VOGELSTEIN, BERT
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; TITLE OF INVENTION: HUMAN TUMORS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

```

```

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/390,516C
; FILING DATE: 07-APR-1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.42798
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX: 197430 BBMB UT
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 64 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: 17q
; US-08-390-516C-1

```

```

Query Match          94.3%; Score 99; DB 1; Length 64;
Best Local Similarity 100.0%; Pred. No. 5.9e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 PPLSQETFSDLWKLLPEN 18
   |||||
Db 12 PPLSQETFSDLWKLLPEN 29

```

## RESULT 10

```

US-08-390-517A-1
; Sequence 1, Application US/08390517A
; Patent No. 5736338
; GENERAL INFORMATION:
; APPLICANT: BURRELL, MARILEE
; APPLICANT: HILL, DAVID E.
; APPLICANT: KINZLER, KENNETH W.
; APPLICANT: VOGELSTEIN, BERT
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/390,517A
; FILING DATE: 07-APR-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.42798
; TELECOMMUNICATION INFORMATION:

```

```

; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX: 197430 BBMB UT
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 64 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: 17q
; US-08-390-517A-1

```

```

Query Match          94.3%; Score 99; DB 1; Length 64;
Best Local Similarity 100.0%; Pred. No. 5.9e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 PPLSQETFSDLWKLLPEN 18
   |||||
Db 12 PPLSQETFSDLWKLLPEN 29

```

## RESULT 11

```

US-08-390-515A-1
; Sequence 1, Application US/08390515A
; Patent No. 5756455
; GENERAL INFORMATION:
; APPLICANT: BURRELL, MARILEE
; APPLICANT: HILL, DAVID E.
; APPLICANT: KINZLER, KENNETH W.
; APPLICANT: VOGELSTEIN, BERT
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/390,515A
; FILING DATE: 07-APR-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.42798
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX: 197430 BBMB UT
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 64 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO

```

FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: 17q  
US-08-390-515A-1

Query Match 94.3%; Score 99; DB 1; Length 64;  
Best Local Similarity 100.0%; Pred. No. 5.9e-09;  
Matches 18; Conservative 0; Mismatches 0; Indels 0;

Qy 1 PPLSQETFSDLWKLLPEN 18  
Db 12 PPLSQETFSDLWKLLPEN 29

RESULT 12  
US-08-801-718-1  
; Sequence 1, Application US/08801718  
; Patent No. 5859976  
; GENERAL INFORMATION:  
; APPLICANT: BURRELL, MARILEE  
; APPLICANT: HILL, DAVID E.  
; APPLICANT: KINZLER, KENNETH W.  
; APPLICANT: VOGELSTEIN, BERT  
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN  
; TITLE OF INVENTION: HUMAN TUMORS  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT  
; STREET: 1001 G STREET, N.W.  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20001  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/801,718  
; FILING DATE: 14-FEB-1997  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/390,515  
; FILING DATE: 07-APR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: KAGAN, SARAH A.  
; REGISTRATION NUMBER: 32,141  
; REFERENCE/DOCKET NUMBER: 01107.42798  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-508-9100  
; TELEFAX: 202-508-9299  
; TELEX: 197430 BBMB UT  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 64 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: N-terminal  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
; POSITION IN GENOME:  
; CHROMOSOME/SEGMENT: 17q  
US-08-801-718-1

Query Match 94.3%; Score 99; DB 2; Length 64;  
Best Local Similarity 100.0%; Pred. No. 5.9e-09;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0.  
Qy 1 PPLSQETFSDLWKLLPEN 18  
Db 12 PPLSQETFSDLWKLLPEN 29

RESULT 13  
US-09-170-159A-1  
; Sequence 1, Application US/09170159A  
; Patent No. 6399755  
; GENERAL INFORMATION:  
; APPLICANT: BURRELL, MARILEE  
; APPLICANT: HILL, DAVID E.  
; APPLICANT: KINZLER, KENNETH W.  
; APPLICANT: VOGELSTEIN, BERT  
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN  
; TITLE OF INVENTION: HUMAN TUMORS  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT  
; STREET: 1001 G STREET, N.W.  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20001  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/170,159A  
; FILING DATE: 13-Oct-1998  
; CLASSIFICATION: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: KAGAN, SARAH A.  
; REGISTRATION NUMBER: 32,141  
; REFERENCE/DOCKET NUMBER: 01107.42798  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-508-9100  
; TELEFAX: 202-508-9299  
; TELEX: 197430 BBMB UT  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 64 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: N-terminal  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
; POSITION IN GENOME:  
; CHROMOSOME/SEGMENT: 17q  
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-170-159A-1

Query Match 94.3%; Score 99; DB 4; Length 64;  
Best Local Similarity 100.0%; Pred. No. 5.9e-09;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLPEN 18  
Db 12 PPLSQETFSDLWKLLPEN 29

RESULT 14  
US-09-414-436-3  
; Sequence 3, Application US/09414436  
; Patent No. 6294384

GENERAL INFORMATION:  
; APPLICANT: Dell'Acqua, Giorgio  
; APPLICANT: Mann, Michael J.  
; APPLICANT: Dzaou, Victor J.  
; TITLE OF INVENTION: Compositions and Methods Based Upon an Isoform of p53  
; FILE REFERENCE: P53f  
; CURRENT APPLICATION NUMBER: US/09/414,436  
; CURRENT FILING DATE: 1999-10-07  
; EARLIER APPLICATION NUMBER: 60/103,849  
; EARLIER FILING DATE: 1999-10-09  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 261  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-414-436-3

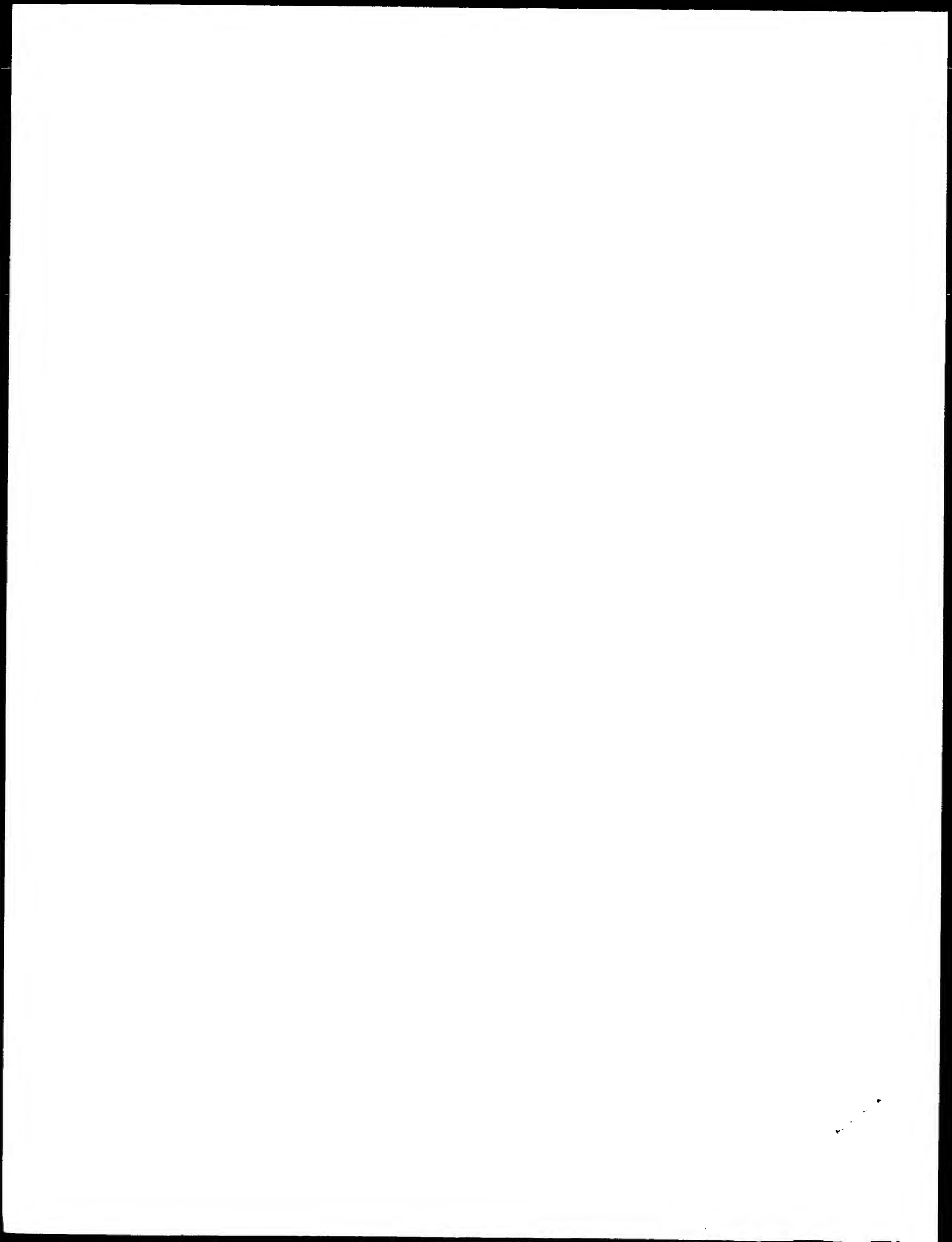
Query Match 94.3%; Score 99; DB 4; Length 261;  
Best Local Similarity 100.0%; Pred. No. 2.8e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLPEN 18  
Db 12 PPLSQETFSDLWKLLPEN 29

RESULT 15  
US-08-697-221-17  
; Sequence 17, Application US/08697221  
; Patent No. 5847083  
; GENERAL INFORMATION:  
; APPLICANT: Halazonetis, Thanos D.  
; TITLE OF INVENTION: Modified p53 Constructs and Uses  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Howson and Howson  
; STREET: Spring House Corporate Cntr., PO Box 457  
; CITY: Spring House  
; STATE: Pennsylvania  
; COUNTRY: USA  
; ZIP: 19477  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/697,221  
; FILING DATE:  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/004,802  
; FILING DATE: 22-SEP-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kodroff, Cathy A.  
; REGISTRATION NUMBER: 33,980  
; REFERENCE/DOCKET NUMBER: WST64AUSA  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-540-9206  
; TELEFAX: 215-540-5818  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 363 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-697-221-17

Query Match 94.3%; Score 99; DB 2; Length 363;  
Best Local Similarity 100.0%; Pred. No. 4e-08;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 PPLSQETFSDLWKLLPEN 18  
Db 12 PPLSQETFSDLWKLLPEN 29  
Search completed: February 12, 2003, 10:36:21  
Job time : 15 secs



GenCore version 5.1.3  
Copyright (C) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 12, 2003, 10:35:07 ; Search time 19 Seconds  
(without alignments)  
83.787 Million cell updates/sec

Title: US-09-403-440A-2

Perfect score: 105

Sequence: 1 PPLSQETFSDLWKLLPENG 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425801 seqs, 83787487 residues

Total number of hits satisfying chosen parameters: 425801

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending Patents AA New.\*  
1: /cgn2\_6/ptodata/1/paa/PCT\_NEW\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/paa/US06\_NEW\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/paa/US07\_NEW\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/paa/US08\_NEW\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/paa/US09\_NEW\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/paa/US10\_NEW\_COMB.pep.\*  
7: /cgn2\_6/ptodata/1/paa/US60\_NEW\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	99	94.3	351	5	US-09-724-676-56463
2	99	94.3	351	5	US-09-724-676-56463
3	99	94.3	353	5	US-09-849-602-24
4	99	94.3	393	1	PCT-US02-21461-3
5	99	94.3	393	5	US-09-860-286-9
6	99	94.3	393	6	US-10-274-874-4
7	99	94.3	393	7	US-60-423-552-118
8	99	94.3	393	7	US-60-427-579-118
9	92	87.6	19	7	US-60-438-805-9
10	91	86.7	32	6	US-10-276-774-2505
11	81	77.1	15	6	US-10-211-088-141
12	70	66.7	13	5	US-09-701-080C-22
13	70	66.7	13	5	US-09-701-080C-27
14	59	56.2	11	5	US-09-189-702A-286
15	51.5	49.0	927	6	US-10-218-140-250
16	51.5	49.0	1009	6	US-10-257-022-5
17	50	47.6	1879	6	US-10-072-012-220
18	46	43.8	323	6	US-10-209-582-898
19	46	43.8	422	6	US-10-233-553-25
20	46	43.8	422	6	US-10-233-553-26
21	46	43.8	422	6	US-10-233-553-27
22	46	43.8	422	6	US-10-233-553-28
23	44	41.9	116	1	PCT-US02-32727-30728
24	44	41.9	260	1	PCT-US02-32727-2767
25	44	41.9	260	6	US-10-057-498-2767
26	44	41.9	397	1	PCT-US02-40225-3137

27 44 41.9 397 6 US-10-320-797-3137 Sequence 3137, Ap  
28 44 41.9 434 6 US-10-092-411A-4695 Sequence 4695, Ap  
29 44 41.9 837 1 PCT-US02-32851-7 Sequence 7, Appli  
30 44 41.9 2828 6 US-10-072-012-607 Sequence 607, App  
31 44 41.9 2828 6 US-10-072-012-608 Sequence 608, App  
32 44 41.9 2828 6 US-10-301-822-49 Sequence 49, Appl  
33 43.5 41.4 70 1 PCT-US02-32727-3470 Sequence 3470, Ap  
34 43.5 41.4 70 6 US-10-057-498-3470 Sequence 3470, Ap  
35 43 41.0 264 6 US-10-245-539-6 Sequence 6, Appli  
36 43 41.0 1481 5 US-09-724-676-77164 Sequence 77164, A  
37 43 41.0 1481 5 US-09-724-676-77166 Sequence 77166, A  
38 43 41.0 1481 5 US-09-724-676A-77164 Sequence 77166, A  
39 43 41.0 1724 6 US-10-163-587A-17 Sequence 17, Appl  
40 43 41.0 1763 6 US-10-276-781-1032 Sequence 1032, Ap  
41 43 41.0 612 1 PCT-US02-32851-29 Sequence 29, Appl  
42 42.5 40.5 617 1 PCT-US03-01363-156 Sequence 156, App  
43 42.5 40.5 208 6 US-10-264-237-2160 Sequence 2160, Ap  
44 42 40.0 271 5 US-09-724-676-80344 Sequence 80344, A  
45 42 40.0 271 5 US-09-724-676-80344 Sequence 80344, A

## ALIGNMENTS

RESULT 1  
US-09-724-676-56463  
; Sequence 56463, Application US/09724676  
; GENERAL INFORMATION:  
; APPLICANT: CompuGen LTD  
; TITLE OF INVENTION: Variants of alternative splicing  
; FILE REFERENCE: 129181.4 CompuGen  
; CURRENT APPLICATION NUMBER: US/09/724,676  
; CURRENT FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 97222  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 56463  
; LENGTH: 351  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-724-676-56463

Query Match 94.3%; Score 99; DB 5; Length 351;  
Best Local Similarity 100.0%; Pred. No. 6.3e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18  
Db 12 PPLSQETFSDLWKLLPEN 29

RESULT 2  
US-09-724-676A-56463  
; Sequence 56463, Application US/09724676A  
; GENERAL INFORMATION:  
; APPLICANT: CompuGen LTD  
; TITLE OF INVENTION: Variants of alternative splicing  
; FILE REFERENCE: 129181.4 CompuGen  
; CURRENT APPLICATION NUMBER: US/09/724,676A  
; CURRENT FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 97222  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 56463  
; LENGTH: 351  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-724-676A-56463

Query Match 94.3%; Score 99; DB 5; Length 351;  
Best Local Similarity 100.0%; Pred. No. 6.3e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18  
Db 12 PPLSQETFSDLWKLLPEN 29





;  
; PRIOR FILING DATE: 1998-03-27  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 4  
; LENGTH: 393  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-274-874-4

Query Match 94.3%; Score 99; DB 6; Length 393;  
Best Local Similarity 100.0%; Pred. No. 7e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18  
| | | | | | | | | | | | | | | | | |  
DB 12 PPLSQETFSDLWKLLPEN 29

## RESULT 7

US-60-423-552-118  
; Sequence 118, Application US/60423552  
; GENERAL INFORMATION:  
; APPLICANT: American Home Product Inc.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING MAJOR DEPRES  
; FILE REFERENCE: AM101250L  
; CURRENT APPLICATION NUMBER: US/60/423,552  
; CURRENT FILING DATE: 2002-11-05  
; NUMBER OF SEQ ID NOS: 256  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 118  
; LENGTH: 393  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-60-423-552-118

Query Match 94.3%; Score 99; DB 7; Length 393;  
Best Local Similarity 100.0%; Pred. No. 7e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18  
| | | | | | | | | | | | | | | | | |  
DB 12 PPLSQETFSDLWKLLPEN 29

## RESULT 8

US-60-427-579-118  
; Sequence 118, Application US/60427579  
; GENERAL INFORMATION:  
; APPLICANT: American Home Product Inc.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING MAJOR DEPRES  
; FILE REFERENCE: AM101250L  
; CURRENT APPLICATION NUMBER: US/60/427,579  
; CURRENT FILING DATE: 2002-11-20  
; NUMBER OF SEQ ID NOS: 256  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 118  
; LENGTH: 393  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-60-427-579-118

Query Match 94.3%; Score 99; DB 7; Length 393;  
Best Local Similarity 100.0%; Pred. No. 7e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18  
| | | | | | | | | | | | | | | | | |  
DB 12 PPLSQETFSDLWKLLPEN 29

## RESULT 9

US-60-438-805-9  
; Sequence 9, Application US/60438805  
; GENERAL INFORMATION:  
; APPLICANT: KODAREK, THOMAS  
; TITLE OF INVENTION: MIXED ELEMENT CAPTURE AGENTS  
; FILE REFERENCE: UTSD:93SUSE1  
; CURRENT APPLICATION NUMBER: US/60/438,805  
; CURRENT FILING DATE: 2003-01-09  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 9  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
US-60-438-805-9

Query Match 87.6%; Score 92; DB 7; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.5e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLSQETFSDLWKLLPEN 18  
| | | | | | | | | | | | | | | | | |  
DB 1 PLSQETFSDLWKLLPEN 17

## RESULT 10

US-10-276-774-2505  
; Sequence 2505, Application US/10276774  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; APPLICANT: Tang, Y. Tom et al  
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides  
; FILE REFERENCE: 21272-030  
; CURRENT APPLICATION NUMBER: US/10/276,774  
; CURRENT FILING DATE: 2002-11-18  
; PRIOR APPLICATION NUMBER: 09/560,875  
; PRIOR FILING DATE: 2000-04-27  
; PRIOR APPLICATION NUMBER: 09/496,914  
; PRIOR FILING DATE: 2000-02-03  
; NUMBER OF SEQ ID NOS: 2700  
; SOFTWARE: Custom  
; SEQ ID NO 2505  
; LENGTH: 32  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-276-774-2505

Query Match 86.7%; Score 91; DB 6; Length 32;  
Best Local Similarity 94.4%; Pred. No. 1.1e-07;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18  
| | | | | | | | | | | | | | | | | |  
DB 12 PPLSQETFSDLWKLLSEN 29

## RESULT 11

US-10-211-088-141  
; Sequence 141, Application US/10211088  
; GENERAL INFORMATION:  
; APPLICANT: Bright, Gary R.  
; APPLICANT: Premkumar, D. David  
; APPLICANT: Chen, Yih-Tai  
; TITLE OF INVENTION: Novel Fusion Proteins And Assays For Molecular Binding  
; FILE REFERENCE: 01-1022-US  
; CURRENT APPLICATION NUMBER: US/10/211,088  
; CURRENT FILING DATE: 2002-10-15  
; PRIOR APPLICATION NUMBER: 60/309,395  
; PRIOR FILING DATE: 2001-08-01  
; PRIOR APPLICATION NUMBER: 60/341,589

; PRIOR FILING DATE: 2001-12-13  
; NUMBER OF SEQ ID NOS: 366  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 141  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Binding domain  
US-10-211-088-141

Query Match 77.1%; Score 81; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLL 15  
| | | | | | | | | | | | | | |  
Db 1 PPLSQETFSDLWKLL 15

## RESULT 12

US-09-701-080C-22  
; Sequence 22, Application US/09701080C  
; GENERAL INFORMATION:  
; APPLICANT: INSTITUTE OF MOLECULAR AND CELL BIOLOGY  
; TITLE OF INVENTION: POLYPEPTIDES FROM CREB BINDING PROTEIN AND RELATED PROTEIN P300 F  
; FILE REFERENCE: N73477C GCW  
; CURRENT APPLICATION NUMBER: US/09/701,080C  
; CURRENT FILING DATE: 2001-02-27  
; PRIOR FILING DATE: 2001-02-27  
; PRIOR FILING DATE: 1998-05-26  
; PRIOR FILING DATE: 1999-01-05  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 22  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: derived from p53  
US-09-701-080C-22

Query Match 66.7%; Score 70; DB 5; Length 13;  
Best Local Similarity 100.0%; Pred. No. 9.6e-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SQETFSDLWKLLP 16  
| | | | | | | | | | | | | | |  
Db 1 SQETFSDLWKLLP 13

## RESULT 13

US-09-701-080C-27  
; Sequence 27, Application US/09701080C  
; GENERAL INFORMATION:  
; APPLICANT: INSTITUTE OF MOLECULAR AND CELL BIOLOGY  
; TITLE OF INVENTION: POLYPEPTIDES FROM CREB BINDING PROTEIN AND RELATED PROTEIN P300 F  
; FILE REFERENCE: N73477C GCW  
; CURRENT APPLICATION NUMBER: US/09/701,080C  
; CURRENT FILING DATE: 2001-02-27  
; PRIOR FILING DATE: 1998-05-26  
; PRIOR FILING DATE: 1999-01-05  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 27  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Artificial Sequence

; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: derived from p53  
US-09-701-080C-27

Query Match 66.7%; Score 70; DB 5; Length 13;  
Best Local Similarity 100.0%; Pred. No. 9.6e-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SQETFSDLWKLLP 16  
| | | | | | | | | | | | | | |  
Db 1 SQETFSDLWKLLP 13

## RESULT 14

US-09-189-702A-286  
; Sequence 286, Application US/09189702A  
; GENERAL INFORMATION:  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Sidney, John  
; APPLICANT: Kast, W. Martin  
; APPLICANT: Southwood, Scott  
; APPLICANT: Epimmune, Inc.  
; TITLE OF INVENTION: HLA Binding Peptides and Their Uses  
; FILE REFERENCE: 39963-20019.20  
; CURRENT APPLICATION NUMBER: US/09/189,702A  
; CURRENT FILING DATE: 1998-11-10  
; PRIOR FILING DATE: 1994-03-04  
; NUMBER OF SEQ ID NOS: 380  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 286  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: p53.14 peptide 34.0324  
US-09-189-702A-286

Query Match 56.2%; Score 59; DB 5; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.0046;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LSQETFSDLWK 13  
| | | | | | | | | | | |  
Db 1 LSQETFSDLWK 11

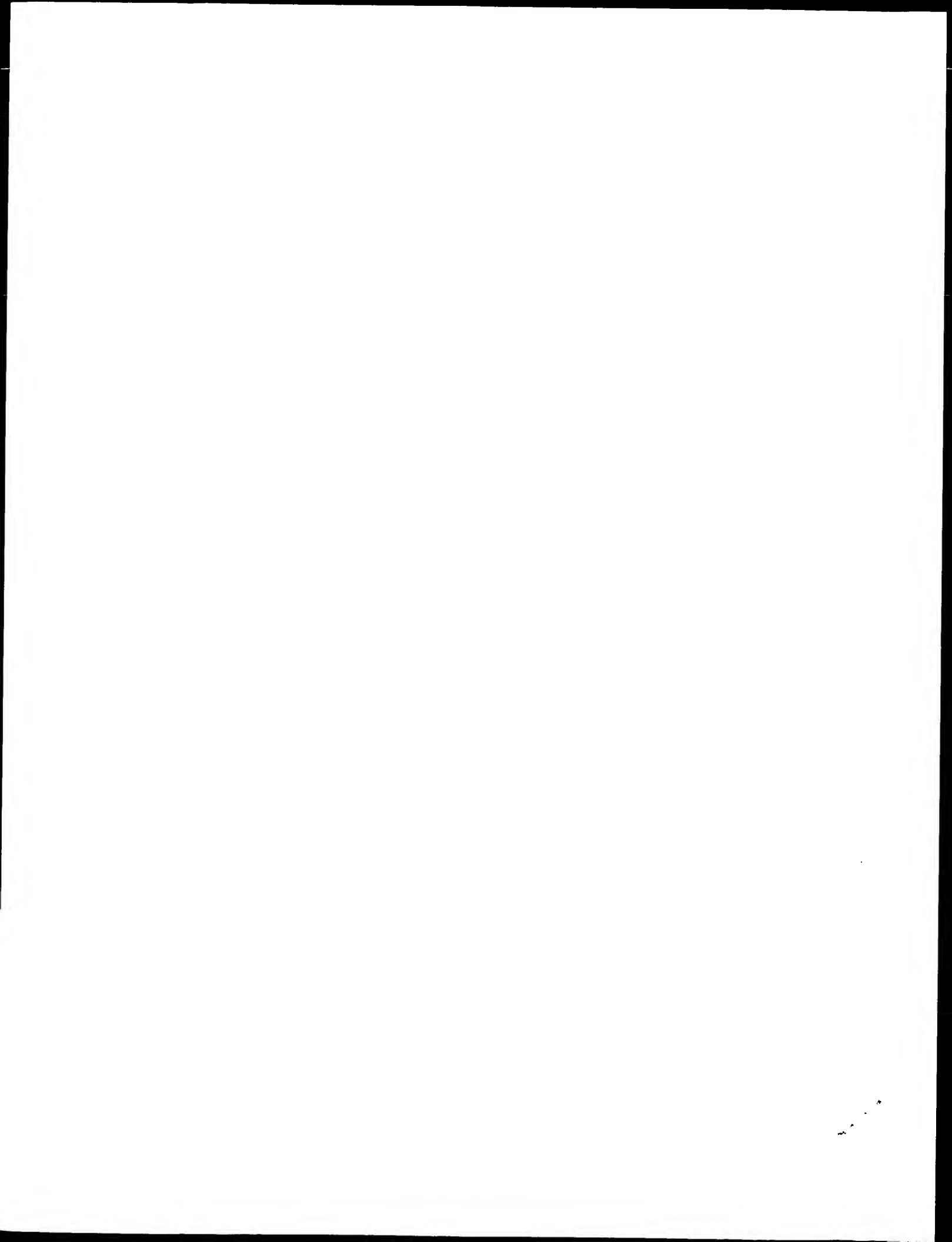
## RESULT 15

US-10-218-140-250  
; Sequence 250, Application US/10218140  
; GENERAL INFORMATION:  
; APPLICANT: Leach, Martin D.  
; APPLICANT: Shimkets, Richard A.  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND POLYPEPTIDES  
; FILE REFERENCE: 15966-543 CON  
; CURRENT APPLICATION NUMBER: US/10/218,140  
; CURRENT FILING DATE: 2002-08-12  
; PRIOR FILING DATE: 2000-03-30  
; PRIOR FILING DATE: 1999-04-05  
; PRIOR FILING DATE: 1999-04-05  
; PRIOR FILING DATE: 1999-04-02  
; PRIOR FILING DATE: 1999-03-31  
; NUMBER OF SEQ ID NOS: 6322  
; SOFTWARE: Curator Version 1.0  
; SEQ ID NO 250  
; LENGTH: 927  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-218-140-250

Query Match 49.0%; Score 51.5; DB 6; Length 927;  
Best Local Similarity 47.4%; Pred. No. 6;  
Matches 9; Conservative 6; Mismatches 3; Indels 1; Gaps 1;

```
QY      2 PLSQE-TFSDLWKLTPENG 19
      |||: ||: ||: : ||
Db     616 PLEQDSTFAELWRTISKNG 634
```

Search completed: February 12, 2003, 10:42:49  
Job time : 20 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 12, 2003, 10:35:42 ; Search time 11 Seconds  
(without alignments)  
44.130 Million cell updates/sec

Title: US-09-403-440A-2

Perfect score: 105

Sequence: 1 PPLSQETFSDLWKLLPENG 19

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 140259 seqs, 25548876 residues

Total number of hits satisfying chosen parameters: 140259

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:\*  
1: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*  
2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*  
7: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep:\*  
8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*  
12: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep:\*  
13: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*  
14: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	99	94.3	18	10	US-09-214-371-74
2	99	94.3	20	12	US-10-155-059-8
3	99	94.3	20	12	US-10-155-059-10
4	99	94.3	20	12	US-10-155-059-11
5	99	94.3	20	12	US-10-155-059-16
6	99	94.3	393	10	US-09-776-695-32
7	99	94.3	393	10	US-09-732-384-3
8	99	94.3	393	10	US-09-860-211-9
9	99	94.3	394	12	US-10-155-059-4
10	94	89.5	20	12	US-10-155-059-14
11	94	89.5	20	12	US-10-155-059-15
12	93	88.6	22	10	US-09-214-371-73
13	92	87.6	19	10	US-09-732-384-7
14	90	85.7	19	12	US-10-155-059-13
15	89	84.8	19	10	US-09-214-371-1
16	86	81.9	20	12	US-10-155-059-19
17	77	73.3	15	10	US-09-732-384-6
18	74	70.5	16	12	US-10-155-059-23
19	74	70.5	20	12	US-10-155-059-20

20	72	68.6	20	12	US-10-155-059-18	Sequence 18, Appl
21	66	62.9	12	10	US-09-214-371-17	Sequence 17, Appl
22	65	61.9	15	10	US-09-950-692-6	Sequence 6, Appli
23	60	57.1	18	12	US-10-155-059-22	Sequence 22, Appl
24	59	56.2	16	10	US-09-214-371-39	Sequence 39, Appl
25	57	54.3	14	9	US-10-024-123-7	Sequence 7, Appli
26	55	52.4	12	10	US-09-214-371-7	Sequence 7, Appli
27	54	51.4	12	10	US-09-214-371-24	Sequence 24, Appl
28	54	51.4	16	10	US-09-214-371-41	Sequence 41, Appl
29	53	50.5	16	10	US-09-214-371-40	Sequence 40, Appl
30	49	46.7	12	10	US-09-214-371-25	Sequence 25, Appl
31	49	46.7	12	10	US-09-214-371-26	Sequence 26, Appl
32	48	45.7	14	10	US-09-214-371-33	Sequence 33, Appl
33	48	45.7	14	10	US-09-214-371-34	Sequence 34, Appl
34	47	44.8	10	12	US-10-155-059-17	Sequence 17, Appl
35	47	44.8	16	10	US-09-019-679-3	Sequence 3, Appli
36	46	43.8	186	10	US-09-811-284-130	Sequence 130, App
37	46	43.8	396	9	US-10-078-770-172	Sequence 172, App
38	45	42.9	837	9	US-10-045-792-12	Sequence 12, Appl
39	44	41.9	11	12	US-10-155-059-21	Sequence 21, Appl
40	44	41.9	12	10	US-09-214-371-20	Sequence 20, Appl
41	44	41.9	2828	10	US-09-905-129-21	Sequence 21, Appl
42	44	41.9	2828	10	US-09-991-630-21	Sequence 21, Appl
43	42.5	40.5	135	9	US-09-796-692-2384	Sequence 2384, Ap
44	42	40.0	15	12	US-10-155-059-24	Sequence 24, Appl
45	42	40.0	573	9	US-09-954-433-8	Sequence 8, Appli

#### ALIGNMENTS

RESULT 1  
US-09-214-371-74  
; Sequence 74, Application US/09214371B  
; Patent No. US2001001851A1  
; GENERAL INFORMATION:  
; APPLICANT: Lane, David  
; APPLICANT: Bottger, Volker  
; APPLICANT: Bottger, Angelica  
; APPLICANT: Pickaley, Stephen  
; APPLICANT: Chene, Patrick  
; APPLICANT: Hochkeppel, Heinz-Kurt  
; APPLICANT: Garcia-Echeverria, Carlos  
; APPLICANT: Furet, Pascal  
; TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2  
; FILE REFERENCE: 4-20937/A/PCT  
; CURRENT APPLICATION NUMBER: US/09/214,371B  
; CURRENT FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: PCT/EP97/03549  
; PRIOR FILING DATE: 1997-07-04  
; NUMBER OF SEQ ID NOS: 83  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 74  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:peptide  
US-09-214-371-74

Query Match 94.3%; Score 99; DB 10; Length 18;  
Best Local Similarity 100.0%; Pred. No. 5.5e-09;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLPEN 18  
Db 1 PPLSQETFSDLWKLLPEN 18

RESULT 2

US-10-155-059-8  
; Sequence 8, Application US/10155059  
; Patent No. US20020147173A1

```
/
/ GENERAL INFORMATION:
/ APPLICANT: Kaelin, William
/           Jost, Christine
/ TITLE OF INVENTION: METHODS OF TREATMENT USING
/           NBS-1, ANTIBODIES AND PROTEINS THEREO, AND USES OF THE
/           ANTIBODIES
/
/ NUMBER OF SEQUENCES: 27
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Nixon Peabody LLP
/ STREET: 101 Federal Street
/ CITY: Boston
/ STATE: MA
/ COUNTRY: USA
/ ZIP: 02110
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: Windows
/ SOFTWARE: FastSeq for Windows Version 2.0b
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/155,059
/ FILING DATE: 24-MAY-2002
/ CLASSIFICATION: <Unknown>
/
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/09/081,975
/ FILING DATE: 12-MAY-1998
/ APPLICATION NUMBER: 60/046,207
/ FILING DATE: 12-MAY-1997
/
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Eisenstein, Ronald I
/ REGISTRATION NUMBER: 30,628
/ REFERENCE/DOCKET NUMBER: 47400
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 617-345-6054
/ TELEFAX: 617-345-1300
/ TELEX: <Unknown>
/
/ INFORMATION FOR SEQ ID NO: 8:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 20 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/
/ SEQUENCE DESCRIPTION: SEQ ID NO: 8:
/
/ US-10-155-059-8
/
/ Query Match          94.3%; Score 99; DB 12; Length 20;
/ Best Local Similarity 100.0%; Pred. No. 6.2e-09;
/ Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
/
/ Qy 1 PPLSQETFSDLWLKLLPEN 18
/ Db 2 PPLSQETFSDLWLKLLPEN 19
/
/ RESULT 3
/ US-10-155-059-10
/ Sequence 10, Application US/10155059
/ Patent No. US20020147173A1
/ GENERAL INFORMATION:
/ APPLICANT: Kaelin, William
/           Jost, Christine
/ TITLE OF INVENTION: METHODS OF TREATMENT USING
/           NBS-1, ANTIBODIES AND PROTEINS THEREO, AND USES OF THE
/           ANTIBODIES
/
/ NUMBER OF SEQUENCES: 27
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Nixon Peabody LLP
/ STREET: 101 Federal Street
/ CITY: Boston
/ STATE: MA
/ COUNTRY: USA
/ ZIP: 02110
/
/ COMPUTER READABLE FORM:
```

```
/
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: Windows
/ SOFTWARE: FastSeq for Windows Version 2.0b
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/155,059
/ FILING DATE: 24-MAY-2002
/ CLASSIFICATION: <Unknown>
/
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/09/081,975
/ FILING DATE: 12-MAY-1998
/ APPLICATION NUMBER: 60/046,207
/ FILING DATE: 12-MAY-1997
/
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Eisenstein, Ronald I
/ REGISTRATION NUMBER: 30,628
/ REFERENCE/DOCKET NUMBER: 47400
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 617-345-6054
/ TELEFAX: 617-345-1300
/ TELEX: <Unknown>
/
/ INFORMATION FOR SEQ ID NO: 10:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 20 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/
/ SEQUENCE DESCRIPTION: SEQ ID NO: 10:
/
/ US-10-155-059-10
/
/ Query Match          94.3%; Score 99; DB 12; Length 20;
/ Best Local Similarity 100.0%; Pred. No. 6.2e-09;
/ Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
/
/ Qy 1 PPLSQETFSDLWLKLLPEN 18
/ Db 2 PPLSQETFSDLWLKLLPEN 19
/
/ RESULT 4
/ US-10-155-059-11
/ Sequence 11, Application US/10155059
/ Patent No. US20020147173A1
/ GENERAL INFORMATION:
/ APPLICANT: Kaelin, William
/           Jost, Christine
/ TITLE OF INVENTION: METHODS OF TREATMENT USING
/           NBS-1, ANTIBODIES AND PROTEINS THEREO, AND USES OF THE
/           ANTIBODIES
/
/ NUMBER OF SEQUENCES: 27
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Nixon Peabody LLP
/ STREET: 101 Federal Street
/ CITY: Boston
/ STATE: MA
/ COUNTRY: USA
/ ZIP: 02110
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: Windows
/ SOFTWARE: FastSeq for Windows Version 2.0b
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/155,059
/ FILING DATE: 24-MAY-2002
/ CLASSIFICATION: <Unknown>
/
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/09/081,975
/ FILING DATE: 12-MAY-1998
/ APPLICATION NUMBER: 60/046,207
/ FILING DATE: 12-MAY-1997
/
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Eisenstein, Ronald I
```

REGISTRATION NUMBER: 30,628  
REFERENCE/DOCKET NUMBER: 47400  
TELEPHONE: 617-345-6054  
TELEFAX: 617-345-1300  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
US-10-155-059-11

Query Match 94.3%; Score 99; DB 12; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.2e-09;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLPEN 18  
Db 2 PPLSQETFSDLWKLLPEN 19

RESULT 5  
US-10-155-059-16  
Sequence 16, Application US/10155059  
Patent No. US20020147173A1  
GENERAL INFORMATION:  
APPLICANT: Kaelin, William  
Jost, Christine

TITLE OF INVENTION: METHODS OF TREATMENT USING  
NBS-1, ANTIBODIES AND PROTEINS THERE TO, AND USES OF THE  
ANTIBODIES

NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nixon Peabody LLP  
STREET: 101 Federal Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/155,059  
FILING DATE: 24-May-2002  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/081,975  
FILING DATE: 12-MAY-1998  
APPLICATION NUMBER: 60/046,207  
FILING DATE: 12-MAY-1997

ATTORNEY/AGENT INFORMATION:  
NAME: Eisenstein, Ronald I  
REGISTRATION NUMBER: 30,628  
REFERENCE/DOCKET NUMBER: 47400  
TELEPHONE: 617-345-6054  
TELEFAX: 617-345-1300  
TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 16:  
US-10-155-059-16

Query Match 94.3%; Score 99; DB 12; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.2e-09;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 PPLSQETFSDLWKLLPEN 18  
Db 2 PPLSQETFSDLWKLLPEN 19

## RESULT 6

US-09-776-695-32  
Sequence 32, Application US/09776695  
Patent No. US20020068283A1  
GENERAL INFORMATION:  
APPLICANT: Boeke, Jef  
Brachmann, Rainer  
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING P53  
MUTATIONS WHICH SUPPRESS P53 CANCER MUTA- TIONS  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Banner & Witcoff  
STREET: 1001 G Street, NW  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20001

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/776,695  
FILING DATE: 26-Feb-2001  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/795,006  
FILING DATE: 2001-03-28  
ATTORNEY/AGENT INFORMATION:  
NAME: Kagan, Sarah A  
REGISTRATION NUMBER: 32141  
REFERENCE/DOCKET NUMBER: 01107.03170

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-508-9100  
TELEFAX: 202-508-9299  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 393 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 32:  
US-09-776-695-32

Query Match 94.3%; Score 99; DB 10; Length 393;  
Best Local Similarity 100.0%; Pred. No. 1.5e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLPEN 18  
Db 12 PPLSQETFSDLWKLLPEN 29

## RESULT 7

US-09-732-384-3  
Sequence 3, Application US/09732384  
Patent No. US20020132977A1  
GENERAL INFORMATION:  
APPLICANT: Yuan, Zhi-Min  
Gu, Jjie  
TITLE OF INVENTION: Inhibition of p53 Degradation  
FILE REFERENCE: 21508-044

; CURRENT APPLICATION NUMBER: US/09/732,384  
 ; PRIOR FILING DATE: 2000-12-07  
 ; PRIOR APPLICATION NUMBER: 60/169,816  
 ; PRIOR FILING DATE: 1999-12-08  
 ; NUMBER OF SEQ ID NOS: 10  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 3  
 ; LENGTH: 393  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-732-384-3

Query Match 94.3%; Score 99; DB 10; Length 393;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18  
 |||||  
 Db 12 PPLSQETFSDLWKLLPEN 29

## RESULT 8

US-09-860-211-9  
 ; Sequence 9, Application US/09860211  
 ; Patent No. US20020137212A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gregory, Richard J.  
 ; Willis, Ken N.  
 ; Maneval, Daniel C.  
 ; TITLE OF INVENTION: Recombinant Adenoviral Vector and  
 ; Methods of Use

; NUMBER OF SEQUENCES: 9  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Townsend and Townsend and Crew LLP  
 ; STREET: Two Embarcadero Center, Eighth Floor  
 ; CITY: San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94111-3834

## COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/860,211  
 ; FILING DATE: 18-May-2001

## CLASSIFICATION: &lt;Unknown&gt;

; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/328,673  
 ; FILING DATE: 15-FEB-2000  
 ; APPLICATION NUMBER: US 08/142,669  
 ; FILING DATE: 25-OCT-1993  
 ; APPLICATION NUMBER: US 08/233,669  
 ; FILING DATE: 26-APR-1994

## ATTORNEY/AGENT INFORMATION:

; NAME: Smith, Timothy S.  
 ; REGISTRATION NUMBER: 35,367  
 ; REFERENCE/DOCKET NUMBER: 016930-000920US  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (415) 576-0200  
 ; TELEFAX: (415) 576-0300

## INFORMATION FOR SEQ ID NO: 9:

## SEQUENCE CHARACTERISTICS:

; LENGTH: 393 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: <Unknown>  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein

## FEATURE:

; NAME/KEY: Protein  
 ; LOCATION: 1..393  
 ; OTHER INFORMATION: /note= "human p53"

; SEQUENCE DESCRIPTION: SEQ ID NO: 9:  
 US-09-860-211-9

Query Match 94.3%; Score 99; DB 10; Length 393;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18  
 |||||  
 Db 12 PPLSQETFSDLWKLLPEN 29

## RESULT 9

US-10-155-059-4  
 ; Sequence 4, Application US/10155059  
 ; Patent No. US20020147173A1

## GENERAL INFORMATION:

; APPLICANT: Kaelin, William

; Jost, Christine

; TITLE OF INVENTION: METHODS OF TREATMENT USING

; NES-1, ANTIBODIES AND PROTEINS THEREO, AND USES OF THE

; ANTIBODIES

; NUMBER OF SEQUENCES: 27

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Nixon Peabody LLP

; STREET: 101 Federal Street

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02110

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: Windows

; SOFTWARE: FastSeq for Windows Version 2.0b

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/155,059

; FILING DATE: 24-May-2002

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/081,975

; FILING DATE: 12-MAY-1998

; APPLICATION NUMBER: 60/046,207

; FILING DATE: 12-MAY-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Eisenstein, Ronald I

; REGISTRATION NUMBER: 30,628

; REFERENCE/DOCKET NUMBER: 47400

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-345-6054

; TELEFAX: 617-345-1300

; TELEX: <Unknown>

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 394 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-10-155-059-4

Query Match 94.3%; Score 99; DB 12; Length 394;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18  
 |||||  
 Db 12 PPLSQETFSDLWKLLPEN 29

## RESULT 10

US-10-155-059-14  
 ; Sequence 14, Application US/10155059



Patent No. US20020147173A1  
GENERAL INFORMATION:  
APPLICANT: Kaelin, William  
TITLE OF INVENTION: METHODS OF TREATMENT USING  
NBS-1, ANTIBODIES AND PROTEINS THERE TO, AND USES OF THE  
ANTIBODIES  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nixon Peabody LLP  
STREET: 101 Federal Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/155,059  
FILING DATE: 24-May-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/081,975  
FILING DATE: 12-MAY-1998  
APPLICATION NUMBER: 60/046,207  
FILING DATE: 12-MAY-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Eisenstein, Ronald I  
REGISTRATION NUMBER: 30,628  
REFERENCE/DOCKET NUMBER: 47400  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-345-6054  
TELEFAX: 617-345-1300  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 14:  
US-10-155-059-14  
Query Match 89.5%; Score 94; DB 12; Length 20;  
Best Local Similarity 94.4%; Pred. No. 3.5e-08;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 PPLSQETFSDLWKLLEN 18  
DB 2 PPLSQETFSDLWKLLEN 19  
RESULT 11  
US-10-155-059-15  
Sequence 15, Application US/10155059  
Patent No. US20020147173A1  
GENERAL INFORMATION:  
APPLICANT: Kaelin, William  
TITLE OF INVENTION: METHODS OF TREATMENT USING  
NBS-1, ANTIBODIES AND PROTEINS THERE TO, AND USES OF THE  
ANTIBODIES  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nixon Peabody LLP  
STREET: 101 Federal Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/155,059  
FILING DATE: 24-May-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/081,975  
FILING DATE: 12-MAY-1998  
APPLICATION NUMBER: 60/046,207  
FILING DATE: 12-MAY-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Eisenstein, Ronald I  
REGISTRATION NUMBER: 30,628  
REFERENCE/DOCKET NUMBER: 47400  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-345-6054  
TELEFAX: 617-345-1300  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 15:  
US-10-155-059-15  
Query Match 89.5%; Score 94; DB 12; Length 20;  
Best Local Similarity 94.4%; Pred. No. 3.5e-08;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 PPLSQETFSDLWKLLEN 18  
DB 2 PPLSQETFSDLWKLLEN 19  
RESULT 12  
US-09-214-371-73  
Sequence 73, Application US/09214371B  
Patent No. US2001001851A1  
GENERAL INFORMATION:  
APPLICANT: Lane, David  
APPLICANT: Bottger, Volker  
APPLICANT: Bottger, Angelica  
APPLICANT: Pinksley, Stephen  
APPLICANT: Chene, Patrick  
APPLICANT: Hochkeppel, Heinz-Kurt  
APPLICANT: Garcia-Echeverria, Carlos  
APPLICANT: Furet, Pascal  
TITLE OF INVENTION: Inhibitors of the Interaction of p53 and MDM2  
FILE REFERENCE: 4-20937/A/PCT  
CURRENT APPLICATION NUMBER: US/09/214,371B  
CURRENT FILING DATE: 1999-03-26  
PRIOR APPLICATION NUMBER: PCT/EP97/03549  
PRIOR FILING DATE: 1997-07-04  
NUMBER OF SEQ ID NOS: 83  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 73  
LENGTH: 22  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: peptide  
NAME/KEY: VARIANT  
LOCATION: (1)  
OTHER INFORMATION: X = Biotin-Ser  
US-09-214-371-73  
Query Match 88.6%; Score 93; DB 10; Length 22;



GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 12, 2003, 10:32:16 ; Search time 36 Seconds  
(without alignments)  
70.327 Million cell updates/sec

Title: US-09-403-440A-2

Perfect score: 105

Sequence: 1 PPLSQETFSDLKLLPENG 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_101002.\*

1: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.\*  
2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*  
3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*  
4: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.\*  
5: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.\*  
6: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.\*  
7: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.\*  
8: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.\*  
9: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.\*  
10: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.\*  
11: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.\*  
12: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.\*  
13: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.\*  
14: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.\*  
15: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.\*  
16: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.\*  
17: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.\*  
18: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.\*  
19: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.\*  
20: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.\*  
21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.\*  
22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*  
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	105	100.0	19	AAW82321	p53 homologue TIP
2	105	100.0	19	AAW82319	p53 homologue TIP
3	99	94.3	18	AAW37228	p53 N-terminal pep
4	99	94.3	25	AAW54907	Immunodominant epi
5	99	94.3	25	AAW51879	Human p53 amino ac
6	99	94.3	26	AAW60202	p53 peptide used t
7	99	94.3	32	AAW30523	Peptide fragment o
8	99	94.3	36	AAW13604	p53 protein amino
9	99	94.3	41	AAW13603	p53 protein amino
10	99	94.3	52	AAW13602	p53 protein amino

11	99	94.3	64	14	AAW42174	p53 N-terminal fra
12	99	94.3	64	17	AAW07886	Human p53, involv
13	99	94.3	64	19	AAW57240	Human p53 N-termin
14	99	94.3	64	19	AAW48243	Human p53 fragment
15	99	94.3	64	19	AAW42878	N-terminal region
16	99	94.3	64	19	AAW42970	Human MDM2 binding
17	99	94.3	64	20	AAW94303	Human p53 fragment
18	99	94.3	71	18	AAW47079	Mammalian two-hybr
19	99	94.3	161	22	AAW36683	Mammalian two-hybr
20	99	94.3	164	22	AAW36689	Mammalian two-hybr
21	99	94.3	211	22	AAW36685	Human p53 amino ac
22	99	94.3	225	22	AAW36690	Human p53 amino ac
23	99	94.3	241	15	AAW51872	Novel human diagno
24	99	94.3	260	22	ABG03222	Novel human diagno
25	99	94.3	261	21	AAW70714	Chimeric p53 prote
26	99	94.3	283	22	ABG01512	Chimeric p53 prote
27	99	94.3	337	18	AAW13962	Chimeric p53 prote
28	99	94.3	355	18	AAW13950	Modified p53 varia
29	99	94.3	359	18	AAW13960	Modified p53 varia
30	99	94.3	361	18	AAW13958	Modified p53 varia
31	99	94.3	361	18	AAW13961	Modified p53 varia
32	99	94.3	363	18	AAW13971	Modified p53 varia
33	99	94.3	363	18	AAW13972	Modified p53 varia
34	99	94.3	363	18	AAW13973	Modified p53 varia
35	99	94.3	363	18	AAW13974	Modified p53 varia
36	99	94.3	363	18	AAW13975	Modified p53 varia
37	99	94.3	363	18	AAW13976	Modified p53 varia
38	99	94.3	363	18	AAW13977	Modified p53 varia
39	99	94.3	363	18	AAW13959	Modified p53 varia
40	99	94.3	363	18	AAW13954	Modified p53 varia
41	99	94.3	368	18	AAW13956	Modified p53 varia
42	99	94.3	370	18	AAW13957	Modified p53 varia
43	99	94.3	393	13	AAW22238	Sequence of 53 KD
44	99	94.3	393	13	AAW26758	p53. Synthetic.
45	99	94.3	393	16	AAW94623	p53 protein. Homo

#### ALIGNMENTS

RESULT 1

AAW82321  
ID AAW82321 standard; Peptide; 19 AA.

XX AAW82321;  
AC AC

XX 22-FEB-1999 (first entry)  
DT

XX p53 homologue TIP peptide.  
DE

XX p53; mdm2; inhibitor; therapy; activator; treatment; cancer; medicament.  
KW

XX Synthetic.  
OS

XX WO9847919-A1.  
PN

XX 29-OCT-1998.  
PD

XX 20-APR-1998; 98WO-GB01140.  
PF

XX 22-APR-1997; 97GB-0008089.  
PR

XX (UYDU-) UNIV DUNDEE.  
PA

XX Lane DP;  
PI

XX WPI; 1998-609975/51.  
DR

XX New substance with a mdm2 binding domain and coupling partner  
PT useful for stabilising in cells without an efficient mdm2-mediated  
PT degradation pathway  
PT

XX Disclosure; Fig 1; 52pp; English.  
PS

Wed Feb 12 11:22:44 2003

XX This sequence is a peptide homologue of a region of p53 which binds  
CC to mdm2. This peptide is used in the construction of a novel agent  
CC capable of disrupting the binding of p53 and mdm2 or inhibiting the  
CC production of mdm2 in a population of cells. This agent is also used in  
CC the preparation of a therapeutic for activating p53, where the population  
CC of cells do not overexpress mdm2. Inhibiting mdm2 production and/or  
CC inhibiting the clearance of p53 by mdm2, and can be used to activate p53  
CC reducing the clearance of p53 by mdm2, and can be used to activate p53  
CC function. The agents for use in therapeutics for activating p53 can be  
CC used for the treatment of cancer, viral conditions or other conditions  
CC associated with non-functional p53.  
XX  
XX SQ

Query Match 100.0%; Score 105; DB 19; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5.7e-10;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLPPENG 19  
Db 1 PPLSQETFSDLWKLPPENG 19

RESULT 2  
AAW82319 standard; Peptide; 19 AA.

XX AAW82319;  
XX 22-FEB-1999 (first entry)  
XX p53 homologue TIP peptide.  
XX p53; mdm2; inhibitor; therapy; activator; treatment; cancer; medicament.  
XX Synthetic.  
XX WO9847525-A1.

XX 29-OCT-1998.  
XX 20-APR-1998; 98WO-GB01144.  
XX 22-APR-1997; 97GB-0008092.  
XX (UYDU-) UNIV DUNDEE.  
XX Lane DP;  
XX WPI; 1998-609932/51.  
XX New agents which inhibit interaction of p53 and mdm2 - useful for  
XX activating p53, e.g. for treating cancers, viral conditions or other  
XX conditions associated with non functional p53 or mdm2  
XX Disclosure; Fig 1; 52pp; English.

XX This sequence is a peptide homologue of a region of p53 which binds  
CC to mdm2. This peptide is used in the construction of a novel agent  
CC capable of disrupting the binding of p53 and mdm2 or inhibiting the  
CC production of mdm2 in a population of cells. This agent is also used in  
CC the preparation of a therapeutic for activating p53, where the population  
CC of cells do not overexpress mdm2. Inhibiting mdm2 production and/or  
CC inhibiting the clearance of p53 by mdm2, and can be used to increase by  
CC reducing the clearance of p53 by mdm2, and can be used to activate p53  
CC function. The agents for use in therapeutics for activating p53 can be  
CC used for the treatment of cancer, viral conditions or other conditions  
CC associated with non-functional p53.  
XX  
XX SQ

Query Match 100.0%; Score 105; DB 19; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5.7e-10;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 5.7e-10;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLPPENG 19  
Db 1 PPLSQETFSDLWKLPPENG 19

RESULT 3  
AAW37228 standard; peptide; 18 AA.

XX AAW37228;  
XX 20-JUL-1998 (first entry)  
XX p53 N-terminal peptide fragment for Elisa TIP assay.

XX MDM2; oncogenic protein; p53; human; inhibition; interaction; cancer;  
XX tumour; diagnosis; binding; viral infection; Elisa TIP assay.

XX Homo sapiens.  
XX WO9801467-A2.

XX 15-JAN-1998.  
XX 04-JUL-1997; 97WO-EP03549.  
XX 07-APR-1997; 97GB-0007041.  
XX 05-JUL-1996; 96GB-0014197.  
XX (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.  
XX (NOVS) NOVARTIS AG.

XX Boettger A, Boettger V, Chene P, Furet P, Garcia-scheverria C;  
XX Hochkeppel H, Lane D, Picksley S;  
XX WPI; 1998-100996/09.

XX Compounds binding to MDM2 protein and inhibit its interaction with  
XX p53 - useful in, e.g. diagnosis and treatment of cancer and viral  
XX infections and identifying binding agents  
XX Disclosure; Page 34; 45pp; English.

XX This represents a p53 N-terminal peptide fragment used in an Elisa TIP  
XX assay for analysing the interaction between human oncogenic protein MDM2  
XX and p53. The invention provides peptide derivatives capable of binding to  
XX the human MDM2. These peptides can specifically inhibit or block the  
XX binding of MDM2 to the human p53 protein, in vitro or in vivo. Inhibiting  
XX the interaction between the p53 and MDM2 can induce growth arrest or  
XX apoptosis in tumour cells comprising a wild-type p53 and non-elevated  
XX levels of MDM2. The peptides may be used to identify molecules that bind  
XX to MDM2 and to identify and design inhibitors of MDM2/p53 binding. They  
XX may also be used to purify binding partners especially MDM2, diagnose  
XX disease by measuring levels of MDM2 in blood of cancer and leukaemia  
XX patients and for treatment or prevention of disease involving p53/MDM2  
XX interactions, especially tumours and viral infections. The peptides can  
XX be administered nasally, rectally, orally or by injection. By interfering  
XX with MDM2/p53 interaction, the peptides can activate p53 function and  
XX accumulation in normal cells. The peptides which mimic the MDM2 binding  
XX site in p53, have a significantly greater blocking activity compared  
XX with wild-type p53.

XX Sequence 18 AA;

Query Match 94.3%; Score 99; DB 19; Length 18;  
Best Local Similarity 100.0%; Pred. No. 4.9e-09;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLPPEN 18  
Db 1 PPLSQETFSDLWKLPPEN 18

Db 1 PPLSQETFSDLWKLLPEN 18

RESULT 4  
AAR54907  
ID AAR54907 standard; peptide; 25 AA.  
XX  
AC AAR54907;  
XX  
DT 29-NOV-1994 (first entry)  
XX  
DE Immunodominant epitope from p53 N-terminal.  
XX  
KW cancer; pre-cancerous state; detection; diagnosis; human p53 gene;  
KW immunodominant epitope; human cellular tumour antigen;  
XX transformation-associated protein.  
XX  
OS Homo sapiens.  
XX  
PN WO9410306-A.  
XX  
PD 11-MAY-1994.  
XX  
PF 02-NOV-1993; 93WO-FR01082.  
XX  
PR 02-NOV-1992; 92FR-0013110.  
XX  
PA (EURO-) LAB EUROBIO SA.  
XX  
PI Legros Y, Lubin R, Soussi T;  
XX  
XX WPI; 1994-167463/20.  
XX  
DR New immuno:dominant epitope(s) of protein p53 - for detecting and  
PT monitoring antibodies indicative of cancer and precancerous  
PT states  
XX  
PS Claim 4; Page 42; 62pp; French.  
XX  
CC Peptides derived from the N-terminal (amino acids 1-112) or the C-  
CC terminal (amino acids 350-393) of protein p53 which specifically  
CC react with anti-p53 antibodies in patients with cancer or  
CC precancerous conditions are claimed. The peptides (AAR54907-R54921)  
CC are useful for detecting and monitoring cancerous and precancerous  
CC conditions.  
XX  
SQ Sequence 25 AA;  
Query Match 94.3%; Score 99; DB 15; Length 25;  
Best Local Similarity 100.0%; Pred. No. 7.1e-09;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 PPLSQETFSDLWKLLPEN 18  
Db 2 PPLSQETFSDLWKLLPEN 19

RESULT 5  
AAR51879  
ID AAR51879 standard; Protein; 25 AA.  
XX  
AC AAR51879;  
XX  
DT 18-NOV-1994 (first entry)  
XX  
DE Human p53 amino acids 9-33.  
XX  
KW Human nuclear phosphoprotein p53; tumour suppressor gene product;  
KW anti-oncogene; cancer; tumour; antibody binding region; epitope.  
XX  
OS Homo sapiens.  
XX  
PN WO9408241-A.

XX 14-APR-1994.  
PD  
XX 30-SEP-1993; 93WO-EP02666.  
PF  
XX 30-SEP-1992; 92DE-4232823.  
PR  
XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM STIFTUNG.  
PA  
XX Klein R, Schranz P, Tessmer C, Volkmann M, Zentgraf H;  
PI  
XX WPI; 1994-135732/16.  
DR  
XX N-PSDB; AAQ62365.  
DR  
XX Non-radioactive detection of p53 specific antibodies - by capture  
PT on immobilised p53 or its fragments, then reaction with labelled  
PT second antibody, for diagnosis of tumours and suitable for  
PT screening  
XX  
XX Claim 11; Page 19; 35pp; German.  
PS  
XX Antibodies specific for p53 are detected by binding to immobilised  
CC fragments of the p53 gene product containing the antibody-binding  
CC region. Preferred fragments contain amino acids 1-241, 40-349,  
CC 40-393, 66-241, 66-393, 237-349, 237-393 and esp. 9-33, 37-52 or  
CC 368-386. See AAR51872-R51881 for sequences of these fragments.  
XX  
SQ Sequence 25 AA;  
Query Match 94.3%; Score 99; DB 15; Length 25;  
Best Local Similarity 100.0%; Pred. No. 7.1e-09;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 PPLSQETFSDLWKLLPEN 18  
Db 4 PPLSQETFSDLWKLLPEN 21

RESULT 6  
AAW60202  
ID AAW60202 standard; peptide; 26 AA.  
XX  
AC AAW60202;  
XX  
DT 18-AUG-1998 (first entry)  
XX  
DE p53 peptide used to detect antibodies against p53.  
XX  
KW Human; p53; antibody; detection; biosensor; cancer patient;  
KW p53 gene therapy; immune response; mutant.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
PN WO9815834-A1.  
XX  
PD 16-APR-1998.  
XX  
PF 01-OCT-1997; 97WO-US16132.  
XX  
PR 07-OCT-1996; 96US-0028533.  
XX  
PA (SCHE ) SCHERING CORP.  
XX  
PI Mytych DT, Swanson SJ;  
XX  
XX WPI; 1998-240965/21.  
XX  
DR Detecting antibodies that bind p53 by reaction with immobilised p53  
PT peptide(s) - attached directly to flow cells in the sensor chip of  
PT bio-sensor, used to analyse serum from cancer patients, e.g. those  
PT being given p53 gene therapy  
XX

Wed Feb 12 11:22:44 2003

CC the whole compound. The methods are useful for producing biologically  
 CC active compounds from inactive precursors. These compounds may be  
 CC inhibitors or stimulators of cellular metabolism, DNA replication, RNA  
 CC transcription, RNA translation, RNA elongation RNA processing, protein  
 CC synthesis, protein processing, cellular differentiation, cell division,  
 CC ion channel transmission, cellular protein and RNA transport, cell division,  
 CC processes of cellular oxidation, toxins, proteins or RNAs. AAB30523-36  
 CC represent peptides which are bound to oligomers AAC62167-80 and  
 CC AAC62181-94. The peptides are fragments of the tumour suppressor p53, and  
 CC the oligomers are antiparallel to human plasminogen antigen activator  
 CC mRNA (AAC62167-80) or human NhOT (AAC62181-94). The method of the  
 CC invention is used to produce the tumour suppressor protein p53 from the  
 CC bound peptides and oligomers.

XX SQ Sequence 32 AA;

Query Match 94.3%; Score 99; DB 22; Length 32;  
 Best Local Similarity 100.0%; Pred. No. 9.2e-09;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18  
 |||||  
 DB 12 PPLSQETFSDLWKLLPEN 29  
 |||||

RESULT 8  
 AAW13604  
 ID AAW13604 standard; peptide; 36 AA.  
 AC AAW13604;  
 XX 16-JAN-1998 (first entry)  
 DT  
 DE p53 protein amino acids 6-41.

XX Mouse; Mdm2; murine double minute; phosphoprotein; binding; modulation;  
 KW tumour suppressor; p53; oncogene; cell cycle arrest; p107; antagonist;  
 KW inhibition; transcription factor; adenocarcinoma; colon; cancer; breast;  
 KW lung; stomach; myeloid leukaemia; lymphoma; hyperproliferative;  
 KW restenosis.  
 XX Homo sapiens.  
 OS  
 XX WO9709343-A2.  
 PN  
 XX 13-MAR-1997.  
 PD  
 XX 02-SEP-1996; 96WO-FR01340.  
 PF  
 XX 04-SEP-1995; 95FR-0010331.  
 PR  
 XX (INRM ) INST NAT SANTE & RECH MEDICALE.  
 PA (RHON ) RHONE FOULENC RORER SA.  
 XX  
 XX Dubs-Poterszman M, Tocque B, Wasylyk B;  
 PI WPI; 1997-192837/17.  
 XX  
 XX Treating cancer with antagonist of oncogenic activity of protein  
 PT Mdm2 - or nucleic acid encoding an antagonist, also viral vectors  
 PT contg. this nucleic acid  
 PT  
 XX Claim 4; Page -; 43pp; French.

XX The peptides AAW13602-6 represent peptide fragments derived from the  
 CC wild type human p53 protein. This peptide corresponds to amino acids  
 CC 6-41 of the p53 sequence. The peptides are claimed peptides which are  
 CC able to bind the N-terminal amino acids (1-134) of the murine double  
 CC minute-2 (mdm2) protein (AAW13600). Mdm2 protein is a 90 kD  
 CC phosphoprotein which binds and modulates the activity of the tumour  
 CC suppressor protein p53. It has now been shown that the mdm2 protein  
 CC itself has oncogenic properties, especially in a p53-null background.  
 CC Mdm2 is observed to unblock cell cycle arrest in G1 caused by

PS Claim 4; Page 5; 41pp; English.

XX Peptides AAW60202-05 are derived from human p53 protein. The present  
 CC peptide corresponds to residues 11-35. The peptides are used in  
 CC the method of the invention. Antibodies that bind to p53 protein are  
 CC detected by immobilising a p53 peptide directly on to a flow cell of  
 CC a sensor chip in a biosensor, treating the peptide with a sample of  
 CC patient serum, diluted in buffer, and measuring binding of antibody  
 CC to the peptide using the biosensor. The method is used to monitor  
 CC cancer patients undergoing p53 gene therapy (to determine if an  
 CC immune response has developed), and also to detect antibodies against  
 CC mutant forms of p53.

XX SQ Sequence 26 AA;

Query Match 94.3%; Score 99; DB 19; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 7.4e-09;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18  
 |||||  
 DB 3 PPLSQETFSDLWKLLPEN 20  
 |||||

RESULT 7  
 AAB30523  
 ID AAB30523 standard; peptide; 32 AA.  
 AC AAB30523;  
 XX 06-MAR-2001 (first entry)  
 DT  
 DE Peptide fragment of a tumour suppressor protein p53.

XX Biologically active compound; cellular metabolism; RNA replication;  
 KW RNA transcription; RNA translation; RNA elongation; RNA processing;  
 KW protein synthesis; protein processing; cellular differentiation;  
 KW cell division; ion channel transmission; cellular protein; toxin;  
 KW RNA transport; cellular oxidation; tumour suppressor p53;  
 KW plasminogen antigen activator.  
 XX Synthetic.  
 OS  
 XX WO200061775-A1.  
 PN  
 XX 19-OCT-2000.  
 PD  
 XX 08-APR-1999; 99WO-IB00616.  
 PF  
 XX 08-APR-1999; 99WO-IB00616.  
 PR  
 XX (SERG/) SERGEEV P.  
 PA  
 XX Sergeev P;  
 PI WPI; 2001-006911/01.  
 XX  
 XX Novel methods for the synthesis of biologically active compounds from  
 PT inactive precursors in the cells of living organisms, useful for  
 PT producing proteins or polynucleotides -  
 PT  
 XX Example 8; Page 29; 65pp; English.

XX The specification describes a method of synthesis of biologically active  
 CC substances of determined structure directly in the cells of living  
 CC organisms containing specific RNA or DNA sequence. The method is based  
 CC on the hybridisation of two or more oligomers bound with biologically  
 CC inactive substances to specific RNA or DNA in vivo in the cells of  
 CC living organisms. After hybridisation of the oligomers, the biologically  
 CC inactive precursors bound to the oligomers can interact with each other  
 CC to make the active form of the substances. This changing of properties  
 CC is due to chemical reactions which bind the biologically inactive  
 CC precursors through a chemical bond into a biologically active form of

CC over-expression of the p107 protein. The p53 peptides are examples of  
 CC antagonists of the invention which are able to inhibit the oncogenic  
 CC activity of mdm2. The antagonists are used to treat e.g. adenocarcinoma  
 CC of the colon; cancer of the breast, lung or stomach; myeloid leukaemia; B  
 CC cell lymphoma, or other hyperproliferative conditions such as  
 CC restenosis. Note: this sequence is not given in the specification but is  
 CC constructed from the wild type human p53 sequence.

XX Sequence 36 AA;

Query Match 94.3%; Score 99; DB 18; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18  
 |||||  
 DB 7 PPLSQETFSDLWKLLPEN 24

# RESULT 9

AAW13603  
 ID AAW13603 standard; peptide; 41 AA.

XX AC AAW13603;

DT 16-JAN-1998 (first entry)

DE p53 protein amino acids 1-41.

XX Mouse; Mdm2; murine double minute; phosphoprotein; binding; modulation;  
 KW tumour suppressor; p53; oncogene; cell cycle arrest; p107; antagonist;  
 KW inhibition; transcription factor; adenocarcinoma; colon; cancer; breast;  
 KW lung; stomach; myeloid leukaemia; lymphoma; hyperproliferative;  
 KW restenosis.

XX Homo sapiens.

XX WO9709343-A2.

XX 13-MAR-1997.

XX 02-SEP-1996; 96WO-FR01340.

XX 04-SEP-1995; 95FR-0010331.

XX (INRM ) INST NAT SANTE & RECH MEDICALE.

XX (RHON ) RHONE POULENC RORER SA.

XX Dubs-Poterszman M, Tocque B, Wasylyk B;

XX WPI; 1997-192837/17.

XX Treating cancer with antagonist of oncogenic activity of protein  
 PT Mdm2 - or nucleic acid encoding an antagonist, also viral vectors  
 PT contg. this nucleic acid

XX Claim 4; Page -; 43pp; French.

XX The peptides AAW13602-6 represent peptide fragments derived from the  
 CC wild type human p53 protein. This peptide corresponds to amino acids  
 CC 1-41 of the p53 sequence. The peptides are claimed peptides which are  
 CC able to bind the N-terminal amino acids (1-134) of the murine double  
 CC minute-2 (mdm2) protein (AAW13600). Mdm2 protein is a 90 kD  
 CC phosphoprotein which binds and modulates the activity of the tumour  
 CC suppressor protein p53. It has now been shown that the mdm2 protein  
 CC itself has oncogenic properties, especially in a p53-null background.  
 CC Mdm2 is observed to unblock cell cycle arrest in G1 caused by  
 CC over-expression of the p107 protein. The p53 peptides are examples of  
 CC antagonists of the invention which are able to inhibit the oncogenic  
 CC activity of mdm2. The antagonists are used to treat e.g. adenocarcinoma  
 CC of the colon; cancer of the breast, lung or stomach; myeloid leukaemia; B  
 CC cell lymphoma, or other hyperproliferative conditions such as  
 CC restenosis. Note: this sequence is not given in the specification but is

CC constructed from the wild type human p53 sequence.

XX Sequence 41 AA;

Query Match 94.3%; Score 99; DB 18; Length 41;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18  
 |||||  
 DB 12 PPLSQETFSDLWKLLPEN 29

# RESULT 10

AAW13602

ID AAW13602 standard; peptide; 52 AA.

XX AC AAW13602;

DT 16-JAN-1998 (first entry)

DE p53 protein amino acids 1-52.

XX Mouse; Mdm2; murine double minute; phosphoprotein; binding; modulation;  
 KW tumour suppressor; p53; oncogene; cell cycle arrest; p107; antagonist;  
 KW inhibition; transcription factor; adenocarcinoma; colon; cancer; breast;  
 KW lung; stomach; myeloid leukaemia; lymphoma; hyperproliferative;  
 KW restenosis.

XX Homo sapiens.

XX WO9709343-A2.

XX 13-MAR-1997.

XX 02-SEP-1996; 96WO-FR01340.

XX 04-SEP-1995; 95FR-0010331.

XX (INRM ) INST NAT SANTE & RECH MEDICALE.

XX (RHON ) RHONE POULENC RORER SA.

XX Dubs-Poterszman M, Tocque B, Wasylyk B;

XX WPI; 1997-192837/17.

XX Treating cancer with antagonist of oncogenic activity of protein  
 PT Mdm2 - or nucleic acid encoding an antagonist, also viral vectors  
 PT contg. this nucleic acid

XX Claim 4; Page -; 43pp; French.

XX The peptides AAW13602-6 represent peptide fragments derived from the  
 CC wild type human p53 protein. This peptide corresponds to amino acids  
 CC 1-52 of the p53 sequence. The peptides are claimed peptides which are  
 CC able to bind the N-terminal amino acids (1-134) of the murine double  
 CC minute-2 (mdm2) protein (AAW13600). Mdm2 protein is a 90 kD  
 CC phosphoprotein which binds and modulates the activity of the tumour  
 CC suppressor protein p53. It has now been shown that the mdm2 protein  
 CC itself has oncogenic properties, especially in a p53-null background.  
 CC Mdm2 is observed to unblock cell cycle arrest in G1 caused by  
 CC over-expression of the p107 protein. The p53 peptides are examples of  
 CC antagonists of the invention which are able to inhibit the oncogenic  
 CC activity of mdm2. The antagonists are used to treat e.g. adenocarcinoma  
 CC of the colon; cancer of the breast, lung or stomach; myeloid leukaemia; B  
 CC cell lymphoma, or other hyperproliferative conditions such as  
 CC restenosis. Note: this sequence is not given in the specification but is  
 CC constructed from the wild type human p53 sequence.

XX Sequence 52 AA;

Query Match 94.3%; Score 99; DB 18; Length 52;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-08;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLPEN 18  
Db 12 PPLSQETFSDLWKLLPEN 29

RESULT 11  
AAAR42174  
ID AAR42174 standard; peptide; 64 AA.  
XX AC AAR42174;  
XX AC AAR42174;  
XX DT 05-MAY-1994 (first entry)  
XX DE p53 N-terminal fragment.  
XX KW p53 gene; tumour suppressor gene; regulation; cellular proliferation;  
XX KW cellular transformation; carcinoma; human; tumour; MDM2; inhibition;  
XX KW gene amplification.  
XX OS Homo sapiens.  
XX FH Key Location/Qualifiers  
FT Binding-site 13..41  
FT /note= "Site of interaction with MDM-2"  
XX WO9320238-A.  
XX PD 14-OCT-1993.  
XX 07-APR-1993; 93WO-US03199.  
XX 07-APR-1992; 92US-0867840.  
XX PR 23-JUN-1992; 92US-0903103.  
XX (UYJO ) UNIV JOHNS HOPKINS.  
XX Burrell M, Hill DE, Kinzler KW, Vogelstein B;  
XX WPI; 1993-336944/42.  
XX Diagnosing neoplasia from amplification of MDM2 gene - or  
XX elevated gene expression, also new DNA, MDM2 protein, antibodies  
XX and treatment of sarcoma by inhibiting MDM2 expression  
XX Disclosure; Page 35; 75pp; English.  
XX This sequence represents the product of the p53 gene. p53 is a  
XX tumour suppressor gene and this protein appears to be a member of a  
XX group of proteins which regulate normal cellular proliferation and  
XX suppression of cellular transformation. Inactivation of the p53  
XX gene has been implicated in the formation, or progression of a wide  
XX variety of carcinoma. p53 is thought to interact with the protein  
XX product of a gene which is amplified in a number of human tumours,  
XX designated MDM2. Polypeptides containing at least amino acids 13-41  
XX of p53, or the DNA encoding these, may be used to inhibit the growth  
XX of tumour cells containing MDM2 gene amplification.

Qy Sequence 64 AA;  
Query Match 94.3%; Score 99; DB 14; Length 64;  
Best Local Similarity 100.0%; Pred. No. 2e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLPEN 18  
Db 12 PPLSQETFSDLWKLLPEN 29

RESULT 12  
AAAW07886  
ID AAW07886 standard; protein; 64 AA.

XX AAW07886;  
XX 28-JAN-1997 (first entry)  
XX DE Human p53, involved in tumour suppression.  
XX KW p53; MDM-2; binding-inhibitor; identification; tumour; cancer;  
XX KW neoplasia; antibody fusion protein; therapy.  
XX OS Homo sapiens.  
XX FH Key Location/Qualifiers  
FT Region 1..41  
FT /note= "MDM-2 binding fragment"  
FT Region 1..50  
FT /note= "MDM-2 binding fragment"  
FT Region 13..57  
FT /note= "MDM-2 binding fragment"  
XX US5550023-A.  
XX 27-AUG-1996.  
XX 07-APR-1992; 92US-0867840.  
XX 07-APR-1993; 93US-0044619.  
XX 07-APR-1992; 92US-0867840.  
XX PR 23-JUN-1992; 92US-0903103.  
XX 18-MAY-1994; 94US-0245500.  
XX (UYJO ) UNIV JOHNS HOPKINS.  
XX Kinzler KW, Vogelstein B;  
XX WPI; 1996-401591/40.  
XX Identification of cpds. interfering with human MDM2/p53 binding -  
XX useful as therapeutic agents to treat human neoplastic cells  
XX Claim 16; Column 19-20; 36pp; English.  
XX AAW07886 represents the human p53 protein which is involved in the  
XX development of many cancers. The protein is used here in a method  
XX for identifying compounds that interfere with the binding of p53 and  
XX MDM-2. In binding the p53 protein, the MDM-2 protein releases a cell  
XX from p53-regulated growth, allowing cancers to develop. Therefore  
XX compounds identified as interfering with the binding of MDM-2 to p53  
XX are potentially useful in the treatment of human neoplastic cells. In  
XX the method pref. one or both of the proteins is a fusion protein esp.  
XX with an antibody or antibody fragment which aids separation and  
XX identification.  
XX Sequence 64 AA;  
Query Match 94.3%; Score 99; DB 17; Length 64;  
Best Local Similarity 100.0%; Pred. No. 2e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLPEN 18  
Db 12 PPLSQETFSDLWKLLPEN 29

RESULT 13  
AAW57240  
ID AAW57240 standard; protein; 64 AA.  
XX AC AAW57240;  
XX 10-AUG-1998 (first entry)  
XX Human p53 N-terminal fragment.



XX KW Human; p53; MDM2; tumour; growth inhibition; amplification;  
 XX KW malignant fibrous histiocytoma; liposarcoma.

XX OS Homo sapiens.

XX PN US5756455-A.

XX PD 26-MAY-1998.

XX PF 17-FEB-1995; 95US-0390515.

XX PR 07-APR-1993; 93US-0044619.

XX PR 07-APR-1992; 92US-0867840.

XX PR 23-JUN-1992; 92US-0903103.

XX PR 17-FEB-1995; 95US-0390515.

XX PA (UYJO ) UNIV JOHNS HOPKINS.

XX PI Kinzler KW, Vogelstein B;

XX DR WPI; 1998-321574/28.

XX PT Inhibiting growth of tumour cells having MDM2 gene amplification -

XX PT with p53 protein fragment

XX PS Claim 1; Column 19-20; 40pp; English.

XX CC A method has been developed for inhibiting the growth of tumour cells  
 CC containing a human MDM2 gene amplification. The method comprises  
 CC treating the tumour cells with a DNA molecule that expresses a  
 CC polypeptide capable of binding to human MDM2 protein. The present  
 CC sequence represents an N-terminal fragment of p53 which can bind to the  
 CC human MDM2 protein. The present invention describes three preferred  
 CC polypeptides for binding human MDM2: (1) the polypeptide comprises  
 CC amino acids 1-50 of p53 (see AAW57240); (2) the polypeptide comprises  
 CC amino acids 13-41 of p53 (see AAW57240) and at least one additional p53  
 CC residues on the N- or C-terminal side, provided that the polypeptide  
 CC lacks the homooligomerisation domain of p53; (3) the polypeptide  
 CC comprises amino acids 13-41 of p53 (see AAW57241) and at least nine  
 CC additional p53 residues on the N- or C-terminal side, provided that the  
 CC polypeptide lacks amino acids 138-393 of p53. Some malignant fibrous  
 CC histiocytomas and liposarcomas have an MDM2 gene amplification, so  
 CC detection of increased expression of MDM2 gene products indicates  
 CC tumorigenesis.

XX SQ Sequence 64 AA;

Query Match 94.3%; Score 99; DB 19; Length 64;

Best Local Similarity 100.0%; Pred. No. 2e-08;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PPLSQETFSDLWKLLPEN 18

|||||

Db 12 PPLSQETFSDLWKLLPEN 29

RESULT 14

AAW48243

ID AAW48243 standard; peptide; 64 AA.

XX AC AAW48243;

XX DT 18-JUN-1998 (first entry)

XX DE Human p53 fragment 13-41.

XX KW Human; MDM2; hMDM2; tumour; cancer; diagnosis; neoplastic disease; p53;  
 XX KW sarcoma; liposarcoma; malignant fibrous histiocytoma; osteosarcoma.

XX OS Homo sapiens.

XX PN US5736338-A.

XX PD 07-APR-1998.

XX PF 17-FEB-1995; 95US-0390517.

XX PR 07-APR-1993; 93US-0044619.

XX PR 07-APR-1992; 92US-0867840.

XX PR 23-JUN-1992; 92US-0903103.

XX PR 17-FEB-1995; 95US-0390517.

XX PA (UYJO ) UNIV JOHNS HOPKINS.

XX PI Burrell M, Hill DE, Kinzler KW, Vogelstein B;

XX DR WPI; 1998-239206/21.

XX PT Cancer diagnosis - by determination of MDM2 protein

XX PS Disclosure; Column 19-20; 35pp; English.

XX CC The present sequence represents a human p53 fragment 13-41 which is  
 CC necessary for the interaction of MDM-2 and p53. The present invention  
 CC describes a method for diagnosing a neoplastic disease caused by  
 CC overexpression of MDM2 protein. The method comprises detecting an  
 CC elevated cellular amount of this protein. The method is useful for the  
 CC diagnosis of sarcoma, especially liposarcoma, malignant fibrous  
 CC histiocytoma or osteosarcoma.

XX SQ Sequence 64 AA;

Query Match 94.3%; Score 99; DB 19; Length 64;

Best Local Similarity 100.0%; Pred. No. 2e-08;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PPLSQETFSDLWKLLPEN 18

|||||

Db 12 PPLSQETFSDLWKLLPEN 29

RESULT 15

AAW42878

ID AAW42878 standard; Protein; 64 AA.

XX AC AAW42878;

XX DT 30-APR-1998 (first entry)

XX DE N-terminal region of p53 (amino acids 13-41).

XX KW MDM2; tumour; diagnosis; neoplasia; DNA binding protein;  
 XX KW p53 polypeptide; binding; tumour cell; p53-regulated growth;  
 XX KW inhibition; anti-cancer agent.

XX OS Homo sapiens.

XX PN US5708136-A.

XX PD 13-JAN-1998.

XX PF 17-FEB-1995; 95US-0390516.

XX PR 07-APR-1993; 93US-0044619.

XX PR 07-APR-1992; 92US-0867840.

XX PR 23-JUN-1992; 92US-0903103.

XX PA (UYJO ) UNIV JOHNS HOPKINS.

XX PI Burrell M, Hill DE, Kinzler KW, Vogelstein B;

XX DR WPI; 1998-100408/09.

XX PT Human MDM2 binding polypeptide - comprises fragments of p53, useful  
 PT in re-establishing p53-regulated growth control in cells

PT over-expressing MDM2

XX Claim 1; Columns 19-20; 41pp; English.

XX  
CC The present sequence represents a N-terminal portion of the p53 protein.  
CC These amino acid residues have been found to be necessary for the  
CC interaction of MDM2 and p53. A cell containing three recombinant  
CC DNA constructs was produced. These constructs encode an MDM2 protein  
CC fused to a sequence-specific DNA binding domain, a p53 polypeptide fused  
CC to a transcriptional activation domain, and a reporter gene downstream  
CC from a DNA element which is recognised by the sequence-specific  
CC DNA-binding domain. The cell is used to identify a compound which  
CC interferes with the binding of MDM2 and p53. Since MDM2 is overexpressed  
CC in tumour cells and since binding of MDM2 to p53 appears to allow tumour  
CC cells to escape from p53-regulated growth, compounds that inhibit such  
CC binding would be useful as anti-cancer agents.

XX SQ Sequence 64 AA;

Query Match 94.3%; Score 99; DB 19; Length 64;

Best Local Similarity 100.0%; Pred. No. 2e-08;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PPLSQETFSDLWKLLPEN 18

Db 12 PPLSQETFSDLWKLLPEN 29

Search completed: February 12, 2003, 10:34:44  
Job time : 37 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 12, 2003, 10:33:46 ; Search time 15 Seconds  
(without alignments)  
121.770 Million cell updates/sec

Title: US-09-403-440A-2

Perfect score: 105

Sequence: 1 PPLSQETFSDLWKLLPENG 19

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 73.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	99	94.3	391	2 JC6193	tumor suppressor p
2	99	94.3	393	1 DNHU53	cellular tumor ant
3	99	94.3	393	1 S06594	cellular tumor ant
4	94	89.5	386	1 S51648	cellular tumor ant
5	86	81.9	393	2 JC6176	tumor suppressor p
6	86	81.9	396	1 JH0633	cellular tumor ant
7	81	77.1	363	1 A29376	cellular tumor ant
8	74	70.5	381	2 S38824	cellular tumor ant
9	74	70.5	390	1 DNWS53	cellular tumor ant
10	72	68.6	391	1 S02192	cellular tumor ant
11	60	57.1	1396	1 JH0631	cellular tumor ant
12	51.5	49.0	1009	2 S28857	glutamate receptor
13	51.5	49.0	1009	2 JH0266	glutamate receptor
14	50	47.6	230	2 C64396	precorrin-2 methyl
15	50	47.6	367	2 G86715	racemase [imported
16	50	47.6	447	2 E96672	Similar to Flavono
17	48	45.7	119	2 C49921	major intracellular
18	48	45.7	308	2 AD3262	methylintransferase
19	48	45.7	1004	2 B25039	outer cell wall pr
20	47	44.8	157	1 VCTMPV	coat protein - pep
21	47	44.8	469	2 G84779	hypothetical prote
22	47	44.8	487	2 D83027	hypothetical prote
23	47	44.8	489	2 T41241	oxysterol-binding
24	47	44.8	956	2 G70327	isoleucine-tRNA li
25	46.5	44.3	250	2 T01604	hypothetical prote
26	46.5	44.3	485	2 C75460	hypothetical prote
27	46	43.8	274	2 S74792	hypothetical prote
28	46	43.8	293	1 D69300	4-hydroxybenzoate
29	45.5	43.3	250	2 T49221	hypothetical prote

30 45 42.9 367 2 E96796 hypothetical prote  
31 45 42.9 405 2 AD2194 hypothetical prote  
32 45 42.9 837 2 I57557 DNA-binding protei  
33 44.5 42.4 211 2 B95064 conserved hypotet  
34 44.5 42.4 211 2 D97931 conserved hypotet  
35 44 41.9 113 1 F3WLB4 L3 protein - bovin  
36 44 41.9 114 2 S03072 hypothetical prote  
37 44 41.9 134 2 A82749 hypothetical prote  
38 44 41.9 209 2 S61204 NEF protein - simi  
39 44 41.9 211 1 ASLJM5 NEF protein - simi  
40 44 41.9 238 2 S61205 NEF protein - simi  
41 44 41.9 239 2 S54852 NEF protein - simi  
42 44 41.9 239 2 S61206 NEF protein - simi  
43 44 41.9 244 2 S61208 NEF protein - simi  
44 44 41.9 246 2 S54853 NEF protein - simi  
45 44 41.9 250 2 S54849 nef protein - simi

#### ALIGNMENTS

##### RESULT 1

JC6193  
tumor suppressor p53 - rabbit  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 11-Apr-1997 #sequence\_revision 09-May-1997 #text\_change 20-Jun-2000  
C:Accession: JC6193  
R:Le Goas, F.; May, P.; Ronco, P.; de Fromental, C.C.  
Gene 185, 169-173, 1997  
A:Title: cDNA cloning and immunological characterization of rabbit p53.  
A:Reference number: JC6193; MUID:97208869; PMID:9055811  
A:Accession: JC6193  
A:Molecule type: mRNA  
A:Residues: 1-391 <LEA>  
A:Cross-references: EMBL:X90592; NID:gl532043; PIDN:CAA62216.1; PID:gl532044  
C:Genetics:  
A:Gene: p53  
C:Superfamily: cellular tumor antigen p53  
C:Keywords: tumor

Query Match 94.3%; Score 99; DB 2; Length 391;  
Best Local Similarity 100.0%; Pred. No. 3e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLPEN 18  
Db 12 PPLSQETFSDLWKLLPEN 29

##### RESULT 2

DNHU53  
cellular tumor antigen p53 [validated] - human  
N:Alternate names: cellular phosphoprotein p53; oncoprotein p53; transformation suppressor p53  
C:Species: Homo sapiens (man)  
C:Date: 05-Oct-1988 #sequence\_revision 18-Nov-1994 #text\_change 15-Sep-2000  
C:Accession: A25224; A43073; JT0436; S40773; S42669; A25397; B25397; S42669; I58354; I78850; I52681; S60153  
R:Lamb, P.; Crawford, L.  
Mol. Cell. Biol. 6, 1379-1385, 1986  
A:Title: Characterization of the human p53 gene.  
A:Reference number: A25224; MUID:87064416; PMID:2946935  
A:Accession: A25224  
A:Molecule type: DNA  
A:Residues: 1-393 <LAM>  
A:Cross-references: EMBL:X01405; GB:M13121; GB:N00032; NID:gl89460; PIDN:AAAS9987.1; PID:AAAS9987.1; Buchman, V.L.; Chumakov, P.M.; Ninkina, N.N.; Samarina, O.P.; Georgiev, G.P.  
Gene 70, 245-252, 1988  
A:Title: A variation in the structure of the protein-coding region of the human p53 gene  
A:Reference number: JT0436; MUID:89108008; PMID:2905688  
A:Accession: A43073  
A:Molecule type: DNA  
A:Residues: 1-393 <BUCL>  
A:Cross-references: EMBL:M22898; NID:gl89474

A;Note: this 72-Arg allele appears to be about 5 times more frequent than the 72-Pro allele  
A;Accession: J0436  
A;Molecule type: DNA  
A;Residues: 1-71,'P',73-393 <BUC2>  
A;Cross-references: EMBL:M22898; NID:g189474; PIDN:AAA59988.1; PID:g189476  
A;Note: this 72-Pro allele was found in both normal and malignant cell lines  
R;Chumakov, P.M.; Almazov, V.P.; Jenkins, J.R.  
Submitted to the EMBL Data Library, August 1990  
A;Reference number: S40773  
A;Accession: S40773  
A;Molecule type: DNA  
A;Residues: 1-393 <CHU>  
A;Cross-references: EMBL:X54156; NID:g35213; PIDN:CAA38095.1; PID:g35214  
R;Matlashewski, G.; Lamb, P.; Pim, D.; Peacock, J.; Crawford, L.; Benchimol, S.  
EMBO J. 3, 3257-3262, 1984  
A;Title: Isolation and characterization of a human p53 cDNA clone: expression of the human p53 cDNA clone in COS cells  
A;Reference number: S42669; MUID:85126934; PMID:6396087  
A;Accession: S42669  
A;Molecule type: mRNA  
A;Residues: 101-393 <MKI1>  
A;Cross-references: EMBL:X01405; NID:g35215; PIDN:CAA25652.1; PID:g642241  
R;Zakut-Houri, R.; Blens-Tadmor, B.; Givol, D.; Oren, M.  
EMBO J. 4, 1251-1255, 1985  
A;Title: Human p53 cellular tumor antigen: cDNA sequence and expression in COS cells.  
A;Reference number: A22837; MUID:85230577; PMID:4006916  
A;Accession: A22837  
A;Molecule type: mRNA  
A;Residues: 1-71,'P',73-393 <ZAK>  
A;Cross-references: EMBL:X02469; EMBL:M60950; NID:g35209; PIDN:CAA26306.1; PID:g35210  
R;Harlow, E.; Williamson, N.M.; Ralston, R.; Helfman, D.M.; Adams, T.E.  
Mol. Cell. Biol. 5, 1601-1610, 1985  
A;Title: Molecular cloning and in vitro expression of a cDNA clone for human cellular tumor antigen p53  
A;Reference number: A55060; MUID:85267676; PMID:3894933  
A;Accession: A55060  
A;Molecule type: mRNA  
A;Residues: 1-71,'P',73-272,'H',274-393 <HAR>  
A;Cross-references: GB:X03199; NID:g189478; PIDN:AAA59989.1; PID:g189479  
R;Harris, N.; Brill, E.; Shohat, O.; Prokocimer, M.; Wolf, D.; Arai, N.; Rotter, V.  
Mol. Cell. Biol. 6, 4650-4656, 1986  
A;Title: Molecular basis for heterogeneity of the human p53 protein.  
A;Reference number: A93086; MUID:87089826; PMID:3025664  
A;Accession: A25397  
A;Molecule type: mRNA  
A;Residues: 1-78,'T',80-393 <HAR1>  
A;Cross-references: EMBL:M14694; NID:g339813; PIDN:AAA61211.1; PID:g339814  
A;Experimental source: clone p53-H-1, transformed hybridoma SV-80 cell line  
A;Accession: B25397  
A;Molecule type: mRNA  
A;Residues: 1-71,'P',73-78,'T',80-393 <HAR2>  
A;Cross-references: EMBL:M14695; NID:g339815; PIDN:AAA61212.1; PID:g339816  
R;Matlashewski, G.J.; Tuck, S.; Pim, D.; Lamb, P.; Schneider, J.; Crawford, L.V.  
Mol. Cell. Biol. 7, 961-963, 1987  
A;Title: Primary structure polymorphism at amino acid residue 72 of human p53.  
A;Reference number: S42452; MUID:87144273; PMID:3547088  
A;Accession: S42452  
A;Molecule type: mRNA; DNA  
A;Residues: 66-71,'P',73-79 <MKI2>  
A;Experimental source: clone lambda C113  
A;Note: 72-Cys was also found, and appears to represent a polymorphism  
A;Accession: S42453  
A;Molecule type: mRNA; DNA  
A;Residues: 66-79 <MKI3>  
A;Experimental source: clone j6K  
R;Farrell, P.J.; Allan, G.J.; Shanahan, F.; Vousden, K.H.; Crook, T.  
EMBO J. 10, 2879-2887, 1991  
A;Title: p53 is frequently mutated in Burkitt's lymphoma cell lines.  
A;Reference number: I38082; MUID:92007731; PMID:1315267  
A;Accession: I38082  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-389,'LLSILSEWKEICWSIWNTEFLFDIIVWCPMSRLRLALT','VPPSTTTTCVTVPAAWA' <F01>

A;Cross-references: EMBL:X60010; NID:g506432; PIDN:CAA42625.1; PID:g506433  
A;Note: deletion of a C nucleotide causes a frameshift at position 566  
A;Accession: I38083  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-192,'R',194-393 <F02>  
A;Cross-references: EMBL:X60011; NID:g506434; PIDN:CAA42626.1; PID:g506435  
A;Accession: I38084  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-393 <F03>  
A;Cross-references: EMBL:X60012; NID:g506436; PIDN:CAA42627.1; PID:g506437  
A;Accession: I38085  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-245,'T',247-393 <F04>  
A;Cross-references: EMBL:X60013; NID:g506438; PIDN:CAA42628.1; PID:g506439  
A;Accession: I38086  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-236,'I',238-393 <F05>  
A;Cross-references: EMBL:X60014; NID:g506440; PIDN:CAA42629.1; PID:g506441  
A;Accession: I38087  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-247,'Q',249-393 <F06>  
A;Cross-references: EMBL:X60015; NID:g506442; PIDN:CAA42630.1; PID:g506443  
A;Accession: I38088  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-71,'P',73-237,'Y',239-393 <F07>  
A;Cross-references: EMBL:X60016; NID:g506444; PIDN:CAA42631.1; PID:g506445  
A;Accession: I38089  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-247,'Q',249-393 <F08>  
A;Cross-references: EMBL:X60017; NID:g506446; PIDN:CAA42632.1; PID:g506447  
A;Accession: I38090  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-71,'P',73-162,'H',164-393 <F09>  
A;Cross-references: EMBL:X60018; NID:g506448; PIDN:CAA42633.1; PID:g506449  
A;Accession: I38091  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-212,'Q',214-393 <F10>  
A;Cross-references: EMBL:X60019; NID:g506450; PIDN:CAA42634.1; PID:g506451  
A;Accession: I38092  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-253,'D',255-393 <F11>  
A;Cross-references: EMBL:X60020; NID:g506452; PIDN:CAA42635.1; PID:g506453  
A;Note: all sequences submitted to the EMBL/GenBank/DBJ databases June 1991  
R;Futreal, P.A.; Barrett, J.C.; Wiseman, R.W.  
Nucleic Acids Res. 19, 6977, 1991  
A;Title: An Alu polymorphism intragenic to the TP53 gene.  
A;Reference number: I38093; MUID:92107726; PMID:1762941  
A;Accession: I38093  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-393 <FUT>  
A;Cross-references: EMBL:X54156; NID:g35213; PIDN:CAA38095.1; PID:g35214  
R;Yamada, Y.; Yoshida, T.; Hayashi, K.; Sekiya, T.; Yokota, J.; Hirohashi, S.; Nakatani  
Cancer Res. 51, 5800-5805, 1991  
A;Title: p53 gene mutations in gastric cancer metastases and in gastric cancer cell line  
A;Reference number: A44905; MUID:92034678; PMID:1933850  
A;Accession: A44905  
A;Molecule type: DNA  
A;Residues: 246-247,'W',249-250 <YAM>  
A;Cross-references: GB:S63157; NID:g237829; PIDN:AA20140.1; PID:g237830  
A;Note: sequence extracted from NCEI backbone (NCBI:63157, NCBIP:63159)  
A;Note: mutation from a liver metastasis of a gastric cancer  
R;Hensel, C.H.; Xiang, R.H.; Sakaguchi, A.Y.; Naylor, S.L.

Oncogene 6', 1067-1071, 1991  
 A>Title: Use of the single strand conformation polymorphism technique and PCR to detect  
 A:Reference number: I58354; PMID:91296386; PMID:1648702  
 A:Accession: I58354  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 244-247, 'W', 249-252 <HEN1>  
 A:Cross-references: GB:S41969; NID:gl679931; PIDN:AAB19324.1; PID:g232814  
 A:Accession: I78850  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 274-277, 'S', 279-282 <HEN2>  
 A:Cross-references: GB:S41977; NID:gl679932; PIDN:AAB19325.1; PID:g232816  
 R:Chow, V.T.; Quek, H.H.; Tock, E.P.C.  
 Cancer Lett. 73, 141-148, 1993  
 A>Title: Alternative splicing of the p53 tumor suppressor gene in the Molt-4 T-lymphoblastoid cell line  
 A:Reference number: I52681; PMID:94036762; PMID:8221626  
 A:Accession: I52681  
 A>Status: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 327-331, 'DOTSFQKENC' <CHO>  
 A:Cross-references: GB:S66666; NID:g436292; PIDN:AAB28601.1; PID:g436293  
 A>Note: mutant sequence with altered splicing and termination expressed in Molt-4 T-lymphoblastoid cell line  
 R:Petersen, G.; Song, D.; Huegle-Doerr, B.; Oldenburg, I.; Bautz, E.K.F.  
 Mol. Gen. Genet. 249, 425-431, 1995  
 A>Title: Mapping of linear epitopes recognized by monoclonal antibodies with gene-fragments  
 A:Reference number: S60151; PMID:96133682; PMID:8552047  
 A:Accession: S60151  
 A:Molecule type: DNA  
 A:Residues: 3-44 <PET>  
 R:Dang, C.V.; Lee, W.M.F.  
 J. Biol. Chem. 264, 18019-18023, 1989  
 A>Title: Nuclear and nucleolar targeting sequences of c-erb-A, c-myc, N-myc, p53, HSP70,

Query Match 94.3%; Score 99; DB 1; Length 393;  
 Best Local Similarity 100.0%; Pred. No. 3e-07;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLEN 18  
 |||||  
 Db 12 PPLSQETFSDLWKLLEN 29

## RESULT 3

cellular tumor antigen p53 - green monkey  
 C:Species: Cercopithecus aethiops (green monkey, grivet)  
 C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
 C:Accession: S06594  
 R:Rigaudy, P.; Eckhart, W.  
 Nucleic Acids Res. 17, 8375, 1989  
 A>Title: Nucleotide sequence of a cDNA encoding the monkey cellular phosphoprotein p53.  
 A:Reference number: S06594; PMID:90045967; PMID:2530498  
 A:Accession: S06594

A:Molecule type: mRNA  
 A:Residues: 1-393 <RIG>  
 A:Cross-references: EMBL:X16384; NID:g22795; PIDN:CAA34420.1; PID:g22796  
 C:Superfamily: cellular tumor antigen p53  
 C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; phosphoprotein; phosphorylation; zinc (Cys, His, Cys) #status predicted  
 F:176,179,238,242/Binding site: zinc (Cys, His, Cys) #status predicted  
 F:392/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 94.3%; Score 99; DB 1; Length 393;  
 Best Local Similarity 100.0%; Pred. No. 3e-07;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLEN 18  
 |||||  
 Db 12 PPLSQETFSDLWKLLEN 29

## RESULT 4

S51648

cellular tumor antigen p53 - bovine  
 N:Alternate names: tumor-suppressor protein p53  
 C:Species: Bos primigenius taurus (cattle)  
 C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
 C:Accession: S51648  
 R:Dequiedt, F.; Willems, L.; Burny, A.; Kettmann, R.  
 submitted to the EMBL Data Library, September 1994  
 A:Description: Nucleotide sequence of the ovine p53 tumor-suppressor gene cDNA and its  
 A:Reference number: S51648  
 A:Accession: S51648  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-396 <DEQ>  
 A:Cross-references: EMBL:X81704; NID:g602332; PIDN:CAA57348.1; PID:g602333  
 C:Superfamily: cellular tumor antigen p53  
 C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; phosphoprotein; phosphorylation; zinc (Cys, His, Cys) #status predicted  
 F:168,171,231,235/Binding site: zinc (Cys, His, Cys) #status predicted  
 F:385/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 89.5%; Score 94; DB 1; Length 386;  
 Best Local Similarity 94.4%; Pred. No. 1.7e-06;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLEN 18  
 |||||  
 Db 12 PPLSQETFSDLWKLLEN 29

## RESULT 5

cellular tumor antigen p53 - Chinese hamster  
 C:Species: Cricetulus griseus (Chinese hamster)  
 C>Date: 11-Apr-1997 #sequence\_revision 09-May-1997 #text\_change 23-Jul-1999  
 C:Accession: JC6176  
 R:Lee, H.; Larner, J.M.; Hamlin, J.L.  
 Gene 184, 177-183, 1997  
 A>Title: Cloning and characterization of Chinese hamster p53 cDNA.  
 A:Reference number: JC6176; PMID:97183659; PMID:9031625  
 A:Contents: liver  
 A:Accession: JC6176

A:Molecule type: mRNA  
 A:Residues: 1-393 <LEE>  
 A:Cross-references: GB:U050395; NID:gl842229; PIDN:AAC53040.1; PID:gl842230  
 C:Comment: This protein is a multimer, it plays the central role in a complex DNA damage

induction, and recombination by protein/protein interactions.

C:Genetics:  
 A:Gene: p53  
 C:Superfamily: cellular tumor antigen p53  
 C:Keywords: liver; tumor

Query Match 81.9%; Score 86; DB 2; Length 393;  
 Best Local Similarity 94.1%; Pred. No. 2.8e-05;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PLSQETFSDLWKLLEN 18  
 |||||  
 Db 13 PLSQETFSDLWKLLEN 29

## RESULT 6

cellular tumor antigen p53 - golden hamster  
 N:Alternate names: tumor-suppressor protein p53  
 C:Species: Mesocricetus auratus (golden hamster)  
 C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
 C:Accession: JH0633  
 R:Legros, Y.; McIntyre, P.; Soussi, T.  
 Gene 112, 247-250, 1992  
 A>Title: The cDNA cloning and immunological characterization of hamster p53.  
 A:Reference number: JH0633; PMID:92210007; PMID:1555773  
 A:Accession: JH0633  
 A:Molecule type: mRNA  
 A:Residues: 1-396 <LEG>

A;Cross-references: GB:W75144; NID:g191414; PIDN:AAA37085.1; PID:g191415  
 A;Experimental source: kidney, strain MP1  
 C;Genetics:

A;Gene: p53  
 C;Superfamily: cellular tumor antigen p53  
 C;Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; phosph  
 F;119,182,241,245/Binding site: zinc (Cys, His, Cys) #status predicted  
 F;395/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 81.9%; Score 86; DB 1; Length 396;  
 Best Local Similarity 94.1%; Pred. No. 2.9e-05;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PLSQETFSDLWKLPPEN 18  
 |||||  
 Db 13 PLSQETFSDLWKLPPN 29

## RESULT 7

A29376  
 C;Keywords: cellular tumor antigen p53 - African clawed frog  
 C;Species: Xenopus laevis (African clawed frog)  
 C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text\_change 10-Sep-1999  
 C;Accession: A29376; S61531; S72313; I51639  
 R;Soussi, T.; de Fromental, C.C.; Mechali, M.; May, P.; Kress, M.  
 Oncogene 1: 71-78, 1987  
 A;Title: Cloning and characterization of a cDNA from Xenopus laevis coding for a protein  
 A;Reference number: A29376; MUID:88143684; PMID:2830576  
 A;Accession: A29376  
 A;Molecule type: mRNA  
 A;Residues: 1-363 <SOU>  
 A;Cross-references: EMBL:X05191; NID:g64961; PIDN:CAA28821.1; PID:g64962  
 R;Hoever, M.; Clement, J.H.; Wedlich, D.; Montenarh, M.; Knoechel, W.  
 Oncogene 9: 109-120, 1994

A;Title: Overexpression of wild-type p53 interferes with normal development in Xenopus 1  
 A;Reference number: I51639; MUID:94134403; PMID:8302570  
 A;Accession: S61531  
 A;Molecule type: mRNA  
 A;Residues: 1-293,295-363 <HOE>  
 A;Cross-references: EMBL:X77546; NID:g468513; PIDN:CAA54672.1; PID:g468514  
 R;Hoever, M.; Clement, J.; Wedlich, D.; Montenarh, M.; Knoechel, W.  
 submitted to the EMBL Data Library, March 1994  
 A;Reference number: S72313  
 A;Accession: S72313  
 A;Molecule type: mRNA  
 A;Residues: 1-51,'S',53-70,72-293,295-363 <HOW>  
 A;Cross-references: EMBL:X77546; NID:g468513; PIDN:CAA54672.1; PID:g468514  
 C;Genetics:

A;Gene: p53  
 C;Superfamily: cellular tumor antigen p53  
 C;Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; phosph  
 F;150,153,213,217/Binding site: zinc (Cys, His, Cys) #status predicted  
 F;362/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 77.1%; Score 81; DB 1; Length 363;  
 Best Local Similarity 82.4%; Pred. No. 0.00015;  
 Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLPE 17  
 |||||  
 Db 11 PPLSQETFSDLWKLPE 27

## RESULT 8

S38824  
 C;Keywords: cellular tumor antigen p53, minor splice form - mouse  
 C;Species: Mus musculus (house mouse)  
 C;Date: 13-Jan-1995 #sequence revision 13-Jan-1995 #text\_change 23-Jul-1999  
 C;Accession: S38824; S35478  
 R;Araki, N.; Nomura, D.; Yokota, K.; Wolf, D.; Brill, E.; Shohat, O.; Rotter, V.  
 Mol. Cell. Biol. 6: 3232-3239, 1986  
 A;Title: Immunologically distinct p53 molecules generated by alternative splicing.  
 A;Reference number: S38822; MUID:87064640; PMID:3023970

A;Accession: S38824  
 A;Molecule type: mRNA  
 A;Residues: 1-381 <ARA>  
 A;Cross-references: GB:M13874; NID:g200202; PIDN:AAA39883.1; PID:g200203  
 R;Han, K.A.; Kulesz-Martin, M.F.  
 Nucleic Acids Res. 20: 1979-1981, 1992  
 A;Title: Alternatively spliced p53 RNA in transformed and normal cells of different tiss  
 A;Reference number: S35478; MUID:92253421; PMID:1579500  
 A;Accession: S35478  
 A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: mRNA  
 A;Residues: 1-381 <HAN>  
 A;Cross-references: EMBL:M13874; NID:g200202; PIDN:AAA39883.1; PID:g200203  
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1988  
 C;Comment: This sequence, produced by alternative splicing of the tenth intron, lacks th  
 s not known.

C;Superfamily: cellular tumor antigen p53  
 C;Keywords: alternative splicing; phosphoprotein; zinc  
 F;1-44/Domain: transcription activation #status predicted <TRA>  
 F;16-26/Region: conserved region I  
 F;99-289/Domain: DNA-binding core #status predicted <DBC>  
 F;108-121/Region: L1 loop  
 F;114-139/Region: conserved region II  
 F;160-192/Region: L2 loop  
 F;168-178/Region: conserved region III  
 F;231-252/Region: conserved region IV  
 F;233-248/Region: L3 loop  
 F;267-283/Region: conserved region V  
 F;313-319/Region: nuclear location signal  
 F;319-357/Region: tetramer association  
 F;7,9,12,18,23,37/Binding site: phosphate (Ser) (covalent) #status predicted  
 F;173,176,235,239/Binding site: zinc (Cys, His, Cys) #status predicted  
 F;312/Binding site: phosphate (Ser) (covalent) (by cdc2 kinase) #status predicted

Query Match 70.5%; Score 74; DB 2; Length 381;  
 Best Local Similarity 93.3%; Pred. No. 0.0018;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PLSQETFSDLWKLPP 16  
 |||||  
 Db 16 PLSQETFSGLWKLPP 30

## RESULT 9

DNMS53  
 C;Keywords: cellular tumor antigen p53 - mouse  
 N;Alternate names: oncoprotein p53  
 C;Species: Mus musculus (house mouse)  
 C;Date: 28-Aug-1985 #sequence revision 04-Oct-1996 #text\_change 11-May-2000  
 C;Accession: A22739; S06336; A02684; S38822; S38823; S40014; I48703  
 R;Bienz, B.; Zakut-Houri, R.; Givol, D.; Oren, M.  
 EMBO J. 3: 2179-2183, 1984  
 A;Title: Analysis of the gene coding for the murine cellular tumour antigen p53.  
 A;Reference number: A22739; MUID:85027173; PMID:6092064  
 A;Accession: A22739  
 A;Molecule type: DNA  
 A;Residues: 1-134,'V',136-390 <BIE>  
 A;Cross-references: GB:X00876; NID:g871420; PIDN:CAA25420.1; PID:g871421; GB:X01237; GB  
 R;Chumakov, P.M.  
 Bioorg. Khim. 13: 1691-1694, 1987  
 A;Title: Primary structure of DNA complementary to murine oncoprotein p53 mRNA.  
 A;Reference number: S06336; MUID:88221682; PMID:3329909  
 A;Accession: S06336  
 A;Status: not compared with conceptual translation

A;Molecule type: mRNA  
 A;Residues: 1-134,'V',136-390 <CHU>  
 R;Zakut-Houri, R.; Oren, M.; Bienz, B.; Lavie, V.; Hazum, S.; Givol, D.  
 Nature 306: 594-597, 1983  
 A;Title: A single gene and a pseudogene for the cellular tumour antigen p53.  
 A;Reference number: A02684; MUID:84068204; PMID:6646235  
 A;Accession: A02684  
 A;Molecule type: mRNA  
 A;Residues: 1-159,'H',161-167,'G',169-233,'I',235-390 <ZAK>

A;Cross-references: GB:X01237; GB:K01700; NID:g53575  
R;Arai, N.; Nomura, D.; Yokota, K.; Wolf, D.; Brill, E.; Shohat, O.; Rotter, V.  
Mol. Cell. Biol. 6, 3232-3239, 1986  
A;Title: Immunologically distinct p53 molecules generated by alternative splicing.  
A;Reference number: S38822; MUID:87064640; PMID:3023970  
A;Accession: S38822  
A;Molecule type: mRNA  
A;Residues: 1-390 <ARA1>  
A;Cross-references: EMBL:M13872; NID:g200198; PIDN:AAA39881.1; PID:g200199  
A;Accession: S38823  
A;Molecule type: mRNA  
A;Residues: 1-167, 'G', 169-233, 'I', 235-390 <ARA2>  
A;Cross-references: EMBL:M13873  
R;Arai, N.; Nomura, D.; Yokota, K.; Wolf, D.; Brill, E.; Shohat, O.; Rotter, V.  
submitted to the EMBL Data Library, July 1988  
A;Reference number: S40014  
A;Accession: S40014  
A;Molecule type: mRNA  
A;Residues: 1-167, 'G', 169-390 <ARA3>  
A;Cross-references: EMBL:M13873; NID:g200200; PIDN:AAA39882.1; PID:g200201  
R;Jenkins, J.R.; Rudge, K.; Redmond, S.; Wade-Evans, A.  
Nucleic Acids Res. 12, 5609-5626, 1984  
A;Title: Cloning and expression analysis of full length mouse cDNA sequences encoding the  
A;Reference number: I48703; MUID:84272240; PMID:6379601  
A;Accession: I48703  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-47, 'R', 49-78, 'QW', 82-390 <RES>  
A;Cross-references: EMBL:X00741; NID:g53570; PIDN:CAA25323.1; PID:g53571  
C;Comment: This DNA-binding protein plays an essential role in the regulation of cell di  
C;Superfamily: The tetramer association region may exhibit a beta-turn, beta-sheet, beta-tu  
C;Comment: cellular tumor antigen p53  
C;Keywords: apoptosis; cell division control; DNA binding; homotetramer; phosphoprotein;  
F;1-44/Domain: transcription activation #status predicted <TRA>  
F;16-26/Region: conserved region I  
F;99-289/Domain: DNA-binding core #status predicted <DBC>  
F;108-121/Region: L1 loop  
F;114-139/Region: conserved region II  
F;160-192/Region: L2 loop  
F;168-178/Region: conserved region III  
F;231-252/Region: conserved region IV  
F;233-248/Region: L3 loop  
F;267-283/Region: conserved region V  
F;313-319/Region: nuclear location signal  
F;319-357/Region: tetramer association  
F;7-9,12,18,23,37/Binding site: phosphate (Ser) (covalent) #status predicted  
F;7-9,12,18,23,37/Binding site: zinc (Cys, His, Cys, Cys) #status predicted  
F;173,176,235,239/Binding site: zinc (Cys, His, Cys, Cys) #status predicted  
F;312/Binding site: phosphate (Ser) (covalent) (by cdc2 kinase) #status predicted  
F;389/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 70.5%; Score 74; DB 1; Length 390;  
Best Local Similarity 93.3%; Pred. No. 0.0018;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PLSQTFSDLWKLLP 16  
|||||  
Db 16 PLSQTFSDLWKLLP 30

RESULT 10  
S02192  
cellular tumor antigen p53 - rat  
N;Alternate names: gene p53 protein; nuclear oncoprotein p53  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
R;Soussi, T.; de Fromental, C.C.; Breugnot, C.; May, E.  
Nucleic Acids Res. 16, 11384, 1988  
A;Title: Nucleotide sequence of a cDNA encoding the rat p53 nuclear oncoprotein.  
A;Reference number: S02192; MUID:89083585; PMID:3060862  
A;Accession: S02192  
A;Molecule type: mRNA  
A;Residues: 1-391 <SOU>

A;Cross-references: EMBL:X13058; NID:g56828; PIDN:CAA31457.1; PID:g56829  
R;Hulla, J.E.; Schneider, R.P.  
Nucleic Acids Res. 21, 713-717, 1993  
A;Title: Structure of the rat p53 tumor suppressor gene.  
A;Reference number: S41149; MUID:93181268; PMID:8441680  
A;Accession: S41149  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-173, 'W', 175-391 <HUL>  
A;Cross-references: EMBL:L07909  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1992  
C;Genetics:  
A;Introns: 25/2; 32/3; 123/3; 185/1; 259/2; 305/1; 329/3; 365/2  
C;Superfamily: cellular tumor antigen p53  
C;Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; phosph  
F;174,177,236,240/Binding site: zinc (Cys, His, Cys, Cys) #status predicted  
F;390/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 68.6%; Score 72; DB 1; Length 391;  
Best Local Similarity 93.3%; Pred. No. 0.0037;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PLSQTFSDLWKLLP 16  
|||||  
Db 13 PLSQTFSDLWKLLP 27

RESULT 11  
JH0631  
cellular tumor antigen p53 - rainbow trout  
C;Species: Oncorhynchus mykiss (rainbow trout)  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C;Accession: JH0631  
R;de Fromental, C.C.; Pakdel, F.; Chapus, A.; Baney, C.; May, P.; Soussi, T.  
Gene 112, 241-245, 1992  
A;Title: Rainbow trout p53: cDNA cloning and biochemical characterization.  
A;Reference number: JH0631; MUID:92210006; PMID:1339362  
A;Accession: JH0631  
A;Molecule type: mRNA  
A;Residues: 1-396 <DEF>  
A;Cross-references: GB:M75145; NID:g213828; PIDN:AAA49605.1; PID:g213829  
A;Experimental source: liver  
A;Comment: This protein is the product of a tumor suppressor gene, p53, whose inactivati  
C;Superfamily: cellular tumor antigen p53  
C;Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; phosph  
F;164,167,227,231/Binding site: zinc (Cys, His, Cys, Cys) #status predicted  
F;395/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 57.1%; Score 60; DB 1; Length 396;  
Best Local Similarity 76.9%; Pred. No. 0.25;  
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 PLSQTFSDLWKLL 14  
|||||  
Db 11 PLSQTFSDLWKLM 23

RESULT 12  
S28857  
Glutamate receptor delta-1 chain precursor - rat  
N;Alternate names: kainate receptor  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 07-Apr-1994 #sequence\_revision 07-Apr-1994 #text\_change 20-Aug-1999  
C;Accession: S28857; S31222  
R;Lomeli, H.; Sprengel, R.; Laurie, D.J.; Koehr, G.; Herb, A.; Seeburg, P.H.; Wisden, W.  
FEBS Lett. 315, 318-322, 1993  
A;Title: The rat delta-1 and delta-2 subunits extend the excitatory amino acid receptor  
A;Reference number: S28857; MUID:93138096; PMID:8422924  
A;Accession: S28857  
A;Status: nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-1009 <LOW>  
A;Cross-references: EMBL:Z17238

R. Sprengel, R.  
submitted to the EMBL Data Library, October 1992  
A:Reference number: S31222  
A:Accession: S31222  
A:Molecule type: mRNA

A:Residues: 83-1009 <SPR>  
A:Cross-references: EMBL:Z12738; NID:G56285; PIDN:CAA78936.1; PID:G56286  
C:Superfamily: glutamate receptor; glutamate receptor homology  
C:Keywords: glycoprotein; ion channel; neurotransmitter receptor; transmembrane protein  
F:1-15/Domain: signal sequence #status predicted <SIG>  
F:16-1009/Product: glutamate receptor delta-1 chain #status predicted <MAT>  
F:441-866/Domain: glutamate receptor homology <GRH>  
F:565-584/Domain: transmembrane #status predicted <TM1>  
F:601-621/Domain: transmembrane #status predicted <TM2>  
F:632-654/Domain: transmembrane #status predicted <TM3>  
F:830-851/Domain: transmembrane #status predicted <TM4>  
F:422/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 49.0%; Score 51.5; DB 2; Length 1009;  
Best Local Similarity 47.4%; Pred. No. 13;  
Matches 9; Conservative 6; Mismatches 3; Indels 1; Gaps 1;

QY 2 PLSQF-TFSDWLKLLPENG 19  
|||: |||: |||: |||:  
Db 698 PLEQDSTFAELWRTISKNG 716

## RESULT 13

JH0266  
glutamate receptor delta-1 chain precursor - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 20-Jun-2000  
C:Accession: JH0266  
R:Yamazaki, M.; Araki, K.; Shibata, A.; Mishina, M.  
Biochem. Biophys. Res. Commun. 183, 886-892, 1992  
A:Title: Molecular cloning of a cDNA encoding a novel member of the mouse glutamate receptor  
A:Reference number: JH0266; MUID:92198486; PMID:1372507  
A:Accession: JH0266  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA

A:Residues: 1-1009 <YAM>  
A:Cross-references: DDBJ:D10171; NID:G220417; PIDN:BA01041.1; PID:G220418  
C:Comment: Glutamate receptor channels mediate most of the fast excitatory synaptic transmission  
C:Superfamily: glutamate receptor; glutamate receptor homology  
C:Keywords: glycoprotein; neurotransmitter receptor; phosphoprotein; transmembrane protein  
F:1-15/Domain: signal sequence #status predicted <SIG>  
F:16-1009/Product: glutamate receptor channel delta-1 chain #status predicted <GLU>  
F:441-866/Domain: glutamate receptor homology <GRH>  
F:565-584/Domain: transmembrane #status predicted <TR1>  
F:603-621/Domain: transmembrane #status predicted <TR2>  
F:632-650/Domain: transmembrane #status predicted <TR3>  
F:831-851/Domain: transmembrane #status predicted <TR4>  
F:131,200,422,498/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:593,713/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 49.0%; Score 51.5; DB 2; Length 1009;  
Best Local Similarity 47.4%; Pred. No. 13;  
Matches 9; Conservative 6; Mismatches 3; Indels 1; Gaps 1;

QY 2 PLSQF-TFSDWLKLLPENG 19  
|||: |||: |||: |||:  
Db 698 PLEQDSTFAELWRTISKNG 716

## RESULT 14

C64396

precorrin-2 methyltransferase homolog - Methanococcus jannaschii  
C:Species: Methanococcus jannaschii  
C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 21-Jul-2000  
C:Accession: C64396  
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, R.; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;  
rson, J.D.; Sadow, F.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.

Science 273, 1058-1073, 1996

A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.  
A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii  
A:Reference number: A64300; MUID:96337999; PMID:8688087  
A:Accession: C64396  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-230 <BUL>  
A:Cross-references: GB:U67522; GB:L77117; NID:G2826315; PIDN:AAB98764.1; PID:G:592306;  
C:Genetics:  
A:Map position: FOR691742-692434  
A:Start codon: GTG  
C:Superfamily: precorrin-3 methylase

Query Match 47.6%; Score 50; DB 2; Length 230;  
Best Local Similarity 55.6%; Pred. No. 4.5;  
Matches 10; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 2 PLSQF-TFSDWLKLLPENG 19  
|||: |||: |||: |||:  
Db 101 PTLYSTFSYVWKLKRG 118

## RESULT 15

G86715

racemase [imported] - Lactococcus lactis subsp. lactis (strain IL1403)  
C:Species: Lactococcus lactis subsp. lactis  
C:Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 03-Aug-2001  
C:Accession: G86715  
R:Botolin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrlich  
Genome Res. 11, 731-753, 2001  
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis  
A:Reference number: A86625; MUID:21235186; PMID:11337471  
A:Accession: G86715  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-367 <STO>  
A:Cross-references: GB:AE005176; PID:gl2723640; PIDN:AAK04825.1; GSPDB:GN00146  
A:Experimental source: strain IL1403  
C:Genetics:  
A:Gene: yhdB

Query Match 47.6%; Score 50; DB 2; Length 367;  
Best Local Similarity 52.9%; Pred. No. 7.5;  
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 PLSQF-TFSDWLKLLPENG 17  
|||: |||: |||: |||:  
Db 54 PFYTSETFADSWKILEE 70

Search completed: February 12, 2003, 10:36:01  
Job time: 17 secs



GenCore version 5.1.1.3

Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 12, 2003, 10:32:56 ; Search time 11 Seconds  
(without alignments)  
71.641 Million cell updates/sec

Title: US-09-403-440A-2

Perfect score: 105

Sequence: 1 PPLSQETFSDLWLLPENG 19

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	99	94.3	386	1 P53 FIG	Q9tub2 sus scrofa
2	99	94.3	391	1 P53_CAVRO	Q9wur6 cavia porce
3	99	94.3	391	1 P53_RABIT	Q95330 oryctolagus
4	99	94.3	393	1 P53_CERAE	P13481 cercopithec
5	99	94.3	393	1 P53_HUMAN	P04637 homo sapien
6	99	94.3	393	1 P53_MACFA	P56423 macaca fasc
7	99	94.3	393	1 P53_MACMU	P56424 macaca mula
8	99	94.3	393	1 P53_TUPGB	Q9ttaa tupai glis
9	94	89.5	382	1 P53_SHEEP	P51664 ovis aries
10	94	89.5	386	1 P53_BOVIN	Q29628 bos taurus
11	94	89.5	391	1 P53_MARMO	Q36006 marmota mon
12	90	85.7	381	1 P53_CANFA	Q29537 canis famil
13	90	85.7	386	1 P53_PELCA	P41685 felis silve
14	86	81.9	393	1 P53_CRIGR	Q09185 cricetus
15	86	81.9	396	1 P53_MESAU	Q00366 mesocricetu
16	81	77.1	363	1 P53_XENLA	P07193 xenopus lae
17	74	70.5	390	1 P53_MOUSE	P02340 mus musculu
18	72	68.6	391	1 P53_RAT	P10361 rattus norv
19	60	57.1	396	1 P53_ONCMY	P25035 oncorhynchu
20	54	51.4	367	1 P53_TETMU	Q9679 tetradodon m
21	53.5	51.0	342	1 P53_XIPHE	Q57538 xiphophorus
22	53.5	51.0	342	1 P53_XIPMA	Q92143 xiphophorus
23	50	47.6	230	1 P53_METJA	Q58181 methanococc
24	48	45.7	119	1 IPI_BACSU	P39804 bacillus su
25	48	45.7	1004	1 SLPO_BACBR	P09333 bacillus br
26	47	44.8	156	1 COAT_PMV2	Q9wdg5 pepper mild
27	47	44.8	156	1 COAT_PMV1	Q94843 pepper mild
28	47	44.8	156	1 COAT_PMV3	P29096 pepper mild
29	47	44.8	156	1 COAT_TOMKO	Q83482 tomato mosa
30	47	44.8	158	1 COAT_PMV0	Q9wdg3 pepper mild
31	47	44.8	314	1 P53_SPEBE	Q84662 spermophilu
32	47	44.8	956	1 SYI_AQUAE	Q66651 aquifex aeo
33	46	43.8	307	1 YA24_SYNY3	P72926 synechocyst

34	45	42.9	837	1 STAC_MOUSE	P52633 mus musculu
35	44.5	42.4	491	1 STRK_HUMAN	Q13188 homo sapien
36	44	41.9	113	1 VL3_BPV4	P08343 bovine papi
37	44	41.9	201	1 HIS7_METKA	P58879 methanopyru
38	44	41.9	207	1 NEF_SIVMK	P05861 simian immu
39	44	41.9	263	1 NEF_SIVNA	P31818 simian immu
40	44	41.9	263	1 NEF_SIVML	P11262 simian immu
41	44	41.9	276	1 Y009_METJA	Q60320 methanococc
42	44	41.9	367	1 P53_CHICK	P10360 gallus gall
43	44	41.9	529	1 SYI_AQUPY	P46207 aquifex pyr
44	44	41.9	1033	1 CC68_KLULA	Q00976 kluyveromyc
45	44	41.9	2555	1 PPS3_BACSU	P39847 bacillus su

## ALIGNMENTS

## RESULT 1

ID	P53 FIG	STANDARD;	PRT;	386 AA.
AC	Q9TUB2;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Cellular tumor antigen p53 (Tumor suppressor p53).			
GN	TP53 OR P53.			
OS	Sus scrofa (Pig).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.			
OX	NCBI_TaxID=9623;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RM	MEDLINE=99422034; PubMed=10490836;			
RA	Burr P.D., Argyle D.J., Reid S.W.J., Nasir L.;			
RT	"Nucleotide sequence of the porcine p53 cDNA, and the detection of			
RT	recombinant porcine p53 expressed in vitro with a variety of anti-p53			
RT	antibodies.";			
RL	Oncogene 18:5005-5009(1999).			
CC	-I- FUNCTION: Acts as a tumor suppressor in many tumor types; induces			
CC	growth arrest or apoptosis depending on the physiological			
CC	circumstances and cell type. Involved in cell cycle regulation as			
CC	a trans-activator that acts to negatively regulate cell division			
CC	by controlling a set of genes required for this process. One of			
CC	the activated genes is an inhibitor of cyclin-dependent kinases.			
CC	Apoptosis induction seems to be mediated either by stimulation of			
CC	BAX and FAS antigen expression, or by repression of Bcl-2			
CC	expression.			
CC	-I- SUBUNIT: Binds DNA as a homotrimer (By similarity).			
CC	-I- SUBCELLULAR LOCATION: Nuclear.			
CC	-I- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY			
CC	OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED			
CC	IN MANY TYPES OF CANCER.			
CC	-I- SIMILARITY: BELONGS TO THE P53 FAMILY.			

-----  
This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use by non-profit institutions as long as its content is in no way  
modified and this statement is not removed. Usage by and for commercial  
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
-----

CC	EMBL; AF098067; AAF04620.1; -.
DR	HSSP; P04637; 1C26
DR	InterPro; IPR002117; P53.
DR	PRINTS; PR00386; P53SUPPRESSR.
DR	PRODOM; PD002681; P53; 2.
DR	PROSITE; PS00348; P53; 1.
KW	Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW	Nuclear protein; Phosphorylation; Apoptosis.
FT	DOMAIN 1 45
FT	DNA_BIND 94 285
FT	BY SIMILARITY.

FT DOMAIN 318 349 OLIGOMERIZATION.  
 FT DOMAIN 361 380 BASIC (REPRESSION OF DNA-BINDING).  
 FT DOMAIN 304 316 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).  
 FT MOD\_RES 385 385 PHOSPHORYLATION (BY SIMILARITY).  
 SQ SEQUENCE 386 AA; 42862 MW; A4C3D8E8DF55162 CRC64;

Query Match 94.3%; Score 99; DB 1; Length 386;  
 Best Local Similarity 100.0%; Pred. No. 7.2e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18  
 |||||  
 Db 12 PPLSQETFSDLWKLLPEN 29

RESULT 2  
 P53\_CAVPO STANDARD; PRT; 391 AA.  
 AC Q9WUR6;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Cellular tumor antigen p53 (Tumor suppressor p53).  
 GN TP53.  
 OS Cavia porcellus (Guinea pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.  
 OX NCBI\_TaxID=10141;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RX MEDLINE=99265972; PubMed=10331945;  
 RA D'Erchia A.M., Pesole G., Tullio A., Saccone C., Sbisa E.;  
 RT "Guinea pig p53 mRNA: identification of new elements in coding and  
 RT untranslated regions and their functional and evolutionary  
 RT implications";  
 RL Genomics 58:50-64(1999).  
 CC -!- FUNCTION: Acts as a tumor suppressor in many tumor types; induces  
 CC growth arrest or apoptosis depending on the physiological  
 CC circumstances and cell type. Involved in cell cycle regulation as  
 CC a trans-activator that acts to negatively regulate cell division  
 CC by controlling a set of genes required for this process. One of  
 CC the activated genes is an inhibitor of cyclin-dependent kinases.  
 CC Apoptosis induction seems to be mediated either by stimulation of  
 CC BAX and FAS antigen expression, or by repression of Bcl-2  
 CC expression.  
 CC -!- SUBUNIT: Binds DNA as a homotetramer (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Nuclear.  
 CC -!- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY  
 CC OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED  
 CC IN MANY TYPES OF CANCER.  
 CC -!- SIMILARITY: BELONGS TO THE P53 FAMILY.

-----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----

DR EMBL; AJ009673; CAB43196.1; -;  
 DR HSP; P04637; LYCS.  
 DR InterPro; IPR002117; P53.  
 DR Pfam; PF00870; P53; 1.  
 DR PRINTS; PR00386; P53SUPPRESSR.  
 DR PRODOM; PD002681; P53; 1.  
 DR PROSITE; PS00348; P53; 1.  
 KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;  
 KW Nuclear protein; Phosphorylation; Apoptosis.  
 FT DOMAIN 1 44 TRANSCRIPTION ACTIVATION (ACIDIC).  
 FT DNA\_BIND 100 290 BY SIMILARITY.  
 FT DOMAIN 323 354 OLIGOMERIZATION.

FT DOMAIN 366 385 BASIC (REPRESSION OF DNA-BINDING).  
 FT DOMAIN 309 321 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).  
 FT MOD\_RES 390 390 PHOSPHORYLATION (BY SIMILARITY).  
 SQ SEQUENCE 391 AA; 43287 MW; 321D40702383573E CRC64;

Query Match 94.3%; Score 99; DB 1; Length 391;  
 Best Local Similarity 100.0%; Pred. No. 7.3e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18  
 |||||  
 Db 12 PPLSQETFSDLWKLLPEN 29

RESULT 3  
 P53\_RABIT STANDARD; PRT; 391 AA.  
 AC Q95330;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Cellular tumor antigen p53 (Tumor suppressor p53).  
 GN TP53.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=New Zealand;  
 RX MEDLINE=97208869; PubMed=9055811;  
 RA le Goss F., May P., Ronco P., Caron de Fromental C.;  
 RT "CDNA cloning and immunological characterization of rabbit p53";  
 RL Gene 185:169-173(1997).  
 CC -!- FUNCTION: Acts as a tumor suppressor in many tumor types; induces  
 CC growth arrest or apoptosis depending on the physiological  
 CC circumstances and cell type. Involved in cell cycle regulation as  
 CC a trans-activator that acts to negatively regulate cell division  
 CC by controlling a set of genes required for this process. One of  
 CC the activated genes is an inhibitor of cyclin-dependent kinases.  
 CC Apoptosis induction seems to be mediated either by stimulation of  
 CC BAX and FAS antigen expression, or by repression of Bcl-2  
 CC expression (By similarity).  
 CC -!- SUBUNIT: Binds DNA as a homotetramer (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Nuclear.  
 CC -!- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY  
 CC OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED  
 CC IN MANY TYPES OF CANCER.  
 CC -!- SIMILARITY: BELONGS TO THE P53 FAMILY.

-----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----

DR EMBL; X90592; CAA62216.1; -;  
 DR HSP; P04637; LYCS.  
 DR InterPro; IPR002117; P53.  
 DR Pfam; PF00870; P53; 1.  
 DR PRINTS; PR00386; P53SUPPRESSR.  
 DR PRODOM; PD002681; P53; 1.  
 DR PROSITE; PS00348; P53; 1.  
 KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;  
 KW Nuclear protein; Phosphorylation; Apoptosis.  
 FT DOMAIN 1 43 TRANSCRIPTION ACTIVATION (ACIDIC).  
 FT DNA\_BIND 99 289 BY SIMILARITY.  
 FT DOMAIN 323 354 OLIGOMERIZATION.  
 FT DOMAIN 366 385 BASIC (REPRESSION OF DNA-BINDING).  
 FT DOMAIN 308 321 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).  
 FT MOD\_RES 390 390 PHOSPHORYLATION (BY SIMILARITY).

SQ SEQUENCE 391 AA; 43435 MW; 86BD5B8D0B726525 CRC64;

Query Match 94.3%; Score 99; DB 1; Length 391;  
Best Local Similarity 100.0%; Pred. No. 7.3e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18  
| | | | | | | | | | | | | | | | | | | | | |  
DB 12 PPLSQETFSDLWKLLPEN 29

## RESULT 4

P53 CERAE STANDARD; PRT; 393 AA.

AC P13481;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-JAN-1990 (Rel. 13, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Cellular tumor antigen p53 (Tumor suppressor p53).  
GN TP53.

OS Cercopithecus aethiops (Green monkey) (Grivet).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;  
OC Cercopithecinae; Cercopithecus.

OX NCBI\_TaxID=9534;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Liver;

RX MEDLINE=90045967; PubMed=2530498;

RA Rigaudy P., Eckhardt W.;

RT "Nucleotide sequence of a cDNA encoding the monkey cellular

phosphoprotein p53.";

RL Nucleic Acids Res. 17:8375-8375(1989).

CC -!- FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2 expression.

CC -!- SUBUNIT: Binds DNA as a homotetramer (By similarity).

CC -!- SUBCELLULAR LOCATION: Nuclear.

CC -!- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY

OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED

IN MANY TYPES OF CANCER.

CC -!- SIMILARITY: BELONGS TO THE P53 FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See [http://www.isb-sib.ch/](http://www.isb-sib.ch/announce/) or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC EMBL; X16384; CAA34420.1; -.

DR FIR; S06594; S06594.

DR HSSP; P04637; 10UG.

DR InterPro; IPR002117; P53.

DR Pfam; PF00870; P53; 1.

DR PRINTS; PR00386; P53SUPPRESSR.

DR PRODOM; PD002681; P53; 1.

DR PROSITE; PS00348; P53; 1.

KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;

Nuclear protein; Phosphorylation; Apoptosis.

FT DOMAIN 1 44 TRANSCRIPTION ACTIVATION (ACIDIC).

FT DNA BIND 102 292 BY SIMILARITY.

FT DOMAIN 325 356 OLIGOMERIZATION.

FT DOMAIN 368 387 BASIC (REPRESSION OF DNA-BINDING).

FT DOMAIN 311 323 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).

FT MOD\_RES 392 392 PHOSPHORYLATION (BY SIMILARITY).

SQ SEQUENCE 393 AA; 43696 MW; 9ED285C9A7855D6E CRC64;

Query Match 94.3%; Score 99; DB 1; Length 393;  
Best Local Similarity 100.0%; Pred. No. 7.3e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18  
| | | | | | | | | | | | | | | | | | | | | |  
DB 12 PPLSQETFSDLWKLLPEN 29

## RESULT 5

P53 HUMAN

ID P53\_HUMAN STANDARD; PRT; 393 AA.

AC P04637; Q16848; Q9UB12;

DT 13-AUG-1987 (Rel. 05, Created)

DT 01-MAR-1989 (Rel. 10, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Cellular tumor antigen p53 (Tumor suppressor p53) (Phosphoprotein

p53) (Antigen NY-CO-13).

GN TP53 OR P53.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=85230577; PubMed=4006916;

RA Zakut-Houri R., Bienz-Tadmor B., Givol D., Oren M.;

RT "Human p53 cellular tumor antigen: cDNA sequence and expression in

COS cells.";

RL EMBO J. 4:1251-1255(1985).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=87064416; PubMed=2946935;

RA Lamb P., Crawford L.;

RT "Characterization of the human p53 gene.";

RL Mol. Cell. Biol. 6:1379-1385(1986).

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=85267676; PubMed=3894933;

RA Harlow E., Williamson N.M., Ralston R., Helfman D.M., Adams T.E.;

RT "Molecular cloning and in vitro expression of a cDNA clone for human

cellular tumor antigen p53.";

RL Mol. Cell. Biol. 5:1601-1610(1985).

RN [4]

RP SEQUENCE FROM N.A.

RX MEDLINE=87083826; PubMed=3025664;

RA Harris N., Brill E., Shohat O., Prokocimer M., Wolf D., Arai N.,

RT "Molecular basis for heterogeneity of the human p53 protein.";

RL Mol. Cell. Biol. 6:4650-4656(1986).

RN [5]

RP SEQUENCE FROM N.A.

RX MEDLINE=85108008; PubMed=2905688;

RA Buchman V.L., Chumakov P.M., Ninkina N.N., Samarina O.P.,

RT "A variation in the structure of the protein-coding region of the

human p53 gene.";

RL Gene 70:245-252(1988).

RN [6]

RP SEQUENCE OF 101-393 FROM N.A.

RX MEDLINE=85126934; PubMed=6396087;

RA Matlashewski G., Lamb P., Pim D., Peacock J., Crawford L.,

RT "Isolation and characterization of a human p53 cDNA clone: expression

of the human p53 gene.";

RL EMBO J. 3:3257-3262(1984).

RN [7]

RP SEQUENCE FROM N.A.

RX MEDLINE=92007731; PubMed=1915267;

RA Farrell P.J., Allan G., Shanahan F., Vousden K.H., Crook T.;

RT "p53 is frequently mutated in Burkitt's lymphoma cell lines.";

EMBO J. 10:2879-2887(1991).  
 [8]  
 RN SEQUENCE FROM N.A.  
 RP Chumakov P.M., Almazov V.P., Jenkins J.R.;  
 RA Submitted (JUN-1991) to the EMBL/GenBank/DBJ databases.  
 [9]  
 RN SEQUENCE FROM N.A.  
 RP Rozenmuller E.H., Tilanus M.G.J.;  
 RA "P53 genomic sequence. Corrections and polymorphism."  
 RT Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.  
 [10]  
 RN SEQUENCE FROM N.A.  
 RP Anderson C.W., Kieleczawa J., Allalunis-Turner J.;  
 RA "Human p53 from the malignant glioma-derived cell lines M059J and  
 RT M059K have a cancer-associated mutation in exon 8."  
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
 [11]  
 RN ALTERNATIVE SPLICING.  
 RP MEDLINE=96197761; PubMed=8632903;  
 RA Flanagan J.-M., Waridel F., Estreicher A., Vannier A., Limacher J.-M.,  
 RT Gilbert D., Iggo R., Frebourg T.;  
 RA "The human tumour suppressor gene p53 is alternatively spliced in  
 RT normal cells."  
 RL Oncogene 12:813-818(1996).  
 [12]  
 RN NUCLEAR LOCALIZATION SIGNAL.  
 RP MEDLINE=90191730; PubMed=2156209;  
 RA Addison C., Jenkins J.R., Sturzbecher H.-W.;  
 RT "The p53 nuclear localisation signal is structurally linked to a  
 RT p34cdc2 kinase motif."  
 RL Oncogene 5:423-426(1990).  
 [13]  
 RN MINIMAL REPRESSION DOMAIN.  
 RP PubMed=11007800;  
 RA Hong T.M., Chen J.J., Peck K., Yang P.C., Wu C.W.;  
 RT "p53 amino acids 339-346 represent the minimal p53 repression  
 RT domain."  
 RL J. Biol. Chem. 276:1510-1515(2001).  
 [14]  
 RN PHOSPHORYLATION BY P60/CDC2 AND CYCLIN B/CDC2.  
 RP MEDLINE=90280456; PubMed=2141171;  
 RA Bischoff J.R., Friedman P.N., Marshak D.R., Prives C., Beach D.;  
 RT "Human p53 is phosphorylated by p60-cdc2 and cyclin B-cdc2."  
 RL Proc. Natl. Acad. Sci. U.S.A. 87:4766-4770(1990).  
 [15]  
 RN DEPHOSPHORYLATION BY PP2A.  
 RP MEDLINE=91172186; PubMed=1848668;  
 RA Scheidtmann K.H., Mumby M.C., Rundell K., Walter G.;  
 RT "Dephosphorylation of simian virus 40 large-T antigen and p53 protein  
 RT by protein phosphatase 2A: inhibition by small-t antigen."  
 RL Mol. Cell. Biol. 11:1996-2003(1991).  
 [16]  
 RN O-GLYCOSYLATION.  
 RP MEDLINE=96197773; PubMed=8632915;  
 RA Shaw P., Freeman J., Bovey R., Iggo R.;  
 RT "Regulation of specific DNA binding by p53: evidence for a role for  
 RT O-glycosylation and charged residues at the carboxy-terminus."  
 RL Oncogene 12:921-930(1996).  
 [17]  
 RN STRUCTURE BY NMR OF 319-360.  
 RP MEDLINE=94294808; PubMed=8023159;  
 RA Clore G.M., Omichinski J.G., Sakaguchi K., Zambrano N., Sakamoto H.,  
 RA Appella E., Gronenborn A.M.;  
 RT "High-resolution structure of the oligomerization domain of p53 by  
 RT multidimensional NMR."  
 RL Science 265:386-391(1994).  
 [18]  
 RN STRUCTURE BY NMR OF 325-355.  
 RP MEDLINE=95292092; PubMed=7773777;  
 RA Lee W., Harvey T.S., Yin Y., Yau P., Litchfield D., Arrowsmith C.H.;  
 RT "Solution structure of the tetrameric minimum transforming domain of  
 RT p53."  
 RL Nat. Struct. Biol. 1:877-890(1994).

[19]  
 RN STRUCTURE BY NMR OF 326-354.  
 RP MEDLINE=98026899; PubMed=9321402;  
 RA McCoy M., Stavridi E.S., Waterman J.L., Wiczorek A.M., Opella S.J.,  
 RA Halazonetis T.D.;  
 RT "Hydrophobic side-chain size is a determinant of the  
 RT three-dimensional structure of the p53 oligomerization domain."  
 RL EMBO J. 16:6230-6236(1997).  
 [20]  
 RN X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 94-289.  
 RP MEDLINE=94294806; PubMed=8023157;  
 RA Cho Y., Gorina S., Jeffrey P.D., Pavletich N.P.;  
 RT "Crystal structure of a p53 tumor suppressor-DNA complex:  
 RT understanding tumorigenic mutations."  
 RL Science 265:346-355(1994).  
 [21]  
 RN X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 325-356.  
 RP MEDLINE=95184011; PubMed=7878469;  
 RA Jeffrey P.D., Gorina S., Pavletich N.P.;  
 RT "Crystal structure of the tetramerization domain of the p53 tumor  
 RT suppressor at 1.7 angstroms."  
 RL Science 267:1498-1502(1995).  
 [22]  
 RN X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 13-29 IN COMPLEX WITH MDM2.  
 RP MEDLINE=97081050; PubMed=8875929;  
 RA Kussie P.H., Gorina S., Marechal V., Elenbaas B., Moreau J.,  
 RA Levine A.J., Pavletich N.P.;  
 RT "Structure of the MDM2 oncoprotein bound to the p53 tumor suppressor  
 RT transactivation domain."  
 RL Science 274:948-953(1996).  
 [23]  
 RN X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 97-287 IN COMPLEX WITH 53BP2.  
 RP MEDLINE=97035414; PubMed=8875926;  
 RA Gorina S., Pavletich N.P.;  
 RT "Structure of the p53 tumor suppressor bound to the ankyrin and SH3  
 RT domains of 53BP2."  
 RL Science 274:1001-1005(1996).  
 [24]  
 RN REVIEW.  
 RP MEDLINE=94090335; PubMed=8266092;  
 RA Harris C.C.;  
 RT "p53: at the crossroads of molecular carcinogenesis and risk  
 RT assessment."  
 RL Science 262:1980-1981(1993).  
 [25]  
 RN REVIEW ON VARIANTS.  
 RP MEDLINE=91289156; PubMed=1905840;  
 RA Hoolstein M., Sidransky D., Vogelstein B., Harris C.C.;  
 RT "p53 mutations in human cancers."  
 RL Science 253:49-53(1991).  
 [26]  
 RN REVIEW ON VARIANTS.  
 RP MEDLINE=96271983; PubMed=8829653;  
 RA de Vries E.M.G., Rieck D.O., de Vries T.N., Hartmann A., Blaszyk H.,  
 RA Liao D., Somsu T., Kovach J.S., Sommer S.S.;  
 RT "Database of mutations in the p53 and APC tumor suppressor genes  
 RT designed to facilitate molecular epidemiological analyses."  
 RL Hum. Mutat. 7:202-213(1996).  
 [27]  
 RN VARIANT ARG-72.  
 RP MEDLINE=91153807; PubMed=1999338;  
 RA Olshwang S., Laurent-Puig P., Vassal A., Salmon R.-J., Thomas G.;  
 RT "Characterization of a frequent polymorphism in the coding sequence  
 RT of the tp53 gene in colonic cancer patients and a control  
 RT population."  
 RL Hum. Genet. 86:369-370(1991).  
 [28]

Query Match 94.3%; Score 99; DB 1; Length 393;  
 Best Local Similarity 100.0%; Pred. No. 7.3e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFDLWKLLEN 18

Db 12 PPLSQETFSDLWKLLPEN 29

## RESULT 6

P53 MACFA  
ID P53 MACFA STANDARD; PRT; 393 AA.  
AC P56423;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Cellular tumor antigen p53 (Tumor suppressor p53).  
GN TP53 OR P53.  
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;  
OC Cercopitheciinae; Macaca.  
OX NCBI\_TaxID=9541;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Khan M.A., Hansen C., Welsh J.A., Bennett W.P.;  
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Acts as a tumor suppressor in many tumor types; induces  
CC growth arrest or apoptosis depending on the physiological  
CC circumstances and cell type. Involved in cell cycle regulation as  
CC a trans-activator that acts to negatively regulate cell division  
CC by controlling a set of genes required for this process. One of  
CC the activated genes is an inhibitor of cyclin-dependent kinases.  
CC Apoptosis induction seems to be mediated either by stimulation of  
CC BAX and FAS antigen expression, or by repression of Bcl-2  
CC expression.  
CC -!- SUBUNIT: Binds DNA as a homotetramer (By similarity).  
CC -!- SUBCELLULAR LOCATION: Nuclear.  
CC -!- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY  
CC OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED  
CC IN MANY TYPES OF CANCER.  
CC -!- SIMILARITY: BELONGS TO THE P53 FAMILY.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; U48957; AAB91535.1; -;  
CC HSPSP; P04637; LOUG.  
CC InterPro; IPR002117; P53.  
CC Pfam; PF00870; P53; 1.  
CC PRINTS; PR00386; P53SUPPRESSR.  
CC ProDom; PD002681; P53; 1.  
CC PROSITE; PS00348; P53; 1.  
CC K0 Anti-oncogene; DNA-binding; Transcription regulation; Activator;  
CC FT Nucleic acid binding; Phosphorylation; Apoptosis.  
CC FT DOMAIN 1 44 TRANSCRIPTION ACTIVATION (ACIDIC).  
CC FT DNA\_BIND 102 292 BY SIMILARITY.  
CC FT DOMAIN 325 356 OLIGOMERIZATION.  
CC FT DOMAIN 368 387 BASIC (REPRESSION OF DNA-BINDING).  
CC FT DOMAIN 311 323 NUCLEAR LOCALIZATION SIGNAL.  
CC FT MOD\_RES 392 392 PHOSPHORYLATION (BY SIMILARITY).  
CC SEQUENCE 393 AA; 43678 MW; EDEEBA1BD3AEAFB8 CRC64;

Query Match 94.3%; Score 99; DB 1; Length 393;  
Best Local Similarity 100.0%; Pred. No. 7.3e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLPEN 18  
Db 12 PPLSQETFSDLWKLLPEN 29

## RESULT 7

P53 MACMU  
ID P53 MACMU STANDARD; PRT; 393 AA.  
AC P56424;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Cellular tumor antigen p53 (Tumor suppressor p53).  
GN TP53 OR P53.  
OS Macaca mulatta (Rhesus macaque).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;  
OC Cercopitheciinae; Macaca.  
OX NCBI\_TaxID=9544;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Kray H.D., Mountjoy C.P., Wu G., Cornish K.G., Smith L.J.;  
RL "Sequence of a cDNA encoding the p53 protein in rhesus monkey (Macaca  
RL mulatta).";  
RL Gene 138:223-226(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Khan M.A., Hansen C., Welsh J.A., Bennett W.P.;  
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Acts as a tumor suppressor in many tumor types; induces  
CC growth arrest or apoptosis depending on the physiological  
CC circumstances and cell type. Involved in cell cycle regulation as  
CC a trans-activator that acts to negatively regulate cell division  
CC by controlling a set of genes required for this process. One of  
CC the activated genes is an inhibitor of cyclin-dependent kinases.  
CC Apoptosis induction seems to be mediated either by stimulation of  
CC BAX and FAS antigen expression, or by repression of Bcl-2  
CC expression.  
CC -!- SUBUNIT: Binds DNA as a homotetramer (By similarity).  
CC -!- SUBCELLULAR LOCATION: Nuclear.  
CC -!- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY  
CC OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED  
CC IN MANY TYPES OF CANCER.  
CC -!- SIMILARITY: BELONGS TO THE P53 FAMILY.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; L20442; AAA17994.1; -;  
CC EMBL; U48956; AAB91534.1; -;  
CC HSPSP; P04637; LOUG.  
CC InterPro; IPR002117; P53.  
CC Pfam; PF00870; P53; 1.  
CC PRINTS; PR00386; P53SUPPRESSR.  
CC ProDom; PD002681; P53; 1.  
CC PROSITE; PS00348; P53; 1.  
CC K0 Anti-oncogene; DNA-binding; Transcription regulation; Activator;  
CC FT Nucleic acid binding; Phosphorylation; Apoptosis.  
CC FT DOMAIN 1 44 TRANSCRIPTION ACTIVATION (ACIDIC).  
CC FT DNA\_BIND 102 292 BY SIMILARITY.  
CC FT DOMAIN 325 356 OLIGOMERIZATION.  
CC FT DOMAIN 368 387 BASIC (REPRESSION OF DNA-BINDING).  
CC FT DOMAIN 311 323 NUCLEAR LOCALIZATION SIGNAL.  
CC FT MOD\_RES 392 392 PHOSPHORYLATION (BY SIMILARITY).  
CC SEQUENCE 393 AA; 43655 MW; E212E5E4FE650103 CRC64;

Query Match 94.3%; Score 99; DB 1; Length 393;  
Best Local Similarity 100.0%; Pred. No. 7.3e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLPEN 18

D'b 12 PPLSQETFSDLWKLLPEN 29

## RESULT 8

RESULT	ID	P53_TUPGB	STANDARD;	PRT;	393 AA.
AC	Q9TTA1;				
DT	16-OCT-2001	(Rel. 40, Created)			
DT	16-OCT-2001	(Rel. 40, Last sequence update)			
DT	15-JUN-2002	(Rel. 41, Last annotation update)			
DE	Cellular tumor antigen p53 (Tumor suppressor p53).				
GN	TP53 OR p53.				
OS	Tupaia glis belangeri (Common tree shrew).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Scandentia; Tupaidae; Tupaia.				
OX	NCBI TaxID=9396;				

CC	EMBL; AF175893; AAF22640.1; -
DR	HSSP; P04637; 1YCS.
DR	InterPro; IPR002117; P53.
DR	Pfam; PF008070; P53; 1
DR	PRINTS; PR00386; P53SUPPRESSR.
DR	ProDom; PD002681; P53; 1.
DR	PROSITE; PS00348; P53; 1.
KW	Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW	Nuclear protein; Phosphorylation; Apoptosis.
FT	DOMAIN 1 44
FT	DNA BIND 102 292
FT	DOMAIN 325 356
FT	DOMAIN 368 387
FT	DOMAIN 311 323
FT	MOD RES 392 392
FT	SEQUENCE 393 AA; 43552 MW; FD9F36603945A1FA CRC64;
CC	EMBL; AF175893; AAF22640.1; -
DR	HSSP; P04637; 1YCS.
DR	InterPro; IPR002117; P53.
DR	Pfam; PF008070; P53; 1
DR	PRINTS; PR00386; P53SUPPRESSR.
DR	ProDom; PD002681; P53; 1.
DR	PROSITE; PS00348; P53; 1.
KW	Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW	Nuclear protein; Phosphorylation; Apoptosis.
FT	DOMAIN 1 44
FT	DNA BIND 102 292
FT	DOMAIN 325 356
FT	DOMAIN 368 387
FT	DOMAIN 311 323
FT	MOD RES 392 392
FT	SEQUENCE 393 AA; 43552 MW; FD9F36603945A1FA CRC64;
CC	EMBL; AF175893; AAF22640.1; -
DR	HSSP; P04637; 1YCS.
DR	InterPro; IPR002117; P53.
DR	Pfam; PF008070; P53; 1
DR	PRINTS; PR00386; P53SUPPRESSR.
DR	ProDom; PD002681; P53; 1.
DR	PROSITE; PS00348; P53; 1.
KW	Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW	Nuclear protein; Phosphorylation; Apoptosis.
FT	DOMAIN 1 44
FT	DNA BIND 102 292
FT	DOMAIN 325 356
FT	DOMAIN 368 387
FT	DOMAIN 311 323
FT	MOD RES 392 392
FT	SEQUENCE 393 AA; 43552 MW; FD9F36603945A1FA CRC64;
CC	EMBL; AF175893; AAF22640.1; -
DR	HSSP; P04637; 1YCS.
DR	InterPro; IPR002117; P53.
DR	Pfam; PF008070; P53; 1
DR	PRINTS; PR00386; P53SUPPRESSR.
DR	ProDom; PD002681; P53; 1.
DR	PROSITE; PS00348; P53; 1.
KW	Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW	Nuclear protein; Phosphorylation; Apoptosis.
FT	DOMAIN 1 44
FT	DNA BIND 102 292
FT	DOMAIN 325 356
FT	DOMAIN 368 387
FT	DOMAIN 311 323
FT	MOD RES 392 392
FT	SEQUENCE 393 AA; 43552 MW; FD9F36603945A1FA CRC64;
CC	EMBL; AF175893; AAF22640.1; -
DR	HSSP; P04637; 1YCS.
DR	InterPro; IPR002117; P53.
DR	Pfam; PF008070; P53; 1
DR	PRINTS; PR00386; P53SUPPRESSR.
DR	ProDom; PD002681; P53; 1.
DR	PROSITE; PS00348; P53; 1.
KW	Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW	Nuclear protein; Phosphorylation; Apoptosis.
FT	DOMAIN 1 44
FT	DNA BIND 102 292
FT	DOMAIN 325 356
FT	DOMAIN 368 387
FT	DOMAIN 311 323
FT	MOD RES 392 392
FT	SEQUENCE 393 AA; 43552 MW; FD9F36603945A1FA CRC64;
CC	EMBL; AF175893; AAF22640.1; -
DR	HSSP; P04637; 1YCS.
DR	InterPro; IPR002117; P53.
DR	Pfam; PF008070; P53; 1
DR	PRINTS; PR00386; P53SUPPRESSR.
DR	ProDom; PD002681; P53; 1.
DR	PROSITE; PS00348; P53; 1.
KW	Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW	Nuclear protein; Phosphorylation; Apoptosis.
FT	DOMAIN 1 44
FT	DNA BIND 102 292
FT	DOMAIN 325 356
FT	DOMAIN 368 387
FT	DOMAIN 311 323
FT	MOD RES 392 392
FT	SEQUENCE 393 AA; 43552 MW; FD9F36603945A1FA CRC64;
CC	EMBL; AF175893; AAF22640.1; -
DR	HSSP; P04637; 1YCS.
DR	InterPro; IPR002117; P53.
DR	Pfam; PF008070; P53; 1
DR	PRINTS; PR00386; P53SUPPRESSR.
DR	ProDom; PD002681; P53; 1.
DR	PROSITE; PS00348; P53; 1.
KW	Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW	Nuclear protein; Phosphorylation; Apoptosis.
FT	DOMAIN 1 44
FT	DNA BIND 102 292
FT	DOMAIN 325 356
FT	DOMAIN 368 387
FT	DOMAIN 311 323
FT	MOD RES 392 392
FT	SEQUENCE 393 AA; 43552 MW; FD9F36603945A1FA CRC64;
CC	EMBL; AF175893; AAF22640.1; -
DR	HSSP; P04637; 1YCS.
DR	InterPro; IPR002117; P53.
DR	Pfam; PF008070; P53; 1
DR	PRINTS; PR00386; P53SUPPRESSR.
DR	ProDom; PD002681; P53; 1.
DR	PROSITE; PS00348; P53; 1.

## RESULT 9

P53	SHEEP		
ID	P53_SHEEP	STANDARD;	PRT; 382 AA.
AC	P51664;		
DT	01-OCT-1996	(Rel. 34, Created)	
DT	01-OCT-1996	(Rel. 34, Last sequence update)	
DT	15-JUN-2002	(Rel. 41, Last annotation update)	
DE	Cellular tumor antigen p53	(Tumor suppressor p53).	
GN	TP53.		
GC	Ovis aries (Sheep).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidae;		
OC	Bovidae; Caprinae; Ovis.		
OX	NCBI_TaxID=9940;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RP	TISSUE=Blood;		
RC	MEDLINE=95352828; PubMed=7626788;		
RX	Dequiedt F., Kettmann R., Burny A., Willems L.;		
RA	"Nucleotide sequence of the ovine p53 tumor-suppressor cDNA and its		
RT	genomic organization.";		
RL	DA SEQ. 5:255-259(1995).		
CC	!- FUNCTION: Acts as a tumor suppressor in many tumor types; induces		
CC	growth arrest or apoptosis depending on the physiological		
CC	circumstances and cell type. Involved in cell cycle regulation		
CC	a trans-activator that acts to negatively regulate cell division		
CC	by controlling a set of genes required for this process. One of		
CC	the activated genes is an inhibitor of cyclin-dependent kinases		
CC	Apoptosis induction seems to be mediated either by stimulation of		
CC	BAX and FAS antigen expression, or by repression of Bcl-2		
CC	expression.		
CC	!- SUBUNIT: Binds DNA as a homotetramer (By similarity).		
CC	!- SUBCELLULAR LOCATION: Nuclear.		
CC	!- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY		
CC	OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED		
CC	IN MANY TYPES OF CANCER.		
CC	!- SIMILARITY: BELONGS TO THE P53 FAMILY.		

```

Query Match      89.5%; Score 94; DB 1; Length 382;
Best Local Similarity 94.4%;
Pred. No. 4.2e-07;
Matches 1; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 PPLSQETFSDLWKLLPEN 18
         ||||| ||||| |||||
Db       12 PPLSQETFSDLWNLLEN 29

```

## RESULT 10

RESULTS TO  
P53 BOVIN

ID AC P53 BOVIN STANDARD; PRT; 386 AA.  
 DT Q29628;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Cellular tumor antigen p53 (tumor suppressor p53).  
 DE TP53.  
 OS Bos taurus (Bovine), and  
 OS Bos indicus (Zebu).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OC NCBI\_TaxID=9913, 9915;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=Bovine; TISSUE=Liver;  
 RX MEDLINE=95352829; PubMed=7626789;  
 RA Dequiedt F., Kettmann R., Burny A., Willems L.;  
 RT "Nucleotide sequence of the bovine p53 tumor-suppressor cDNA.";  
 RL DNA Seq. 5:261-264 (1995).  
 RN [2]  
 RP SEQUENCE OF 13-386 FROM N.A.  
 RC SPECIES=Bovine; STRAIN=Holstein; TISSUE=Thymus;  
 RX MEDLINE=96401400; PubMed=8807776;  
 RA Komori H., Ishiguro N., Horiuchi M., Shinagawa M., Aida Y.;  
 RT "Predominant p53 mutations in enzootic bovine leukemic cell lines.";  
 RL Vet. Immunol. Immunopathol. 52:53-63 (1996).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=B. indicus; STRAIN=Boran; TISSUE=Blood;  
 RX Bishop R.P., Gobright E.E.I.;  
 RA Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.  
 RL  
 CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces  
 CC growth arrest or apoptosis depending on the physiological  
 CC circumstances and cell type. Involved in cell cycle regulation as  
 CC a trans-activator that acts to negatively regulate cell division  
 CC by controlling a set of genes required for this process. One of  
 CC the activated genes is an inhibitor of cyclin-dependent kinases.  
 CC Apoptosis induction seems to be mediated either by stimulation of  
 CC BAX and FAS antigen expression, or by repression of Bcl-2  
 CC expression.  
 CC -1- SUBUNIT: Binds DNA as a homotetramer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Nuclear.  
 CC -1- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY  
 CC OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED  
 CC IN MANY TYPES OF CANCER.  
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 DR EMBL; X81704; CAA57348.1; -;  
 DR EMBL; D49825; BAA08629.1; -;  
 DR EMBL; U74486; AAB51214.1; -;  
 DR HSSP; P04637; ITUP.  
 DR InterPro: IPR002117; P53.  
 DR Pfam; PF00870; P53; 1.  
 DR PRINTS; PR00386; P53SUPPRESSOR.  
 DR ProDom; PD002681; P53; 1.  
 DR PROSITE; PS00348; P53; 1.  
 DR Anti-oncogene; DNA-binding; Transcription regulation; Activator;  
 KW Nuclear protein; Phosphorylation; Apoptosis.  
 FT DOMAIN 1 44 TRANSCRIPTION ACTIVATION (ACIDIC).  
 FT DOMAIN 94 285 BY SIMILARITY.  
 FT DOMAIN 318 349 OLIGOMERIZATION.  
 FT DOMAIN 361 380 BASIC (REPRESSION OF DNA-BINDING).  
 FT DOMAIN 304 316 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).  
 FT MOD\_RES 385 385 PHOSPHORYLATION (BY SIMILARITY).

FT CONFLICT 380 380 R -> T (IN REF. 2).  
 SQ SEQUENCE 386 AA; 43255 MW; 222473F28C548F31 CRC64;  
 Query Match 89.5%; Score 94; DB 1; Length 386;  
 Best Local Similarity 94.4%; Pred. No. 4.3e-07;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 PPLSQETFSDLWKLLEN 18  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 12 PPLSQETFSDLWKLLEN 29  
 | | | | | | | | | | | | | | | | | | | | | |  
 RESULT 11  
 ID P53 MARMO STANDARD; PRT; 391 AA.  
 AC O3606;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Cellular tumor antigen p53 (tumor suppressor p53).  
 DE TP53.  
 OS Marmota monax (Woodchuck).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;  
 OC Marmota.  
 OC NCBI\_TaxID=9995;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97376996; PubMed=9233767;  
 RA Feitelson M.A., Ranganathan P.N., Clayton M.M., Zhang S.M.;  
 RT "Partial characterization of the woodchuck tumor suppressor, p53, and  
 RT its interaction with woodchuck hepatitis virus X antigen in  
 RT hepatocarcinogenesis.";  
 RL Oncogene 15:327-336 (1997).  
 CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces  
 CC growth arrest or apoptosis depending on the physiological  
 CC circumstances and cell type. Involved in cell cycle regulation as  
 CC a trans-activator that acts to negatively regulate cell division  
 CC by controlling a set of genes required for this process. One of  
 CC the activated genes is an inhibitor of cyclin-dependent kinases.  
 CC Apoptosis induction seems to be mediated either by stimulation of  
 CC BAX and FAS antigen expression, or by repression of Bcl-2  
 CC expression.  
 CC -1- SUBUNIT: Binds DNA as a homotetramer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Nuclear.  
 CC -1- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY  
 CC OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED  
 CC IN MANY TYPES OF CANCER.  
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 DR EMBL; AJ001022; CAA04478.1; -;  
 DR HSSP; P04637; ITUP.  
 DR InterPro: IPR002117; P53.  
 DR Pfam; PF00870; P53; 1.  
 DR PRINTS; PR00386; P53SUPPRESSOR.  
 DR ProDom; PD002681; P53; 1.  
 DR PROSITE; PS00348; P53; 1.  
 DR Anti-oncogene; DNA-binding; Transcription regulation; Activator;  
 KW Nuclear protein; Phosphorylation; Apoptosis.  
 FT DOMAIN 1 44 TRANSCRIPTION ACTIVATION (ACIDIC).  
 FT DOMAIN 100 290 BY SIMILARITY.  
 FT DOMAIN 323 354 OLIGOMERIZATION.  
 FT DOMAIN 366 385 BASIC (REPRESSION OF DNA-BINDING).  
 FT DOMAIN 309 321 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).  
 FT MOD\_RES 390 390 PHOSPHORYLATION (BY SIMILARITY).



SQ SEQUENCE 391 AA; 43468 MW; E1DB5DB84BA40182 CRC64;

Query Match 89.5%; Score 94; DB 1; Length 391;  
Best Local Similarity 94.4%; Pred. No. 4.3e-07;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18  
DB 12 PPLSQETFSDLWNLLEN 29

RESULT 12

ID P53\_CANFA STANDARD; PRT; 381 AA.

AC Q29537; Q9TV78;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Cellular tumor antigen p53 (Tumor suppressor p53).  
GN TP53 OR P53  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
OX NCBI\_TaxID=9615;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Leukocyte;  
RX MEDLINE=98178696; PubMed=9519881;  
RA Veldhoen N., Milner J.;  
RT "Isolation of canine p53 cDNA and detailed characterization of the  
RT full length canine p53 protein.";  
RL Oncogene 16:1077-1084(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RA Setoguchi A., Sakai T., Okuda M., Minehata K., Yazawa M., Ishizaka T.,  
RA Watari T., Hasegawa A., Tsujimoto H.;  
RT "Aberrations of p53 tumor suppressor gene in various spontaneous  
RT tumors in the dog.";  
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE OF 25-300 FROM N.A.  
RC STRAIN=Beagle;  
RX MEDLINE=95323915; PubMed=7600529;  
RA Kraegel S.A., Pazzi K.A., Madewell B.R.;  
RT "Sequence analysis of canine p53 in the region of exons 3-8.";  
RL Cancer Lett. 92:181-186(1995).  
CC -!- FUNCTION: Acts as a tumor suppressor in many tumor types; induces  
CC growth arrest or apoptosis depending on the physiological  
CC circumstances and cell type. Involved in cell cycle regulation as  
CC a trans-activator that acts to negatively regulate cell division  
CC by controlling a set of genes required for this process. One of  
CC the activated genes is an inhibitor of cyclin-dependent kinases.  
CC Apoptosis induction seems to be mediated either by stimulation of  
CC BAX and P53 antigen expression, or by repression of Bcl-2  
CC expression.  
CC -!- SUBUNIT: Binds DNA as a homotetramer (By similarity).  
CC -!- SUBCELLULAR LOCATION: Nuclear.  
CC -!- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY  
CC OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED  
CC IN MANY TYPES OF CANCER.  
CC -!- SIMILARITY: BELONGS TO THE P53 FAMILY.

-----  
This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use by non-profit institutions as long as its content is in no way  
modified and this statement is not removed. Usage by and for commercial  
entities requires a license agreement (see <http://www.isb-sib.ch/announce/>  
or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
-----

DR EMBL; AF060514; AAC16909.1; -;  
DR EMBL; AR020761; BAA78379.1; -;

DR EMBL; S77819; AAB42022.1; -;  
DR HSFP; P04637; IOLG.  
DR InterPro; IPR002117; P53.  
DR Pfam; PF00870; P53; 1.  
DR PRINTS; PR00386; P53SUPPRESSR.  
DR ProDom; PD002681; P53; 1.  
DR PROSITE; PS00348; P53; 1.  
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;  
KW Nuclear protein; Phosphorylation; Apoptosis.  
FT DOMAIN 1 44  
FT DOMAIN 89 280  
FT DOMAIN 313 344  
FT DOMAIN 356 375  
FT DOMAIN 299 311  
FT MOD\_RES 380 380  
FT CONFLICT 1 4  
FT CONFLICT 378 378 L -> P (IN REF. 2).  
SQ SEQUENCE 381 AA; 42486 MW; 761A718FDC93DA59 CRC64;

Query Match 85.7%; Score 90; DB 1; Length 381;  
Best Local Similarity 88.9%; Pred. No. 1.7e-06;  
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18  
DB 12 PPLSQETFSDLWNLLEN 29

RESULT 13

ID P53\_FELCA STANDARD; PRT; 386 AA.

AC P41685;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Cellular tumor antigen p53 (tumor suppressor p53).  
GN TP53 OR TRP53.  
OS Felis silvestris catus (Cat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
OX NCBI\_TaxID=9685;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lymph node;  
RX MEDLINE=94333960; PubMed=8056458;  
RA Okuda M., Umeda A., Sakai T., Ohashi T., Momoi Y., Youn H.Y.,  
RA Watari T., Goitsuka R., Tsujimoto H., Hasegawa A.;  
RT "Cloning of feline p53 tumor-suppressor gene and its aberration in  
RT hematopoietic tumors.";  
RL Int. J. Cancer 58:602-607(1994).  
RN [2]  
RP SEQUENCE OF 34-354 FROM N.A.  
RX MEDLINE=94114699; PubMed=8286534;  
RA Okuda M., Umeda A., Matsumoto Y., Momoi Y., Watari T., Goitsuka R.,  
RA O'Brien S.J., Tsujimoto H., Hasegawa A.;  
RT "Molecular cloning and chromosomal mapping of feline p53 tumor  
RT suppressor gene.";  
RL J. Vet. Med. Sci. 55:801-805(1993).  
CC -!- FUNCTION: Acts as a tumor suppressor in many tumor types; induces  
CC growth arrest or apoptosis depending on the physiological  
CC circumstances and cell type. Involved in cell cycle regulation as  
CC a trans-activator that acts to negatively regulate cell division  
CC by controlling a set of genes required for this process. One of  
CC the activated genes is an inhibitor of cyclin-dependent kinases.  
CC Apoptosis induction seems to be mediated either by stimulation of  
CC BAX and P53 antigen expression, or by repression of Bcl-2  
CC expression.  
CC -!- SUBUNIT: Binds DNA as a homotetramer (By similarity).  
CC -!- SUBCELLULAR LOCATION: Nuclear.  
CC -!- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY  
CC OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED  
CC IN MANY TYPES OF CANCER.  
CC -!- SIMILARITY: BELONGS TO THE P53 FAMILY.



CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC EMBL; D26608; BAA05653.1; -;  
 CC EMBL; D16450; BAA03927.1; -;  
 CC HSSP; P04637; IOUG.  
 CC InterPro; IPR002117; P53.  
 CC PRINTS; PR00386; P53SUPPRESSR.  
 CC ProDom; PD002681; P53; 1.  
 CC PROSITE; PS00348; P53; 1.

KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;  
 KW Nuclear protein; Phosphorylation; Apoptosis.

FT DOMAIN 1 44 TRANSCRIPTION ACTIVATION (ACIDIC).  
 FT DNA BIND 94 285 BY SIMILARITY.  
 FT DOMAIN 318 349 OLIGOMERIZATION.  
 FT DOMAIN 361 380 BASIC (REPRESSION OF DNA-BINDING).  
 FT DOMAIN 304 316 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).  
 FT MOD\_RES 385 385 PHOSPHORYLATION (BY SIMILARITY).  
 FT CONFLICT 285 285 K -> R (IN REF. 2).  
 SQ SEQUENCE 386 AA; 42692 MW; D08B43BA1BC8EB78 CRC64;

Query Match 85.7%; Score 90; DB 1; Length 386;  
 Best Local Similarity 88.9%; Pred. No. 1.8e-06;  
 Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 PLSQETFSDLWKLLPEN 18  
 DB 12 PLSQETFSSELNLLPEN 29

## RESULT 14

P53 CRIGR  
 ID\_P53 CRIGR STANDARD; PRT; 393 AA.  
 AC Q09185; Q64397; P97258; P97788;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Cellular tumor antigen p53 (Tumor suppressor p53).  
 GN TP53 OR P53.  
 OS Cricetulus griseus (Chinese hamster).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
 OC Cricetulus.  
 OX NCBI\_TaxID=10029;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Chuang W., Mi L.J., Boorstein R.J.;  
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=97183659; PubMed=9031625;  
 RA Lee H., Larner J.M., Hamlin J.L.;  
 RT "Cloning and characterization of Chinese hamster p53 cDNA."  
 RL Gene 184:177-183(1997).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Embryonic fibroblast;  
 RA Shimizu T., Nikaudo O., Suzuki F.;  
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces  
 CC growth arrest or apoptosis depending on the physiological  
 CC circumstances and cell type. Involved in cell cycle regulation as  
 CC a trans-activator that acts to negatively regulate cell division  
 CC by controlling a set of genes required for this process. One of  
 CC the activated genes is an inhibitor of cyclin-dependent kinases.

CC Apoptosis induction seems to be mediated either by stimulation of  
 CC BAX and FAS antigen expression, or by repression of Bcl-2  
 CC expression.

CC -1- SUBUNIT: Binds DNA as a homotetramer (By similarity).

CC -1- SUBCELLULAR LOCATION: Nuclear.

CC -1- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY  
 CC OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED  
 CC IN MANY TYPES OF CANCER.

CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC EMBL; Y08900; CAA70108.1; -;  
 CC EMBL; Y08901; CAA70109.1; -;  
 CC EMBL; U50395; AAC53040.1; -;  
 CC EMBL; D86070; BAA13004.1; -;  
 CC HSSP; P04637; ITUP.

CC InterPro; IPR002117; P53.

CC PRINTS; PR00386; P53SUPPRESSR.

CC ProDom; PD002681; P53; 1.

CC PROSITE; PS00348; P53; 1.

KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;  
 KW Nuclear protein; Phosphorylation; Apoptosis.

FT DOMAIN 1 45 TRANSCRIPTION ACTIVATION (ACIDIC).  
 FT DNA BIND 102 292 BY SIMILARITY.  
 FT DOMAIN 325 356 OLIGOMERIZATION.  
 FT DOMAIN 368 387 BASIC (REPRESSION OF DNA-BINDING).  
 FT DOMAIN 311 323 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).  
 FT MOD\_RES 392 392 PHOSPHORYLATION (BY SIMILARITY).

FT VARIANT 133 133 L -> Q (IN CELL LINE V79-4).

FT VARIANT 135 135 C -> W (IN CELL LINE V79-4).

FT CONFLICT 103 103 Y -> F (IN REF. 2).

SQ SEQUENCE 393 AA; 43378 MW; 2A7830E788311689 CRC64;

Query Match 81.9%; Score 86; DB 1; Length 393;

Best Local Similarity 94.1%; Pred. No. 7.4e-06;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 PLSQETFSDLWKLLPEN 18

DB 13 PLSQETFSDLWKLLPPN 29

## RESULT 15

P53 MESAU  
 ID\_P53 MESAU STANDARD; PRT; 396 AA.

AC Q00366; P97276;

DT 01-DEC-1992 (Rel. 24, Created)

DT 01-DEC-1992 (Rel. 24, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Cellular tumor antigen p53 (Tumor suppressor p53).

GN TP53.

OS Mesocricetus auratus (Golden hamster).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;

OC Mesocricetus.

OX NCBI\_TaxID=10036;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Syrain; TISSUE=Kidney;

RX MEDLINE=92210007; PubMed=1555773;

RA Legros Y., McIntyre P., Soussi T.;

RT "The cDNA cloning and immunological characterization of hamster p53.";

RL Gene 112:247-250(1992).

RN [2]

RP SEQUENCE FROM N.A.

```

RA Hou E.W., Wiseman R.;
RL Submitted (APR-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
CC growth arrest or apoptosis depending on the physiological
CC circumstances and cell type. Involved in cell cycle regulation as
CC a trans-activator that acts to negatively regulate cell division
CC by controlling a set of genes required for this process. One of
CC the activated genes is an inhibitor of cyclin-dependent kinases.
CC Apoptosis induction seems to be mediated either by stimulation of
CC BAX and FAS antigen expression, or by repression of Bcl-2
CC expression.
CC -!- SUBUNIT: Binds DNA as a homotetramer (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY
CC OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED
CC IN MANY TYPES OF CANCER.
CC -!- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M75144; AAA37085.1; -.
DR EMBL; U07182; AAB41344.1; -.
DR PIR; JH0633; JH0633.
DR HSSP; P04637; 1TUP.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR PRODOM; PD002681; P53; 1.
DR PROSITE; PS00348; P53; 1.
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; Phosphorylation; Apoptosis.
FT DOMAIN 1 45 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNA_BIND 105 295 BY SIMILARITY..
FT DOMAIN 328 359 OLIGOMERIZATION.
FT DOMAIN 371 390 BASIC (REPRESSION OF DNA-BINDING).
FT DOMAIN 314 326 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 395 395 PHOSPHORYLATION (BY SIMILARITY).
FT CONFLICT 188 188 G -> S (IN REF. 2).
SQ SEQUENCE 396 AA; 43631 MW; 906EF02568099BE3 CRC64;

```

```

Query Match      81.9%; Score 86; DB 1; Length 396;
Best Local Similarity 94.1%; Pred. No. 7.5e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 2 PLSQETFSDLWKLPPEN 18
   |||||
Db 13 PLSQETFSDLWKLPPN 29

```

```

Search completed: February 12, 2003, 10:35:02
Job time : 12 secs

```

GenCore version 5.1.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 12, 2003, 10:33:27 ; Search time 29 Seconds  
(without alignments)  
134.996 Million cell updates/sec

Title: US-09-403-440A-2

Perfect score: 105  
Sequence: 1 PPLSQETFSDLWKLLENPENG 19

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_21.\*  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phase.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_virus.\*  
16: sp\_bacteriap.\*  
17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	99	94.3	32	4 Q9NZD0	Q9nzdo homo sapien
2	99	94.3	387	6 Q8SPZ3	Q8spz3 delphinape
3	99	94.3	393	4 Q9UQ61	Q9uq61 homo sapien
4	99	94.3	393	4 Q9HAQ8	Q9haq8 homo sapien
5	99	94.3	393	4 Q16811	Q16811 homo sapien
6	99	94.3	393	4 Q16807	Q16807 homo sapien
7	99	94.3	393	4 Q15086	Q15086 homo sapien
8	99	94.3	393	4 Q15087	Q15087 homo sapien
9	99	94.3	393	4 Q15088	Q15088 homo sapien
10	99	94.3	393	4 Q16808	Q16808 homo sapien
11	99	94.3	393	4 Q16809	Q16809 homo sapien
12	99	94.3	393	4 Q16810	Q16810 homo sapien
13	99	94.3	393	4 Q9BTM4	Q9btm4 homo sapien
14	99	94.3	393	4 Q16535	Q16535 homo sapien
15	94	89.5	387	6 Q9N252	Q9n252 sus scrofa
16	88	83.8	390	11 Q920Y0	Q920y0 meriones un

17	77	73.3	25	4	Q9NP68	Q9np68 homo sapien
18	74	70.5	307	11	Q9ER40	Q9er40 mus musculus
19	74	70.5	390	11	O70366	O70366 mus musculus
20	74	70.5	391	11	Q91XH8	Q91xh8 mus musculus
21	72	68.6	170	11	Q9EPP9	Q9epp9 rattus norv
22	72	68.6	271	11	Q9EQL0	Q9eqlo rattus norv
23	69	65.7	378	11	P89002	P89002 pracomys nat
24	60	57.1	265	13	Q9W680	Q9w680 oncorhynch
25	60	57.1	265	13	Q9W681	Q9w681 oncorhynch
26	60	57.1	265	13	Q9W682	Q9w682 oncorhynch
27	55	52.4	515	16	Q92QD2	Q92qd2 rhizobium m
28	52	49.5	443	5	Q9NGC8	Q9ngc8 mya arenari
29	52	49.5	621	5	Q9NGC7	Q9ngc7 mya arenari
30	51.5	49.0	791	4	Q9ULK0	Q9ulk0 homo sapien
31	51.5	49.0	1009	11	Q62640	Q62640 rattus norv
32	51.5	49.0	1009	11	O61627	O61627 mus musculus
33	50	47.6	367	16	Q9CHK4	Q9chk4 lactococcus
34	50	47.6	447	10	Q9XIQ5	Q9xiq5 arabidopsis
35	49.5	47.1	692	16	Q8RAS7	Q8ras7 thermoplas
36	49	46.7	160	17	Q8TWJ0	Q8twj0 methanopyru
37	49	46.7	474	5	Q8T4N3	Q8t4n3 rhipicephal
38	48	45.7	308	16	O8VJK2	O8vjk2 brucella me
39	47.5	45.2	591	5	Q8T7V3	Q8t7v3 spissula sol
40	47	44.8	157	12	Q9IU98	Q9iu98 pepper mild
41	47	44.8	157	12	Q9IU97	Q9iu97 pepper mild
42	47	44.8	157	12	Q9IE32	Q9ie32 tobacco mos
43	47	44.8	158	12	Q83483	Q83483 tobacco mos
44	47	44.8	469	10	Q9SJM2	Q9sjm2 arabidopsis
45	47	44.8	487	16	Q9HUK7	Q9huk7 pseudomonas

## ALIGNMENTS

### RESULT 1

Q9NZD0 ID Q9NZD0 PRELIMINARY; PRT; 32 AA.  
AC Q9NZD0;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE P53 tumor suppressor protein (Fragment).  
GN TP53.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
[1]  
RN  
RP SEQUENCE FROM N.A.  
RC TISSUE=GLIOMAS AND ASSOCIATED NORMAL TISSUES;  
RA Thompson-Hehir J., Davies M.P.A., Green J.A., Halliwell N.,  
RA Joyce K.A., Salisbury J., Sibson D.R., Vergote I., Walker C.;  
RT "Mutation Detection Utilizing a Novel PCR Approach for Amplification  
RT of the p53 Gene from Microdissected Tissue: Application to Archival  
RT Tumor Samples.";  
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF210309; AAF63442.1; -;  
DR EMBL; AF210308; AAF63442.1; JOINED.  
DR InterPro; IPR002117; P53.  
DR Pfam; PF00870; P53; 1.  
DR ProDom; PD002681; P53; 1.  
FT NON TER 32  
SQ SEQUENCE 32 AA; 3670 MW; F0E0EA983A90B917 CRC64;

Query Match 94.3%; Score 99; DB 4; Length 32;  
Best Local Similarity 100.0%; Pred. No. 6.4e-09;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLEN 18  
Db 12 PPLSQETFSDLWKLLEN 29

```

RESULT 2
Q8SPZ3 Q8SPZ3 PRELIMINARY; PRT; 387 AA.
AC Q8SPZ3;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE P53.
GN P53.
OS Delphinapterus leucas (Beluga whale).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti;
OC Monodontidae; Delphinapterus.
OX NCBI_TaxID=9749;
RN [1]
RP SEQUENCE FROM N.A.
RA Xu N., Shiraki T., Yamada T., Nakajima M., Gauthier J.M.,
RA Pfeiffer C.J., Sato S.;
RT "Nucleotide sequence of the p53 cDNA of beluga whale (Delphinapterus
RT leucas).";
RL Gene 0-0-0(2002).
DR EMBL; AF475081; AAL83290.1; -. B4C8BEDBF34A540E CRC64;
SQ SEQUENCE 387 AA; 43033 MW; 43033 MW; 43033 MW; 43033 MW;

Query Match 94.3%; Score 99; DB 6; Length 387;
Best Local Similarity 100.0%; Pred. No. 9e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLEN 18
Db 12 PPLSQETFSDLWKLLEN 29

RESULT 3
Q9UQ61 Q9UQ61 PRELIMINARY; PRT; 393 AA.
AC Q9UQ61;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 20, Last annotation update)
DE Cellular tumor antigen p53.
GN TP53 OR P53.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Allalunis-Turner M.J., Barron G.M., Day R.S. III, Dobler K.D.,
RA Mirzayans R.;
RX MEDLINE=93303270; PubMed=8316628;
RT "Isolation of two cell lines from a human malignant glioma specimen
RT differing in sensitivity to radiation and chemotherapeutic drugs.";
RL Radiat. Res. 134:349-354(1993).
RN [2]
RP SEQUENCE FROM N.A.
RA Anderson C.W., Kiehlczawa J., Allalunis-Turner M.J.;
RT "Human p53 from malignant glioma-derived M059J and M059K cells has a
RT cancer-associated mutation in exon 8.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES
CC GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL
CC CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN
CC TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION, IS A TRANS-
CC ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY
CC CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE
CC ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.
CC APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF
CC RAX AND FAS ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2
CC EXPRESSION (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY OF
CC TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED IN
CC MANY TYPES OF CANCER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL; AF307851; AAG28785.1; -.
DR HSSP; P04637; 1TUP.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR PRODOM; PD002681; P53; 1.
DR PROSITE; PS00348; P53; 1.
DR PROSITE; PS00348; P53; 1.
KW Activator; Anti-oncogene; Apoptosis; DNA-binding; Nuclear protein;
KW Phosphorylation; Transcription regulation.
KW SEQUENCE 393 AA; 43712 MW; AC611E4938C7BC3B CRC64;

Query Match 94.3%; Score 99; DB 4; Length 393;
Best Local Similarity 100.0%; Pred. No. 9.2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC -1- MANY TYPES OF CANCER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL; AF135121; AAD28535.1; -.
DR EMBL; AF135120; AAD28535.1; JOINED.
DR HSSP; P04637; 1OLG.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR PRODOM; PD002681; P53; 1.
DR PROSITE; PS00348; P53; 1.
DR PROSITE; PS00348; P53; 1.
KW Activator; Anti-oncogene; Apoptosis; DNA-binding; Nuclear protein;
KW Phosphorylation; Transcription regulation.
KW SEQUENCE 393 AA; 43711 MW; 0C6BB4E4581CD18D CRC64;

Query Match 94.3%; Score 99; DB 4; Length 393;
Best Local Similarity 100.0%; Pred. No. 9.2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLEN 18
Db 12 PPLSQETFSDLWKLLEN 29

RESULT 4
Q9HAQ8 Q9HAQ8 PRELIMINARY; PRT; 393 AA.
AC Q9HAQ8;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Cellular tumor antigen p53.
GN TP53.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Chang N.-S., Pratt N., Heath J., Schultz L., Sleve D., Carey G.B.,
RA Zevotek N.;
RT "Hyaluronidase Induction of a WW Domain-Containing Oxidoreductase that
RT Enhances Tumor Necrosis Factor Cytotoxicity.";
RL J. Biol. Chem. 276:3361-3370(2001).
CC -1- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES
CC GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL
CC CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN
CC TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION, IS A TRANS-
CC ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY
CC CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE
CC ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.
CC APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF
CC BAX AND FAS ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2
CC EXPRESSION (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY OF
CC TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED IN
CC MANY TYPES OF CANCER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL; AF307851; AAG28785.1; -.
DR HSSP; P04637; 1TUP.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR PRODOM; PD002681; P53; 1.
DR PROSITE; PS00348; P53; 1.
DR PROSITE; PS00348; P53; 1.
KW Activator; Anti-oncogene; Apoptosis; DNA-binding; Nuclear protein;
KW Phosphorylation; Transcription regulation.
KW SEQUENCE 393 AA; 43712 MW; AC611E4938C7BC3B CRC64;

Query Match 94.3%; Score 99; DB 4; Length 393;
Best Local Similarity 100.0%; Pred. No. 9.2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Db 12 PPLSQETFSDLWKLLPEN 29  
|||||  
RESULT 6  
Q16807 ID Q16807 PRELIMINARY; PRT; 393 AA.  
AC Q16807;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE Cellular tumor antigen p53 (Fragment).  
GN TP53 OR P53.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92007731; PubMed=1915267;  
RA Farrell P.J., Allan G., Shanahan F., Voutsen K.H., Crook T.;  
RT "p53 is frequently mutated Burkitt's lymphoma cell lines.";  
RL EMBO J. 10:2879-2887(1991).  
CC -!- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES  
CC GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL  
CC CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN  
CC TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION, IS A TRANS-  
CC ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY  
CC CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE  
CC ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.  
CC APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF  
CC BAX AND FAS ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2  
CC EXPRESSION (BY SIMILARITY).  
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
CC -!- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY OF  
CC TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED IN  
CC MANY TYPES OF CANCER (BY SIMILARITY).  
CC -!- SIMILARITY: BELONGS TO THE P53 FAMILY.  
DR EMBL; X60011; CAA42626.1; -.  
DR HSSP; P04637; 10LG.  
DR InterPro: IPR002117; P53.  
DR Pfam; PF00870; P53; 1.  
DR PRINTS; PR00386; P53SUPPRESSR.  
DR PRODOM; PD002681; P53; 1.  
DR PROSITE; PS00348; P53; 1.  
KW Activator; Anti-oncogene; Apoptosis; DNA-binding; Nuclear protein;  
KW Phosphorylation; Transcription regulation.  
FT VARIANT 193 193 R -> H.  
FT NON\_TER 393 393  
SQ SEQUENCE 393 AA; 43731 MW; 3A3580718E932E27 CRC64;  
Query Match 94.3%; Score 99; DB 4; Length 393;  
Best Local Similarity 100.0%; Pred. No. 9.2e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 PPLSQETFSDLWKLLPEN 18  
|||||  
Db 12 PPLSQETFSDLWKLLPEN 29  
|||||  
RESULT 7  
Q15086 ID Q15086 PRELIMINARY; PRT; 393 AA.  
AC Q15086;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE P53 transformation suppressor (Fragment).  
GN P53.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;

Qy 1 PPLSQETFSDLWKLLPEN 18  
|||||  
Db 12 PPLSQETFSDLWKLLPEN 29  
|||||  
RESULT 5  
Q16811 ID Q16811 PRELIMINARY; PRT; 393 AA.  
AC Q16811;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE Cellular tumor antigen p53.  
GN TP53.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=85126934; PubMed=6396087;  
RA Matlaehewski G., Lamb P., Pim D., Peacock J., Crawford L.,  
RT BenChimol S.;  
RL "Isolation and characterization of a human p53 cDNA clone: expression  
of the human p53 gene.";  
RL EMBO J. 3:3257-3262(1984).  
CC [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=87064416; PubMed=2946935;  
RA Lamb P., Crawford L.;  
RT "Characterization of the human p53 gene.";  
RL Mol. Cell. Biol. 6:1379-1385(1986).  
CC -!- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES  
CC GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL  
CC CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN  
CC TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION, IS A TRANS-  
CC ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY  
CC CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE  
CC ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.  
CC APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF  
CC BAX AND FAS ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2  
CC EXPRESSION (BY SIMILARITY).  
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
CC -!- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY OF  
CC TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED IN  
CC MANY TYPES OF CANCER (BY SIMILARITY).  
CC -!- SIMILARITY: BELONGS TO THE P53 FAMILY.  
DR EMBL; M13121; AAA59987.1; -.  
DR EMBL; M13112; AAA59987.1; JOINED.  
DR EMBL; M13113; AAA59987.1; JOINED.  
DR EMBL; M13114; AAA59987.1; JOINED.  
DR EMBL; M13115; AAA59987.1; JOINED.  
DR EMBL; M13116; AAA59987.1; JOINED.  
DR EMBL; M13117; AAA59987.1; JOINED.  
DR EMBL; M13118; AAA59987.1; JOINED.  
DR EMBL; M13119; AAA59987.1; JOINED.  
DR EMBL; M13120; AAA59987.1; JOINED.  
DR HSSP; P04637; ITUP.  
DR InterPro: IPR002117; P53.  
DR Pfam; PF00870; P53; 1.  
DR PRINTS; PR00386; P53SUPPRESSR.  
DR PRODOM; PD002681; P53; 1.  
DR PROSITE; PS00348; P53; 1.  
KW Activator; Anti-oncogene; Apoptosis; DNA-binding; Nuclear protein;  
KW Phosphorylation; Transcription regulation.  
SQ SEQUENCE 393 AA; 43698 MW; AD1979573AFA1DA5 CRC64;  
Query Match 94.3%; Score 99; DB 4; Length 393;  
Best Local Similarity 100.0%; Pred. No. 9.2e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 PPLSQETFSDLWKLLPEN 18  
|||||

```

RN SEQUENCE FROM N.A.
RX MEDLINE=92007731; PubMed=1915267;
RA Farrell P.J., Allan G., Shanahan F., Vousden K.H., Crook T.;
RT "p53 is frequently mutated Burkitt's lymphoma cell lines.";
RL EMBO J. 10:2879-2887(1991).
DR EMBL; X60013; CAA42628.1; -.
DR HSSP; P04637; IOLG.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR ProDom; PD002681; P53; 1.
FT VARIANT 246 246 T -> M.
FT NON TER 393 393
SQ SEQUENCE 393 AA; 43682 MW; AC798FCA1EAC0BCB CRC64;

Query Match 94.3%; Score 99; DB 4; Length 393;
Best Local Similarity 100.0%; Pred. No. 9.2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETPSDLWKLLPEN 18
Db 12 PPLSQETPSDLWKLLPEN 29

RESULT 8
ID Q15087 PRELIMINARY; PRT; 393 AA.
AC Q15087;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE P53 transformation suppressor (Fragment).
GN P53.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE=92007731; PubMed=1915267;
RA Farrell P.J., Allan G., Shanahan F., Vousden K.H., Crook T.;
RT "p53 is frequently mutated Burkitt's lymphoma cell lines.";
RL EMBO J. 10:2879-2887(1991).
DR EMBL; X60014; CAA42629.1; -.
DR HSSP; P04637; IOLG.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR ProDom; PD002681; P53; 1.
FT VARIANT 237 237 I -> M.
FT NON TER 393 393
SQ SEQUENCE 393 AA; 43694 MW; C6A118E50EB96BB CRC64;

Query Match 94.3%; Score 99; DB 4; Length 393;
Best Local Similarity 100.0%; Pred. No. 9.2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETPSDLWKLLPEN 18
Db 12 PPLSQETPSDLWKLLPEN 29

RESULT 9
ID Q15088 PRELIMINARY; PRT; 393 AA.
AC Q15088;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE P53 transformation suppressor (Fragment).
GN P53.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE=92007731; PubMed=1915267;
RA Farrell P.J., Allan G., Shanahan F., Vousden K.H., Crook T.;
RT "p53 is frequently mutated Burkitt's lymphoma cell lines.";
RL EMBO J. 10:2879-2887(1991).
DR EMBL; X60015; CAA42631.1; -.
DR HSSP; P04637; IOLG.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR ProDom; PD002681; P53; 1.
FT VARIANT 238 238 Y -> C.
FT NON TER 393 393
SQ SEQUENCE 393 AA; 43713 MW; AD48ABDB26FA208B CRC64;

Query Match 94.3%; Score 99; DB 4; Length 393;
Best Local Similarity 100.0%; Pred. No. 9.2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETPSDLWKLLPEN 18
Db 12 PPLSQETPSDLWKLLPEN 29

RESULT 10
ID Q16808 PRELIMINARY; PRT; 393 AA.
AC Q16808;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Cellular tumor antigen p53 (Fragment).
GN TP53 OR P53.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE=92007731; PubMed=1915267;
RA Farrell P.J., Allan G., Shanahan F., Vousden K.H., Crook T.;
RT "p53 is frequently mutated Burkitt's lymphoma cell lines.";
RL EMBO J. 10:2879-2887(1991).
CC -!- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION. IS A TRANS- ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES. APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF BAX AND BCL-2 ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2 EXPRESSION (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED IN MANY TYPES OF CANCER (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL; X60018; CAA42633.1; -.
DR HSSP; P04637; IOLG.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR ProDom; PD002681; P53; 1.
DR PROSITE; PS00348; P53; 1.
KW Activator; Anti-oncogene; Apoptosis; DNA-binding; Nuclear protein; Phosphorylation; Transcription regulation.
FT VARIANT 163 163 H -> Y.
FT NON TER 393 393

```

SQ SEQUENCE 393 AA; 43627 MW; 3325FAE63F8E1E61 CRC64;  
 Query Match 94.3%; Score 99; DB 4; Length 393;  
 Best Local Similarity 100.0%; Pred. No. 9.2e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18  
 DB 12 PPLSQETFSDLWKLLPEN 29

RESULT 11

Q16809 Q16809 PRELIMINARY; PRT; 393 AA.  
 AC Q16809;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
 DE Cellular tumor antigen p53 (Fragment).  
 GN TP53 OR P53.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92007731; PubMed=1915267;  
 RA Farrell P.J., Allan G., Shanahan F., Vousden K.H., Crook T.;  
 RT "p53 is frequently mutated Burkitt's lymphoma cell lines."  
 RL EMBO J. 10:2879-2887(1991).  
 CC -1- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES  
 CC GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL  
 CC CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN  
 CC TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION, IS A TRANS-  
 CC ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY  
 CC CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE  
 CC ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.  
 CC APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF  
 CC BAX AND BCL-2 ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2  
 CC EXPRESSION (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
 CC -1- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY OF  
 CC TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED IN  
 CC MANY TYPES OF CANCER (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.  
 DR EMBL; X60019; CA42634.1; --  
 DR HSP; P04637; IOLG.  
 DR InterPro; IPR002117; P53.  
 DR Pfam; PF00870; P53; 1.  
 DR PRINTS; PR00386; P53SUPPRESSR.  
 DR ProDom; PD002681; P53; 1.  
 DR PROSITE; PS00348; P53; 1.  
 DR Activator; Anti-oncogene; Apoptosis; DNA-binding; Nuclear protein;  
 KW Phosphorylation; Transcription regulation.  
 FT VARIANT 254 254 D -> N.  
 FT NON TER 393 393  
 FT SEQUENCE 393 AA; 43684 MW; 3DB21E4A398CD0C7 CRC64;

Query Match 94.3%; Score 99; DB 4; Length 393;  
 Best Local Similarity 100.0%; Pred. No. 9.2e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18  
 DB 12 PPLSQETFSDLWKLLPEN 29

RESULT 12

Q16810 Q16810 PRELIMINARY; PRT; 393 AA.  
 AC Q16810;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)

DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
 DE Cellular tumor antigen p53 (Fragment).  
 GN TP53 OR P53.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92007731; PubMed=1915267;  
 RA Farrell P.J., Allan G., Shanahan F., Vousden K.H., Crook T.;  
 RT "p53 is frequently mutated Burkitt's lymphoma cell lines."  
 RL EMBO J. 10:2879-2887(1991).  
 CC -1- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES  
 CC GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL  
 CC CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN  
 CC TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION, IS A TRANS-  
 CC ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY  
 CC CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE  
 CC ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.  
 CC APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF  
 CC BAX AND BCL-2 ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2  
 CC EXPRESSION (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
 CC -1- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY OF  
 CC TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED IN  
 CC MANY TYPES OF CANCER (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.  
 DR EMBL; X60020; CA42635.1; --  
 DR HSP; P04637; IOLG.  
 DR InterPro; IPR002117; P53.  
 DR Pfam; PF00870; P53; 1.  
 DR PRINTS; PR00386; P53SUPPRESSR.  
 DR ProDom; PD002681; P53; 1.  
 DR PROSITE; PS00348; P53; 1.  
 DR Activator; Anti-oncogene; Apoptosis; DNA-binding; Nuclear protein;  
 KW Phosphorylation; Transcription regulation.  
 FT VARIANT 254 254 D -> N.  
 FT NON TER 393 393  
 FT SEQUENCE 393 AA; 43714 MW; AC69737F2CF9C53B CRC64;

Query Match 94.3%; Score 99; DB 4; Length 393;  
 Best Local Similarity 100.0%; Pred. No. 9.2e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18  
 DB 12 PPLSQETFSDLWKLLPEN 29

RESULT 13

Q9BTM4 Q9BTM4 PRELIMINARY; PRT; 393 AA.  
 AC Q9BTM4;  
 DT 01-JUN-2001 (TREMBlrel. 17, Created)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
 DE Cellular tumor antigen p53.  
 GN TP53.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX Strausberg R.;  
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES  
 CC GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL  
 CC CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN  
 CC TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION, IS A TRANS-

CC ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY  
 CC CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE  
 CC ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.  
 CC APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF  
 CC BAX AND FAS ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2  
 CC EXPRESSION (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
 CC -1- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY OF  
 CC TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED IN  
 CC MANY TYPES OF CANCER (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.  
 DR EMBL; BC003596; AA03596.1; -.  
 DR HSSP; P04637; 10LG.  
 DR InterPro; IPR002117; P53.  
 DR Pfam; PF00870; P53; 1.  
 DR PRINTS; PR00386; P53SUPPRESSR.  
 DR PRODOM; PD002681; P53; 1.  
 DR PROSITE; PS00348; P53; 1.  
 KW Activator; Anti-oncogene; Apoptosis; DNA-binding; Nuclear protein;  
 KW Phosphorylation; Transcription regulation.  
 SQ SEQUENCE 393 AA; 43686 MW; 5C701E458E016756 CRC64;

Query Match 94.3%; Score 99; DB 4; Length 393;  
 Best Local Similarity 100.0%; Pred. No. 9.2e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18  
 |||||  
 DB 12 PPLSQETFSDLWKLLPEN 29

## RESULT 14

Q16535  
 ID Q16535 PRELIMINARY; PRT; 393 AA.  
 AC Q16535;  
 DT 01-NOV-1996 (TRENBLrel. 01, Created)  
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)  
 DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)  
 DE P53 transformation suppressor (Fragment).  
 GN P53.  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP MEDLINE=92007731; PubMed=1915267;  
 RA Farrell P.J., Allan G., Shanahan F., Vousden K.H., Crook T.;  
 RT "p53 is frequently mutated in Burkitt's lymphoma cell lines.";  
 RL EMO J. 10:2879-2887(1991).  
 DR EMBL; X60017; CAA42632.1; -.  
 DR EMBL; X60015; CAA42630.1; -.  
 DR HSSP; P04637; 10LG.  
 DR InterPro; IPR002117; P53.  
 DR Pfam; PF00870; P53; 1.  
 DR PRINTS; PR00386; P53SUPPRESSR.  
 DR PRODOM; PD002681; P53; 1.  
 FT VARIANT 248 248 Q -> R.  
 FT NON TER 393 393  
 SQ SEQUENCE 393 AA; 43684 MW; FC5343E85557BC39 CRC64;

Query Match 94.3%; Score 99; DB 4; Length 393;  
 Best Local Similarity 100.0%; Pred. No. 9.2e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18  
 |||||  
 DB 12 PPLSQETFSDLWKLLPEN 29

## RESULT 15

Q9N252  
 ID Q9N252 PRELIMINARY; PRT; 387 AA.

AC Q9N252;  
 DT 01-OCT-2000 (TRENBLrel. 15, Created)  
 DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)  
 DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)  
 DE Cellular tumor antigen p53.  
 GN TP53.  
 OS Sus scrofa (Pig).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=URINARY BLADDER EPITHELIUM;  
 RA Plasm M., Hartmann E., Mueller O., Kuhlmann J.;  
 RT "Identification of a Sus scrofa gene encoding a protein with high  
 RT similarity to p53 from Homo sapiens, Bos taurus and Ovis aries.";  
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES  
 CC GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL  
 CC CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN  
 CC TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION, IS A TRANS-  
 CC ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY  
 CC CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE  
 CC ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.  
 CC APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF  
 CC BAX AND FAS ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2  
 CC EXPRESSION (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
 CC -1- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY OF  
 CC TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED IN  
 CC MANY TYPES OF CANCER (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.  
 DR EMBL; AF124298; AAF28891.1; -.  
 DR HSSP; P04637; 1C26.  
 DR InterPro; IPR002117; P53.  
 DR Pfam; PF00870; P53; 1.  
 DR PRINTS; PR00386; P53SUPPRESSR.  
 DR PRODOM; PD002681; P53; 1.  
 DR PROSITE; PS00348; P53; 1.  
 KW Activator; Anti-oncogene; Apoptosis; DNA-binding; Nuclear protein;  
 KW Phosphorylation; Transcription regulation.  
 SQ SEQUENCE 387 AA; 43475 MW; 3BB49AA32B0053FA CRC64;

Query Match 89.5%; Score 94; DB 6; Length 387;  
 Best Local Similarity 94.4%; Pred. No. 5.8e-07;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18  
 |||||  
 DB 12 PPLSQETFSDLWKLLPEN 29

Search completed: February 12, 2003, 10:35:38  
 Job time : 30 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 12, 2003, 10:49:54 ; Search time 15 seconds

(without alignments)  
32.045 Million cell updates/sec

Title: US-09-403-440A-1

Perfect score: 23

Sequence: 1 FXXLW 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 120

Minimum DB seq length: 5

Maximum DB seq length: 5

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

PIR 73.\*

1: PIR1.\*

2: PIR2.\*

3: PIR3.\*

4: PIR4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11	47.8	5	2	A32516
2	11	47.8	5	2	cholecystokinin-5
3	11	47.8	5	2	neuropeptide - sea
4	11	47.8	5	2	gut pentapeptide -
5	11	47.8	5	2	Bradykinin-potenti
6	11	47.8	5	2	Ig heavy chain CRD
7	11	47.8	5	2	Ig heavy chain CRD
8	11	47.8	5	2	T-cell receptor be
9	11	47.8	5	2	T-cell receptor be
10	8	34.8	5	2	Ig heavy chain CRD
11	6	26.1	5	2	alkanal monooxygen
12	6	26.1	5	2	endo-1,4-beta-xyla
13	6	26.1	5	2	angiotensin-conver
14	6	26.1	5	2	ribulose-bisphosph
15	6	26.1	5	2	actin I - malaria
16	6	26.1	5	2	fulicin - giant Af
17	6	26.1	5	2	Leu-enkephalin - b
18	6	26.1	5	2	Met-enkephalin - b
19	6	26.1	5	2	subesophageal gang
20	6	26.1	5	2	cocoonase (BC 3.4.
21	6	26.1	5	2	T-cell receptor be
22	4	17.4	5	1	Serrawettin W2 - S
23	4	17.4	5	2	proctolin - Americ
24	4	17.4	5	2	peptidyl-di-peptida
25	4	17.4	5	2	copper resistance
26	4	17.4	5	2	flagellar protein
27	4	17.4	5	2	R-phycocerythrin al
28	4	17.4	5	2	zinc-binding prote
29	4	17.4	5	2	proctolin - Atlant
					hypothetical prote

30	4	17.4	5	2	D44823
31	4	17.4	5	2	synaptosomal-assoc
32	4	17.4	5	2	T-cell receptor be
33	4	17.4	5	2	T-cell receptor be
34	4	17.4	5	2	T-cell receptor be
35	4	17.4	5	2	27.5 kda structural
36	4	17.4	5	2	27.5K structural p
37	4	17.4	5	2	28.5K structural p
38	4	17.4	5	2	28K structural p
39	4	17.4	5	2	34.5K structural p
40	4	17.4	5	2	35K structural p
41	4	17.4	5	2	surface protein te
42	4	17.4	5	3	phytosulfokine alp
43	3	13.0	5	2	pap fibmbrial regul
44	3	13.0	5	2	ribosomal protein
45	3	13.0	5	2	ribosomal protein
46	3	13.0	5	2	ribosomal protein
47	3	13.0	5	2	dnazx-like protein
48	3	13.0	5	2	major protein anti
49	3	13.0	5	2	R-phycocerythrin ga
50	3	13.0	5	2	photosystem I 10.4
51	3	13.0	5	2	blood cell protein
52	2	8.7	5	2	glycogen phosphory
53	2	8.7	5	2	peptidyl-di-peptida
54	2	8.7	5	2	copper resistance
55	2	8.7	5	2	URF2 protein - Xan
56	2	8.7	5	2	primase - Citrobac
57	2	8.7	5	2	biotin B - Citrobac
58	2	8.7	5	2	20K protein - RICK
59	2	8.7	5	2	hypothetical prote
60	2	8.7	5	2	hypothetical prote
61	2	8.7	5	2	hypothetical prote
62	2	8.7	5	2	acid proteinase li
63	2	8.7	5	2	hypoxanthine phosph
64	2	8.7	5	2	myosin light chain
65	2	8.7	5	2	seminal plasma pro
66	2	8.7	5	2	synaptosomal-assoc
67	2	8.7	5	2	T-cell receptor be
68	2	8.7	5	2	T-cell receptor be
69	2	8.7	5	2	T-cell receptor be
70	2	8.7	5	2	T-cell receptor be
71	2	8.7	5	2	34.5K structural p
72	1	4.3	5	2	S11127
73	0	0.0	5	2	phosphoprotein, bo
74	0	0.0	5	2	spinal cord peptid
75	0	0.0	5	2	mitosis inhibiting
76	0	0.0	5	2	copper resistance
77	0	0.0	5	2	tram protein - Bsc
78	0	0.0	5	2	major protein anti
79	0	0.0	5	2	major protein anti
80	0	0.0	5	2	cadmium-binding pe
81	0	0.0	5	2	alpha-amylase - ri
82	0	0.0	5	2	hemoglobin, extrac
83	0	0.0	5	2	alcohol dehydrogen
84	0	0.0	5	2	Ig heavy chain CRD
85	0	0.0	5	2	Ig heavy chain CRD
86	0	0.0	5	2	Ig kappa chain V-I
87	0	0.0	5	2	T-cell receptor be
88	0	0.0	5	2	T-cell receptor be
89	0	0.0	5	2	T-cell receptor be
90	0	0.0	5	2	T-cell receptor be
91	0	0.0	5	2	T-cell receptor be
92	0	0.0	5	2	T-cell receptor be
93	0	0.0	5	2	T-cell receptor be
94	0	0.0	5	2	T-cell receptor be
95	0	0.0	5	2	T-cell receptor be
96	0	0.0	5	2	T-cell receptor be
97	0	0.0	5	2	T-cell receptor be
98	0	0.0	5	2	T-cell receptor be
99	0	0.0	5	2	T-cell receptor be
100	0	0.0	5	2	T-cell receptor be

## ALIGNMENTS

RESULT 1  
A32516  
cholecystokinin-5 - dog  
N/Alternate names: CCK-5  
C/Species: Canis lupus familiaris (dog)  
C/Date: 18-Oct-1989 #sequence\_revision 18-Oct-1989 #text\_change 18-Aug-2000  
C/Accession: A32516  
R/Shively, J.; Reeve Jr., J.R.; Eysselein, V.E.; Ben-Avram, C.; Vigna, S.R.; Walsh, J.H.  
Am. J. Physiol. 252, G272-G275, 1987  
A/Title: CCK-5: sequence analysis of a small cholecystokinin from canine brain and intestine  
A/Reference number: A32516; MUID:87153871; PMID:3826354  
A/Accession: A32516  
A/Molecule type: protein  
A/Residues: 1-5 <SH1>  
C/Comment: This peptide corresponds to the five carboxyl-terminal residues of cholecystokinin  
C/Superfamily: gastrin  
C/Keywords: amidated carboxyl end; neuropeptide  
F/5/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 47.8%; Score 11; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5  
DB 2 W 2

RESULT 2  
A60803  
neuropeptide - sea anemone (Anthopleura elegantissima)  
C/Species: Anthopleura elegantissima  
C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
C/Accession: A60803  
R/Graff, D.; Grimmelikhuijzen, C.J.P.  
Brain Res. 442, 354-358, 1988  
A/Title: Isolation of <Glu-Ser-Lu-Arg-Trp-NH-2, a novel neuropeptide from sea anemones.  
A/Reference number: A60803; MUID:88222764; PMID:2897223  
A/Accession: A60803  
A/Molecule type: protein  
A/Residues: 1-5 <GRA>  
C/Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid  
F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F/5/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 47.8%; Score 11; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5  
DB 5 W 5

RESULT 3  
JH0253  
gut pentapeptide - Japanese eel  
C/Species: Anguilla japonica (Japanese eel)  
C/Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 11-Apr-1995  
C/Accession: JH0253  
R/Uesaka, T.; Ikeda, T.; Kubota, I.; Muneoka, Y.; Ando, M.  
Biochem. Biophys. Res. Commun. 180, 828-832, 1991  
A/Title: Structure and function of a pentapeptide isolated from the gut of the eel.  
A/Reference number: JH0253; MUID:92062113; PMID:1953755  
A/Accession: JH0253  
A/Molecule type: protein  
A/Residues: 1-5 <UES>  
A/Experimental source: gut  
C/Comment: This peptide increased basal tone of the circular muscle of the esophagogastric  
, and of the circular muscle of the gastro-intestinal junction.

Query Match 47.8%; Score 11; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5  
DB 3 W 3

RESULT 4  
G37196  
bradykinin-potentiating peptide 7 - island jararaca  
C/Species: Bothrops insularis (island jararaca)  
C/Date: 14-Feb-1992 #sequence\_revision 01-Dec-1992 #text\_change 05-Aug-1994  
C/Accession: G37196  
R/Cintrà, A.C.O.; Vieira, C.A.; Giglio, J.R.  
J. Protein Chem. 9, 221-227, 1990  
A/Title: Primary structure and biological activity of bradykinin potentiating peptides  
A/Reference number: A37196; MUID:90351557; PMID:2386615  
A/Accession: G37196  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-5 <CIN>  
C/Keywords: pyroglutamic acid  
F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 47.8%; Score 11; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5  
DB 3 W 3

RESULT 5  
PT0281  
Ig heavy chain CRD3 region (clone 4-91C) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
C/Accession: PT0281  
R/Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991  
A/Title: Preferential utilization of specific immunoglobulin heavy chain diversity and  
A/Reference number: PT0222; MUID:91108337; PMID:1899102  
A/Accession: PT0281  
A/Molecule type: DNA  
A/Residues: 1-5 <YAM>  
A/Experimental source: B lymphocyte  
C/Keywords: heterotetramer; immunoglobulin

Query Match 47.8%; Score 11; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5  
DB 4 W 4

RESULT 6  
PT0308  
Ig heavy chain CRD3 region (clone 6-88) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
C/Accession: PT0308  
R/Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991  
A/Title: Preferential utilization of specific immunoglobulin heavy chain diversity and  
A/Reference number: PT0222; MUID:91108337; PMID:1899102  
A/Accession: PT0308  
A/Molecule type: DNA

A;Residues: 1-5 <YAM>  
A;Experimental source: B lymphocyte  
C;Keywords: heterotetramer; immunoglobulin

Query Match 47.8%; Score 11; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5  
DB 2 W 2

RESULT 7  
PT0729  
T-cell receptor beta chain V-D-J region (120-1J) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C;Accession: PT0640; PT0685; PT0729  
R;Feeney, A.J.

J;Exp. Med. 174, 115-124, 1991  
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A;Reference number: PT0509; MUID:91277601; PMID:1711558  
A;Accession: PT0640  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-5 <FE>  
A;Experimental source: newborn thymus, strain BALB/c, clone 120-1J  
A;Accession: PT0685  
A;Status: translation not shown  
A;Molecule type: DNA  
A;Residues: 1-5 <FE>  
A;Experimental source: day 18 fetal thymus, strain BALB/c, clone 154-1C  
A;Accession: PT0729  
A;Status: translation not shown  
A;Molecule type: DNA  
A;Residues: 1-5 <FE>  
A;Experimental source: newborn thymus, strain BALB/c, clone 135-1AG  
C;Keywords: T-cell receptor

Query Match 47.8%; Score 11; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5  
DB 5 W 5

RESULT 8  
PT0580  
T-cell receptor beta chain V-D-J region (159-2B) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C;Accession: PT0580  
R;Feeney, A.J.

J;Exp. Med. 174, 115-124, 1991  
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A;Reference number: PT0509; MUID:91277601; PMID:1711558  
A;Accession: PT0580  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-5 <FE>  
A;Experimental source: day 19 fetal thymus, strain BALB/c  
C;Keywords: T-cell receptor

Query Match 47.8%; Score 11; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5  
DB 4 W 4

# RESULT 9

PT0278  
IG heavy chain CRD3 region (clone 4-88) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
C;Accession: PT0278  
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
J;Exp. Med. 173, 395-407, 1991  
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and

A;Reference number: PT0222; MUID:91108337; PMID:1899102  
A;Accession: PT0278  
A;Molecule type: DNA  
A;Residues: 1-5 <YAM>  
A;Experimental source: B lymphocyte  
C;Keywords: heterotetramer; immunoglobulin

Query Match 34.8%; Score 8; DB 2; Length 5;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXL 4  
DB 2 FGVL 5

# RESULT 10

A44955  
alkanal monooxygenase (FMN-linked) (EC 1.14.14.3) alpha chain - Vibrio harveyi (fragment)  
C;Species: Vibrio harveyi  
C;Date: 03-Jun-1993 #sequence\_revision 03-Jun-1993 #text\_change 26-May-2000  
C;Accession: A44955  
R;Paquette, O.; Tu, S.C.  
Photochem. Photobiol. 50, 817-825, 1989  
A;Title: Chemical modification and characterization of the alpha cysteine 106 at the Vib

A;Reference number: A44955; MUID:90175700; PMID:2626493  
A;Accession: A44955  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-5 <PAQ>  
C;Keywords: FMN; luminescence; monooxygenase; oxidoreductase

Query Match 26.1%; Score 6; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
DB 1 F 1

# RESULT 11

S70615  
endo-1,4-beta-xylanase (EC 3.2.1.8) - Streptomyces sp. (Chainia sp. NCL 82.5.1) (fragment)  
N;Alternate names: xylanase  
C;Species: Streptomyces sp.  
A;Variety: Chainia sp. NCL 82.5.1  
C;Date: 19-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 07-May-1999  
C;Accession: S70615  
R;Rao, M.; Khadilkar, S.; Bandivadekar, K.R.; Deshpande, V.  
Biochem. J. 316, 771-775, 1996  
A;Title: Structural environment of an essential cysteine residue of xylanase from Chainia

A;Reference number: S70615; MUID:96265041; PMID:8670151  
A;Accession: S70615  
A;Molecule type: protein  
A;Residues: 1-5 <RAO>  
A;Experimental source: Chainia sp. strain NCL 82.5.1  
A;Note: the source is designated as Chainia sp.  
C;Function:

A;Description: endohydrolyzation of beta-1,4-xylosidic linkages in xylans  
A;Pathway: fermentation of hemicellulose into ethanol  
C;Keywords: glycosidase; hydrolase

Query Match 26.1%; Score 6; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 F 1  
 Db 3 F 3

RESULT 12  
 PQ0009  
 angiotensin-converting enzyme inhibitor (FLP-2) - common fig  
 N;Alternate names: ficus latex peptide 2  
 C;Species: Ficus carica (common fig)  
 C;Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 08-Dec-1995  
 C;Accession: PQ0009  
 R;Maruyama, S.; Miyoshi, S.; Tanaka, H.  
 Agric. Biol. Chem. 53, 2763-2767, 1989  
 A;Title: Angiotensin I-converting enzyme inhibitors derived from Ficus carica.  
 A;Reference number: PQ0008  
 A;Accession: PQ0009  
 A;Molecule type: protein  
 A;Residues: 1-5 <MAR>  
 A;Experimental source: latex  
 C;Keywords: angiotensin-converting enzyme inhibitor

Query Match 26.1%; Score 6; DB 2; Length 5;  
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5  
 Db 1 LY 2

RESULT 13  
 PS0324  
 ribulose-bisphosphate carboxylase activase III - rice (strain Nihonbare) (fragment)  
 C;Species: Oryza sativa (rice)  
 C;Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 02-Jul-1998  
 C;Accession: PS0324  
 R;Tsugita, A.  
 submitted to JIPID, April 1993  
 A;Reference number: PS0206  
 A;Accession: PS0324  
 A;Molecule type: protein  
 A;Residues: 1-5 <TSU>  
 A;Experimental source: leaf, chlorophyll

Query Match 26.1%; Score 6; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 F 1  
 Db 1 F 1

RESULT 14  
 B45525  
 actin I - malaria parasite (Plasmodium falciparum) (fragments)  
 C;Species: Plasmodium falciparum  
 C;Date: 03-Jun-1993 #sequence\_revision 28-Oct-1994 #text\_change 09-Jun-2000  
 C;Accession: B45525  
 R;Wesseling, J.G.; Snijders, P.J.F.; van Someren, P.; Jansen, J.; Smits, M.A.; Schoenmak  
 Mol. Biochem. Parasitol. 35, 167-176, 1989  
 A;Title: Stage-specific expression and genomic organization of the actin genes of the ma  
 A;Reference number: A45525; MUID:89364996; PMID:2671721  
 A;Accession: B45525  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-5 <WES>

A;Cross-references: GB:J03988  
 A;Note: the authors translated the codon GAA for residue 3 as Gly  
 C;Comment: The actin I gene contains no introns.

Query Match 26.1%; Score 6; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 F 1  
 Db 5 F 5

RESULT 15  
 A44692  
 fulicin - giant African snail  
 C;Species: Achatina fulica (giant African snail)  
 C;Date: 23-Mar-1995 #sequence\_revision 05-Apr-1995 #text\_change 11-Jul-1997  
 C;Accession: A44692  
 R;Ohta, N.; Kubota, I.; Takao, T.; Shimonishi, Y.; Yasuda-Kamatani, Y.; Minakata, H.; No  
 Biochem. Biophys. Res. Commun. 178, 486-493, 1991  
 A;Title: Fulicin, a novel neuropeptide containing a D-amino acid residue isolated from t  
 A;Reference number: A44692; MUID:91315471; PMID:1859408  
 A;Accession: A44692  
 A;Molecule type: protein  
 A;Residues: 1-5 <OHT>  
 C;Keywords: amidated carboxyl end; D-amino acid; neuropeptide  
 F;2/Modified site: D-asparagine (Asn) #status experimental  
 F;5/Modified site: amidated carboxyl end (Val) #status experimental

Query Match 26.1%; Score 6; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 F 1  
 Db 1 F 1

RESULT 16  
 B61445  
 Leu-enkephalin - blue mussel  
 C;Species: Mytilus edulis (blue mussel)  
 C;Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 21-Jan-2000  
 C;Accession: B61445  
 R;Leung, M.K.; Stefano, G.B.  
 Proc. Natl. Acad. Sci. U.S.A. 81, 955-958, 1984  
 A;Title: Isolation and identification of enkephalins in pedal ganglia of Mytilus edulis  
 A;Reference number: A61445; MUID:84144823; PMID:6583690  
 A;Accession: B61445  
 A;Molecule type: protein  
 A;Residues: 1-5 <LEU>  
 A;Experimental source: pedal ganglia  
 C;Keywords: neuropeptide; opioid peptide

Query Match 26.1%; Score 6; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 F 1  
 Db 4 F 4

RESULT 17  
 A61445  
 Met-enkephalin - blue mussel  
 C;Species: Mytilus edulis (blue mussel)  
 C;Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 21-Jan-2000  
 C;Accession: A61445  
 R;Leung, M.K.; Stefano, G.B.  
 Proc. Natl. Acad. Sci. U.S.A. 81, 955-958, 1984  
 A;Title: Isolation and identification of enkephalins in pedal ganglia of Mytilus edulis

A;Reference number: A61445; MUID:84144823; PMID:6593690  
 A;Accession: A61445  
 A;Molecule type: protein  
 A;Residues: 1-5 <LEU>  
 A;Experimental source: pedal ganglia  
 C;Keywords: neuropeptide; opioid peptide

Query Match 26.1%; Score 6; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
 Db 4 F 4

## RESULT 18

JS0319  
 subesophageal ganglion pentapeptide - house cricket  
 C;Species: Acheta domesticus (house cricket)  
 C;Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 20-Jun-2000  
 C;Accession: JS0319  
 R;Wicker, C.; Wicker, C.  
 Comp. Biochem. Physiol. C 88, 185-187, 1987  
 A;Title: Isolation and structure of a peptide isolated from the subesophageal ganglion  
 A;Reference number: JS0319  
 A;Accession: JS0319  
 A;Molecule type: protein  
 A;Residues: 1-5 <NIC>

Query Match 26.1%; Score 6; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
 Db 5 F 5

## RESULT 19

B61168  
 cocoanase (EC 3.4.21.-) - Chinese oak silkmoth (fragment)  
 C;Species: Antherea pernyi (Chinese oak silkmoth)  
 C;Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 07-May-1999  
 C;Accession: B61168  
 R;Kramer, K.J.; Felsted, R.L.; Law, J.H.  
 J. Biol. Chem. 248, 3021-3028, 1973  
 A;Title: Cocoanase. V. Structural studies on an insect serine protease.  
 A;Reference number: A61168; MUID:73166540; PMID:4735570  
 A;Accession: B61168  
 A;Molecule type: protein  
 A;Residues: 1-5 <KRA>  
 C;Keywords: hydrolase; serine proteinase; zymogen  
 F;1-5/Product: cocoanase (fragment) #status experimental <MAT>

Query Match 26.1%; Score 6; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
 Db 5 F 5

## RESULT 20

PT0644  
 T-cell receptor beta chain V-D-J region (111-1G) - mouse (fragment)  
 C;Species: Mus musculus (house mouse)  
 C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
 C;Accession: PT0644  
 R;Peeney, A.J.  
 J. Exp. Med. 174, 115-124, 1991  
 A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A;Reference number: PT0509; MUID:91277601; PMID:1711558  
 A;Accession: PT0644  
 A;Status: translation not shown  
 A;Molecule type: mRNA  
 A;Residues: 1-5 <FE>  
 A;Experimental source: newborn thymus, strain BALB/c  
 C;Keywords: T-cell receptor

Query Match 26.1%; Score 6; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
 Db 4 F 4

## RESULT 21

A58728  
 serrawettin W2 - Serratia marcescens  
 C;Species: Serratia marcescens  
 C;Date: 10-Feb-1998 #sequence\_revision 12-Feb-1998 #text\_change 12-Feb-1998  
 C;Accession: A58728  
 R;Matsuyama, I.; Kaneda, K.; Nakagawa, Y.; Isa, K.; Hara-Hotta, H.; Yano, I.  
 J. Bacteriol. 174, 1769-1776, 1992  
 A;Title: A novel extracellular cyclic lipopeptide which promotes flagellum-dependent and  
 A;Reference number: A58728; MUID:92193260; PMID:1548227  
 A;Accession: A58728  
 A;Status: unencoded polypeptide  
 A;Molecule type: protein  
 A;Residues: 1-5 <MAT>  
 A;Experimental source: strain NS 25  
 C;Comment: A surfactant lipopeptide promoting flagellum-independent surface translocation  
 C;Keywords: blocked amino end; blocked carboxyl end; D-amino acid; lipoprotein; unencoded  
 F;1/Modified site: D-leucine (Leu) #status experimental  
 F;4/Modified site: D-phenylalanine (Phe) #status experimental  
 F;1-5/Cross-link: 3-hydroxydecanoyl amino end, ester carboxyl end (Leu-Ile) #status experimental

Query Match 26.1%; Score 6; DB 4; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
 Db 4 F 4

## RESULT 22

H0ROHA  
 proctolin - American cockroach  
 C;Species: Periplaneta americana (American cockroach)  
 C;Date: 29-Jul-1981 #sequence\_revision 29-Jul-1981 #text\_change 23-Aug-1996  
 C;Accession: A01644  
 R;Starratt, A.N.; Brown, B.E.  
 Life Sci. 17, 1253-1256, 1975  
 A;Title: Structure of the pentapeptide proctolin, a proposed neurotransmitter in insects  
 A;Reference number: A93048; MUID:76074708; PMID:576  
 A;Accession: A01644  
 A;Molecule type: protein  
 A;Residues: 1-5 <STA>  
 A;Note: the synthetic peptide had the same chromatographic, electrophoretic, and pharmacological  
 R;O'Shea, M.; Adams, M.E.  
 Science 213, 567-569, 1981  
 A;Title: Pentapeptide (proctolin) associated with an identified neuron.  
 A;Reference number: A94260; MUID:81225865; PMID:6113690  
 A;Contents: annotation; biological source  
 C;Comment: This peptide is found in the lateral white neurons, which occur (in the cockroach) innervate the striated hindgut muscles in insects and stimulate contraction of these muscles  
 C;Superfamily: proctolin  
 C;Keywords: neuropeptide

Query Match 17.4%; Score 4; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 L 4  
|  
Db 3 L 3

RESULT 23  
JN0860  
peptidyl-dipeptidase A inhibitory peptide C107 - striped bonito  
C;Species: Sarda orientalis (striped bonito)  
C;Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 07-May-1999  
C;Accession: JN0860  
R;Watanabe, N.; Fujii, M.; Takeda, Y.; Shimizu, T.  
Biochem. Biotechnol. Biochem. 57, 1743-1744, 1993  
A;Title: Isolation and characterization of angiotensin I-converting enzyme inhibitory peptide  
A;Reference number: JN0859; MUID:94080036; PMID:7764272  
A;Accession: JN0860  
A;Molecule type: protein  
A;Residues: 1-5 <MAT>  
A;Experimental source: intestine  
A;Comment: The carboxyl-terminus is essential for the protein's expression of angiotensin  
C;Superfamily: bradykinin-potentiating peptide  
C;Keywords: angiotensin-converting enzyme inhibitor

Query Match 17.4%; Score 4; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 L 4  
|  
Db 2 L 2

RESULT 24  
C41225  
copper resistance protein - Pseudomonas syringae pv. tomato (fragment)  
C;Species: Pseudomonas syringae pv. tomato  
C;Date: 19-Jun-1992 #sequence\_revision 19-Jun-1992 #text\_change 24-Jun-1993  
C;Accession: C41225  
R;Chen, J.S.; Cooksey, D.A.  
Proc. Natl. Acad. Sci. U.S.A. 88, 8915-8919, 1991  
A;Title: Copper resistance in Pseudomonas syringae mediated by periplasmic and outer membrane  
A;Reference number: A41225; MUID:92020961; PMID:1924351  
A;Accession: C41225  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-5 <CHA>

Query Match 17.4%; Score 4; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 L 4  
|  
Db 4 L 4

RESULT 25  
E42364  
flagellar protein fljR - Salmonella typhimurium (fragment)  
C;Species: Salmonella typhimurium  
C;Date: 24-Jul-1992 #sequence\_revision 24-Jul-1992 #text\_change 30-Sep-1993  
C;Accession: E42364  
R;Vogler, A.P.; Homma, M.; Irikura, V.M.; Macnab, R.M.  
J. Bacteriol. 173, 3564-3572, 1991  
A;Title: Salmonella typhimurium mutants defective in flagellar filament regrowth and secretion  
A;Reference number: A42364; MUID:91258342; PMID:1646201  
A;Accession: E42364  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-5 <VOG>  
A;Cross-references: GB:M62408

Query Match 17.4%; Score 4; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 L 4  
|  
Db 4 L 4

RESULT 26  
B22565  
R-phycoerythrin alpha-2 chain - red alga (Gastrocloonium coulteri) (fragment)  
C;Species: Gastrocloonium coulteri  
C;Date: 07-Mar-1988 #sequence\_revision 07-Mar-1988 #text\_change 23-Mar-1993  
C;Accession: B22565  
R;Klotz, A.V.; Glazer, A.N.  
J. Biol. Chem. 260, 4856-4863, 1985  
A;Title: Characterization of the bilin attachment sites in R-phycoerythrin.  
A;Reference number: A22565; MUID:85182601; PMID:3886644  
A;Accession: B22565  
A;Molecule type: protein  
A;Residues: 1-5 <KLO>

Query Match 17.4%; Score 4; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 L 4  
|  
Db 1 L 1

RESULT 27  
S55237  
zinc-binding protein ZBP14 - maize (fragment)  
C;Species: Zea mays (maize)  
C;Date: 27-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 07-May-1999  
C;Accession: S55237  
R;Robinson, K.; Jones, D.; Howell, S.; Soneji, Y.; Martin, S.; Aitken, A.  
Biochem. J. 307, 267-272, 1995  
A;Title: Expression and characterization of maize ZBP14, a member of a new family of zinc  
A;Reference number: S55237; MUID:95234046; PMID:7717986  
A;Accession: S55237  
A;Molecule type: protein  
A;Residues: 1-5 <ROB>

Query Match 17.4%; Score 4; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 L 4  
|  
Db 1 L 1

RESULT 28  
A60411  
proctolin - Atlantic horseshoe crab  
C;Species: Limulus polyphemus (Atlantic horseshoe crab)  
C;Date: 03-Feb-1993 #sequence\_revision 03-Feb-1993 #text\_change 17-Mar-1999  
C;Accession: A60411  
R;Groome, J.R.; Tillinghast, E.K.; Townley, M.A.; Vetrovs, A.; Watson III, W.H.; Hunt, D.  
Peptides 11, 205-211, 1990  
A;Title: Identification of proctolin in the central nervous system of the horseshoe crab  
A;Reference number: A60411; MUID:90287800; PMID:2356151  
A;Accession: A60411  
A;Molecule type: protein  
A;Residues: 1-5 <GRO>  
A;Comment: This neuropeptide stimulates cardiac output and hindgut motility in the horse  
C;Keywords: neuropeptide

Query Match 17.4%; Score 4; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 L 4  
|  
Db 3 L 3

## RESULT 29

S53595

hypothetical protein (upstream of transcription factor, CCAAT-binding) - chicken

C:Species: Gallus gallus (chicken)

C:Date: 15-Jul-1995 #sequence\_revision 01-Sep-1995 #text\_change 07-May-1999

C:Accession: S53595

R:Calhoun, C.F.; Bouwman, P.R.J.; Snippe, L.; Ab, G.

Nucleic Acids Res. 22, 5540-5547, 1994

A:Title: Translation start site multiplicity of the CCAAT/enhancer binding protein alpha

A:Reference number: S53595; MUID:95140613; PMID:7838705

A:Accession: S53595

A&gt;Status: preliminary

A:Molecule type: DNA

A:Residues: 1-5 &lt;CAL&gt;

A:Cross-references: EMBL:X66844

## Query Match

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 L 4  
|  
Db 5 L 5

## RESULT 30

D44823

synaptosomal-associated protein SNAP-25 peptide 2 - rabbit (fragment)

N:Alternate names: superprotein peptide 2

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 31-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 15-Jun-1996

C:Accession: D44823

R:Loewy, A.; Liu, W.S.; Baittinger, C.; Willard, M.B.

J. Neurosci. 11, 3412-3421, 1991

A:Title: The major 35S-methionine-labeled rapidly transported protein (superprotein) is

A:Reference number: A44823; MUID:92044785; PMID:1941090

A:Accession: D44823

A&gt;Status: preliminary

A:Molecule type: protein

A:Residues: 1-5 &lt;LOE&gt;

A:Experimental source: visual tissue

A&gt;Note: sequence extracted from NCBI backbone (NCBIP:64250)

C:Keywords: membrane trafficking

## Query Match

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 L 4  
|  
Db 2 L 2

## RESULT 31

PT0624

T-cell receptor beta chain V-D-J region (120-1K) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997

C:Accession: PT0624

R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A:Reference number: PT0509; MUID:91277601; PMID:1711558

A:Accession: PT0624

A&gt;Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-5 &lt;FEE&gt;

A:Experimental source: newborn thymus, strain BALB/c

C:Keywords: T-cell receptor

## Query Match

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 L 4  
|  
Db 4 L 4

## RESULT 32

PT0625

T-cell receptor beta chain V-D-J region (120-2S) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997

C:Accession: PT0625

R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A:Reference number: PT0509; MUID:91277601; PMID:1711558

A:Accession: PT0625

A&gt;Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-5 &lt;FEE&gt;

A:Experimental source: newborn thymus, strain BALB/c

C:Keywords: T-cell receptor

## Query Match

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 L 4  
|  
Db 4 L 4

## RESULT 33

PT0713

T-cell receptor beta chain V-D-J region (165-3C) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997

C:Accession: PT0713

R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A:Reference number: PT0509; MUID:91277601; PMID:1711558

A:Accession: PT0713

A&gt;Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-5 &lt;FEE&gt;

A:Experimental source: newborn thymus, strain BALB/c

C:Keywords: T-cell receptor

## Query Match

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 L 4  
|  
Db 4 L 4

## RESULT 34

G44817

27.5 kDa structural protein - Leuconostoc oenos phase P32 (fragment)

C:Species: Leuconostoc oenos phase P32

C:Date: 31-Mar-1993 #sequence\_revision 22-May-1998 #text\_change 22-May-1998

C:Accession: G44817

R:Arendt, E.K.; Lonvaud, A.; Hammes, W.P.

J. Gen. Microbiol. 137, 2135-2139, 1991  
 A;Title: Lysogeny in Leuconostoc oenos.  
 A;Reference number: A44817; MUID:92085033; PMID:1748868  
 A;Accession: G44817  
 A;Molecule type: protein  
 A;Residues: 1-5 <ARE>  
 A;Note: sequence extracted from NCBI backbone (NCBIP:70333)

Query Match 17.4%; Score 4; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 L 4  
 |  
 Db 5 L 5

## RESULT 35

I44817  
 27.5K structural protein - Leuconostoc oenos phase P37 (fragment)

C;Species: Leuconostoc oenos phase P37  
 C;Date: 31-Mar-1993 #sequence\_revision 22-May-1998 #text\_change 22-May-1998  
 C;Accession: I44817

R;Arendt, E.K.; Lonvaud, A.; Hammes, W.P.

J. Gen. Microbiol. 137, 2135-2139, 1991

A;Title: Lysogeny in Leuconostoc oenos.

A;Reference number: A44817; MUID:92085033; PMID:1748868

A;Accession: I44817

A;Molecule type: protein

A;Residues: 1-5 <ARE>

A;Note: sequence extracted from NCBI backbone (NCBIP:70330)

Query Match 17.4%; Score 4; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 L 4  
 |  
 Db 5 L 5

## RESULT 36

E44817  
 27.5K structural protein - Leuconostoc oenos phase P54 (fragment)

C;Species: Leuconostoc oenos phase P54  
 C;Date: 31-Mar-1993 #sequence\_revision 22-May-1998 #text\_change 22-May-1998  
 C;Accession: E44817

R;Arendt, E.K.; Lonvaud, A.; Hammes, W.P.

J. Gen. Microbiol. 137, 2135-2139, 1991

A;Title: Lysogeny in Leuconostoc oenos.

A;Reference number: A44817; MUID:92085033; PMID:1748868

A;Accession: E44817

A;Molecule type: protein

A;Residues: 1-5 <ARE>

A;Note: sequence extracted from NCBI backbone (NCBIP:70336)

Query Match 17.4%; Score 4; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 L 4  
 |  
 Db 5 L 5

## RESULT 37

C44817  
 28.5K structural protein - Leuconostoc oenos phase Pat5-12 (fragment)

C;Species: Leuconostoc oenos phase Pat5-12  
 C;Date: 31-Mar-1993 #sequence\_revision 22-May-1998 #text\_change 22-May-1998  
 C;Accession: C44817

R;Arendt, E.K.; Lonvaud, A.; Hammes, W.P.

J. Gen. Microbiol. 137, 2135-2139, 1991

A;Title: Lysogeny in Leuconostoc oenos.  
 A;Reference number: A44817; MUID:92085033; PMID:1748868  
 A;Accession: C44817  
 A;Molecule type: protein  
 A;Residues: 1-5 <ARE>  
 A;Note: sequence extracted from NCBI backbone (NCBIP:70341)

Query Match 17.4%; Score 4; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 L 4  
 |  
 Db 5 L 5

## RESULT 38

A44817

28K structural protein - Leuconostoc oenos phase PZtl1-15 (fragment)

C;Species: Leuconostoc oenos phase PZtl1-15

C;Date: 31-Mar-1993 #sequence\_revision 22-May-1998 #text\_change 22-May-1998  
 C;Accession: A44817

R;Arendt, E.K.; Lonvaud, A.; Hammes, W.P.

J. Gen. Microbiol. 137, 2135-2139, 1991

A;Title: Lysogeny in Leuconostoc oenos.

A;Reference number: A44817; MUID:92085033; PMID:1748868

A;Accession: A44817

A;Molecule type: protein

A;Residues: 1-5 <ARE>

A;Note: sequence extracted from NCBI backbone (NCBIP:70343)

Query Match 17.4%; Score 4; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 L 4  
 |  
 Db 5 L 5

## RESULT 39

B44817

34.5K structural protein - Leuconostoc oenos phase PZtl1-15 (fragment)

C;Species: Leuconostoc oenos phase PZtl1-15

C;Date: 31-Mar-1993 #sequence\_revision 22-May-1998 #text\_change 22-May-1998  
 C;Accession: B44817

R;Arendt, E.K.; Lonvaud, A.; Hammes, W.P.

J. Gen. Microbiol. 137, 2135-2139, 1991

A;Title: Lysogeny in Leuconostoc oenos.

A;Reference number: A44817; MUID:92085033; PMID:1748868

A;Accession: B44817

A;Molecule type: protein

A;Residues: 1-5 <ARE>

A;Note: sequence extracted from NCBI backbone (NCBIP:70342)

Query Match 17.4%; Score 4; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 L 4  
 |  
 Db 1 L 1

## RESULT 40

D44817

35K structural protein - Leuconostoc oenos phase Pat5-12 (fragment)

C;Species: Leuconostoc oenos phase Pat5-12

C;Date: 31-Mar-1993 #sequence\_revision 22-May-1998 #text\_change 22-May-1998  
 C;Accession: D44817

R;Arendt, E.K.; Lonvaud, A.; Hammes, W.P.

J. Gen. Microbiol. 137, 2135-2139, 1991

A;Title: Lysogeny in Leuconostoc oenos.



A;Reference number: A44817; MUID:92085033; PMID:1748868  
 A;Accession: D44817  
 A;Molecule type: protein  
 A;Residues: 1-5 <ARE>  
 A;Note: sequence extracted from NCBI backbone (NCBIP:70340)

Query Match 17.4%; Score 4; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 L 4  
 |  
 Db 1 L 1

## RESULT 41

S69237  
 surface protein tetraabrachion heavy chain - Staphylothermus marinus (fragment)  
 C;Species: Staphylothermus marinus

C;Date: 04-Dec-1997 #sequence\_revision 04-Dec-1997 #text\_change 17-Mar-1999  
 C;Accession: S69237

R;Peters, J.; Nitsch, M.; Kuehlmoegen, B.; Golbik, R.; Lupas, A.; Kellermann, J.; Engelh  
 J. Mol. Biol. 245, 385-401, 1995

A;Title: Tetraabrachion: a filamentous archaeobacterial surface protein assembly of unusua  
 A;Reference number: S69237; MUID:95139068; PMID:7837271

A;Accession: S69237

A;Molecule type: protein

A;Residues: 1-5 <PET>

A;Experimental source: strain F1, DSM 3639

C;Keywords: cell wall; glycoprotein; heat-stable protein

Query Match 17.4%; Score 4; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 L 4  
 |  
 Db 3 L 3

## RESULT 42

JT0870

phytoulfokine alpha - garden asparagus (fragment)

C;Species: Asparagus officinalis (garden asparagus)

C;Date: 02-Apr-2002 #sequence\_revision 02-Apr-2002 #text\_change 19-Apr-2002

C;Accession: JT0870

R;Matsumabayashi, Y.; Sakagami, Y.

Proc. Natl. Acad. Sci. U.S.A. 93, 7623-7627, 1996

A;Title: Phytoulfokine, sulfated peptides that induce the proliferation of single mesoph

A;Reference number: JT0870

A;Accession: JT0870

A;Molecule type: protein

A;Residues: 1-5 <NAT>

Query Match 17.4%; Score 4; DB 3; Length 5;  
 Best Local Similarity 0.0%; Pred. No. 2.8e+05;  
 Matches 0; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5  
 |  
 Db 2 IV 3

## RESULT 43

B37325

pap fibrillar regulatory protein papI - Escherichia coli (fragment)

C;Species: Escherichia coli

C;Date: 11-Sep-1992 #sequence\_revision 11-Sep-1992 #text\_change 23-Mar-1993

C;Accession: B37325

R;Braaten, B.A.; Blyn, L.B.; Skinner, B.S.; Low, D.A.

J. Bacteriol. 173, 1789-1800, 1991

A;Title: Evidence for a methylation-blocking factor (mbf) locus involved in pap pilus ex

A;Reference number: A37325; MUID:91154136; PMID:1671857

A;Accession: B37325

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-5 <BRA>

A;Cross-references: GB:M63747

Query Match 13.0%; Score 3; DB 2; Length 5;  
 Best Local Similarity 0.0%; Pred. No. 2.8e+05;  
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
 |  
 Db 4 Y 4

## RESULT 44

I39964

ribosomal protein S4 - Bacillus circulans (fragment)

C;Species: Bacillus circulans

C;Date: 19-Jul-1996 #sequence\_revision 19-Jul-1996 #text\_change 19-Jul-1996

C;Accession: I39964

R;Grundy, F.J.; Henkin, T.M.

J. Bacteriol. 174, 6763-6770, 1992

A;Title: Characterization of the Bacillus subtilis rpsD regulatory target site.

A;Reference number: I39963; MUID:93015735; PMID:1400226

A;Accession: I39964

A;Status: preliminary; translated from GB/EMBL/DBDJ

A;Molecule type: DNA

A;Residues: 1-5 <RES>

A;Cross-references: GB:M99041; NID:g143471

C;Genetics:

A;Gene: rpsD

Query Match 13.0%; Score 3; DB 2; Length 5;  
 Best Local Similarity 0.0%; Pred. No. 2.8e+05;  
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
 |  
 Db 4 Y 4

## RESULT 45

I39966

ribosomal protein S4 - Bacillus licheniformis (fragment)

C;Species: Bacillus licheniformis

C;Date: 19-Jul-1996 #sequence\_revision 19-Jul-1996 #text\_change 19-Jul-1996

C;Accession: I39966

R;Grundy, F.J.; Henkin, T.M.

J. Bacteriol. 174, 6763-6770, 1992

A;Title: Characterization of the Bacillus subtilis rpsD regulatory target site.

A;Reference number: I39963; MUID:93015735; PMID:1400226

A;Accession: I39966

A;Status: preliminary; translated from GB/EMBL/DBDJ

A;Molecule type: DNA

A;Residues: 1-5 <RES>

A;Cross-references: GB:M99043; NID:g143475

C;Genetics:

A;Gene: rpsD

Query Match 13.0%; Score 3; DB 2; Length 5;  
 Best Local Similarity 0.0%; Pred. No. 2.8e+05;  
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
 |  
 Db 4 Y 4

## RESULT 46

I39965

ribosomal protein S4 - Bacillus megaterium (fragment)

C;Species: Bacillus megaterium

C;Date: 19-Jul-1996 #sequence\_revision 19-Jul-1996 #text\_change 19-Jul-1996

C;Accession: I39965

J;Brundy, F.J.; Henkin, T.M.

J;Bacteriol. 174, 6763-6770, 1992

A;Title: Characterization of the *Bacillus subtilis* rpsD regulatory target site.

A;Reference number: I39963; MUID:93015735; PMID:1400226

A;Accession: I39965

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-5 <RES>

A;Cross-references: GB:M99042; NID:g143473

C;Genetics:

A;Gene: rpsD

Query Match 13.0%; Score 3; DB 2; Length 5;  
Best Local Similarity 0.0%; Pred. No. 2.8e+05;  
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 F 1  
: :  
Db 4 Y 4

RESULT 47

I40469

dnazX-like protein - *Bacillus subtilis* (fragment)

C;Species: *Bacillus subtilis*

C;Date: 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text\_change 21-Jul-2000

C;Accession: I40469

R;Struck, J.C.; Hartmann, R.K.; Toschka, H.Y.; Erdmann, V.A.

Mol. Gen. Genet. 215, 478-482, 1989

A;Title: Transcription and processing of *Bacillus subtilis* small cytoplasmic RNA.

A;Reference number: I40469; MUID:89218958; PMID:2468993

A;Accession: I40469

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-5 <RES>

A;Cross-references: EMBL:X14796; NID:g40130; PIDN:CAA32902.1; PID:g4376204

C;Genetics:

A;Start codon: GTG

Query Match 13.0%; Score 3; DB 2; Length 5;  
Best Local Similarity 0.0%; Pred. No. 2.8e+05;  
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 F 1  
: :  
Db 3 Y 3

RESULT 48

E60274

major protein antigen MPT63 - *Mycobacterium tuberculosis* (fragment)

C;Species: *Mycobacterium tuberculosis*

C;Date: 11-Dec-1992 #sequence\_revision 11-Dec-1992 #text\_change 30-Sep-1993

C;Accession: E60274

R;Negai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.

Infect. Immun. 59, 372-382, 1991

A;Title: Isolation and partial characterization of major protein antigens in the culture

A;Reference number: A60274; MUID:9109989; PMID:1898899

A;Accession: E60274

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-5 <NAG>

Query Match 13.0%; Score 3; DB 2; Length 5;  
Best Local Similarity 0.0%; Pred. No. 2.8e+05;  
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 F 1  
: :  
Db 2 Y 2

RESULT 49

F22565

R-phycoerythrin gamma-A chain - red alga (*Gastrocionium coulteri*) (fragment)

C;Species: *Gastrocionium coulteri*

C;Date: 07-Mar-1988 #sequence\_revision 07-Mar-1988 #text\_change 23-Mar-1993

C;Accession: F22565

J;Klotz, A.V.; Glazer, A.N.

J. Biol. Chem. 260, 4856-4863, 1985

A;Title: Characterization of the bilin attachment sites in R-phycoerythrin.

A;Reference number: A22565; MUID:85182601; PMID:3886644

A;Accession: F22565

A;Molecule type: protein

A;Residues: 1-5 <KLO>

Query Match 13.0%; Score 3; DB 2; Length 5;  
Best Local Similarity 0.0%; Pred. No. 2.8e+05;  
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 F 1  
: :  
Db 4 Y 4

RESULT 50

PQ0689

Photosystem I 10.4K H1 chain - common tobacco (fragment)

C;Species: *Nicotiana tabacum* (common tobacco)

C;Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 17-Mar-1999

C;Accession: PQ0689

R;Obokata, J.; Mikami, K.; Hayashida, N.; Nakamura, M.; Sugiyama, M.

Plant Physiol. 102, 1259-1267, 1993

A;Title: Molecular heterogeneity of photosystem I. psaD, psaE, psaF, psaH and psaL are a

A;Reference number: PQ0667; MUID:94105345; PMID:8278548

A;Accession: PQ0689

A;Molecule type: protein

A;Residues: 1-5 <OBO>

C;Keywords: chloroplast; photosynthesis; photosystem I; thylakoid

Query Match 13.0%; Score 3; DB 2; Length 5;  
Best Local Similarity 0.0%; Pred. No. 2.8e+05;  
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 F 1  
: :  
Db 2 Y 2

RESULT 51

S68326

blood cell protein B - *Ascidia ceratodes* (fragment)

N;Alternate names: Abcp-B

C;Species: *Ascidia ceratodes*

C;Date: 19-Mar-1997 #sequence\_revision 29-Aug-1997 #text\_change 11-Jun-1999

C;Accession: S68326

R;Taylor, S.W.; Ross, M.M.; Waite, J.H.

Arch. Biochem. Biophys. 324, 228-240, 1995

A;Title: Novel 3,4-di- and 3,4,5-trihydroxyphenylalanine-containing polypeptides from th

A;Reference number: S68325; MUID:96132650; PMID:8554314

A;Accession: S68326

A;Molecule type: protein

A;Residues: 1-5 <TAY>

F;2/Modified site: 3',4',5'-trihydroxyphenylalanine (Tyr) #status experimental

F;4/Modified site: 3',4'-dihydroxyphenylalanine (Tyr) #status experimental

Query Match 13.0%; Score 3; DB 2; Length 5;  
Best Local Similarity 0.0%; Pred. No. 2.8e+05;  
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 F 1  
: :  
Db 2 Y 2

## RESULT 52

A60521  
glycogen phosphorylase (EC 2.4.1.1), muscle - mullet (Liza ramada) (fragment)  
N:Alternate names: glycogen phosphorylase b  
C:Species: Liza ramada  
C:Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 11-May-2000  
C:Accession: A60521  
R:Bonamusa, L.; Baanante, I.V.  
Comp. Biochem. Physiol. B 95, 295-301, 1990  
A:Title: Purification and characterization of glycogen phosphorylase B from skeletal muscle  
A:Reference number: A60521; MUID:90227907; PMID:2103669  
A:Accession: A60521  
A:Molecule type: protein  
A:Residues: 1-5 <BON>  
C:Superfamily: phosphorylase  
C:Keywords: glycyltransferase; hexosyltransferase; phosphoprotein  
F:3/Binding site: phosphate (Ser) (covalent) (by phosphorylase b kinase) #status experiment

Query Match 8.7%; Score 2; DB 2; Length 5;  
Best Local Similarity 0.0%; Pred.No. 2.8e+05;  
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 L 4  
;  
DB 2 I 2

## RESULT 53

JN0862  
peptidyl-dipeptidase A inhibitory peptide C112 - striped bonito  
C:Species: Sarda orientalis (striped bonito)  
C:Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 07-May-1999  
C:Accession: JN0862  
R:Matsumura, N.; Fujii, M.; Takeda, Y.; Shimizu, T.  
Biosci. Biotechnol. Biochem. 57, 1743-1744, 1993  
A:Title: Isolation and characterization of angiotensin I-converting enzyme inhibitory peptide  
A:Reference number: JN0859; MUID:94080036; PMID:7764272  
A:Accession: JN0862  
A:Molecule type: protein  
A:Residues: 1-5 <MAT>  
A:Experimental source: intestine  
A:Comment: The amino terminal tripeptide of this protein inhibits angiotensin I-converting enzyme  
C:Superfamily: bradykinin-potentiating peptide  
C:Keywords: angiotensin-converting enzyme inhibitor

Query Match 8.7%; Score 2; DB 2; Length 5;  
Best Local Similarity 0.0%; Pred.No. 2.8e+05;  
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 L 4  
;  
DB 1 I 1

## RESULT 54

B41225  
copper resistance protein B - Pseudomonas syringae pv. tomato (fragment)  
C:Species: Pseudomonas syringae pv. tomato  
C:Date: 19-Jun-1992 #sequence\_revision 19-Jun-1992 #text\_change 24-Jun-1993  
C:Accession: B41225  
R:Cha, J.S.; Cooksey, D.A.  
Proc. Natl. Acad. Sci. U.S.A. 88, 8915-8919, 1991  
A:Title: Copper resistance in Pseudomonas syringae mediated by periplasmic and outer membrane proteins  
A:Reference number: A41225; MUID:92020961; PMID:1924351  
A:Accession: B41225  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-5 <CHA>

Query Match 8.7%; Score 2; DB 2; Length 5;  
Best Local Similarity 0.0%; Pred.No. 2.8e+05;  
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 L 4  
;  
DB 5 M 5

## RESULT 55

S70154  
URF2 protein - Xanthomonas sp.  
C:Species: Xanthomonas sp.  
C:Date: 15-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 08-Oct-1999  
C:Accession: S70154  
R:Kholodil, G.Y.; Mindlin, S.Z.; Baas, I.A.; Yurieva, O.V.; Minakhina, S.V.; Nikiforov, M.I. Microbiol. 17, 1189-1200, 1995  
A:Title: Four genes, two ends, and a res region are involved in transposition of Tn5053  
A:Reference number: S70140; MUID:96130850; PMID:8594337  
A:Accession: S70154  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-5 <KHO>  
A:Cross-references: EMBL:L40585; NID:G710572; PIDN:AAA98329.1; PID:G735909  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1995

Query Match 8.7%; Score 2; DB 2; Length 5;  
Best Local Similarity 0.0%; Pred.No. 2.8e+05;  
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 L 4  
;  
DB 1 M 1

## RESULT 56

I40702  
primase - Citrobacter diversus (fragment)  
C:Species: Citrobacter diversus  
C:Date: 16-Aug-1996 #sequence\_revision 16-Aug-1996 #text\_change 16-Aug-1996  
C:Accession: I40702  
R:Versalovic, J.; Lupski, J.R.  
Mol. Microbiol. 8, 343-355, 1993  
A:Title: Conservation and evolution of the rpsU-dnaG-rpoD macromolecular synthesis (MMS) genes  
A:Reference number: I40702; MUID:93302510; PMID:8316085  
A:Accession: I40702  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-5 <RES>  
A:Cross-references: GB:L01754; NID:G144439  
C:Genetics: dnaG  
A:Gene: dnaG

Query Match 8.7%; Score 2; DB 2; Length 5;  
Best Local Similarity 0.0%; Pred.No. 2.8e+05;  
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 L 4  
;  
DB 1 M 1

## RESULT 57

I40698  
biotin B - Citrobacter freundii (fragment)  
C:Species: Citrobacter freundii  
C:Date: 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text\_change 12-Aug-1996  
C:Accession: I40698  
R:Shiuan, D.; Campbell, A.  
Gene 67, 203-211, 1988  
A:Title: Transcriptional regulation and gene arrangement of Escherichia coli, Citrobacter  
A:Reference number: I40697; MUID:89006280; PMID:2971595  
A:Accession: I40698  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-5 <RES>

A;Cross-references: GB:M21922; NID:gl44434

Query Match 8.7%; Score 2; DB 2; Length 5;  
Best Local Similarity 0.0%; Pred. No. 2.8e+05;  
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 L 4  
;  
Db 1 M 1

# RESULT 58

B31836  
20K protein - Rickettsia rickettsii (fragment)  
C;Species: Rickettsia rickettsii  
C;Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 28-May-1999  
C;Accession: B31836  
R;Anderson, B.E.; Baumstark, B.R.; Bellini, W.J.  
J. Bacteriol. 170, 4493-4500, 1988  
A;Title: Expression of the gene encoding the 17-kilodalton antigen from Rickettsia rickettsii  
A;Reference number: A91885; MUID:8908059; PMID:3139629  
A;Accession: B31836  
A;Molecule type: DNA  
A;Residues: 1-5 <AND>  
A;Cross-references: GB:J03371; NID:gl52455; PIDN:AAI15030.1; PID:g4262874

Query Match 8.7%; Score 2; DB 2; Length 5;  
Best Local Similarity 0.0%; Pred. No. 2.8e+05;  
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 L 4  
;  
Db 1 M 1

# RESULT 59

T10954  
hypothetical protein 3 - spring vetch  
C;Species: Vicia sativa (spring vetch, tare)  
C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999  
C;Accession: T10954  
R;Christiansen, A.; Hansen, A.C.; Vijn, I.; Pallisgaard, N.; Larsen, K.; Yang, W.C.; Bisse  
submitted to the EMBL Data Library, December 1995  
A;Description: A novel type of DNA binding protein interacts with a conserved sequence in  
A;Reference number: Z17228  
A;Accession: T10954  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-5 <CHR>  
A;Cross-references: EMBL:X95995; NID:gl360633; PID:e225862

Query Match 8.7%; Score 2; DB 2; Length 5;  
Best Local Similarity 0.0%; Pred. No. 2.8e+05;  
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 L 4  
;  
Db 1 M 1

# RESULT 60

T14908  
hypothetical protein - parsley  
C;Species: Petroselinum crispum (parsley)  
C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 21-Jul-2000  
C;Accession: T14908  
R;Kircher, S.; Ledger, S.; Hayashi, H.; Weisshaar, B.; Schafer, E.; Frohnmeyer, H.  
Mol. Gen. Genet. 257, 595-605, 1998  
A;Title: CPRF4a, a novel plant bZIP protein of the CPRF family: comparative analysis of  
A;Reference number: Z18261; MUID:98265918; PMID:9604882  
A;Accession: T14908  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA

A;Residues: 1-5 <KIR>

A;Cross-references: EMBL:Y10809; NID:g3336901; PIDN:CAA71767.1; PID:g3336902  
A;Experimental source: Hamburger Schnitt

Query Match 8.7%; Score 2; DB 2; Length 5;  
Best Local Similarity 0.0%; Pred. No. 2.8e+05;  
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 L 4  
;  
Db 1 M 1

# RESULT 61

T14910  
hypothetical protein - parsley  
C;Species: Petroselinum crispum (parsley)  
C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 21-Jul-2000  
C;Accession: T14910  
R;Kircher, S.; Ledger, S.; Hayashi, H.; Weisshaar, B.; Schafer, E.; Frohnmeyer, H.  
Mol. Gen. Genet. 257, 595-605, 1998  
A;Title: CPRF4a, a novel plant bZIP protein of the CPRF family: comparative analysis of  
A;Reference number: Z18261; MUID:98265918; PMID:9604882  
A;Accession: T14910  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-5 <KIR>  
A;Cross-references: EMBL:Y10810; NID:g3336904; PIDN:CAA71769.1; PID:g3336905  
A;Experimental source: ssp. Hamburger Schnitt

Query Match 8.7%; Score 2; DB 2; Length 5;  
Best Local Similarity 0.0%; Pred. No. 2.8e+05;  
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 L 4  
;  
Db 1 M 1

# RESULT 62

B37988  
acid proteinase light chain - slime mold (Physarum polycephalum) (fragment)  
C;Species: Physarum polycephalum  
C;Date: 28-Jun-1991 #sequence\_revision 28-Jun-1991 #text\_change 30-Sep-1993  
C;Accession: B37988  
R;Murakami-Murofushi, K.; Takahashi, T.; Minowa, Y.; Iino, S.; Takeuchi, T.; Kitagaki-Og  
J. Biol. Chem. 265, 19898-19903, 1990  
A;Title: Purification and characterization of a novel intracellular acid proteinase from  
A;Reference number: A37988; MUID:91060608; PMID:2246266  
A;Accession: B37988  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-5 <MUR>

Query Match 8.7%; Score 2; DB 2; Length 5;  
Best Local Similarity 0.0%; Pred. No. 2.8e+05;  
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 L 4  
;  
Db 5 I 5

# RESULT 63

A37114  
hypoxanthine phosphoribosyltransferase (EC 2.4.2.8) - fluke (Schistosoma mansoni) (fragm  
C;Species: Schistosoma mansoni  
C;Date: 28-Mar-1991 #sequence\_revision 28-Mar-1991 #text\_change 23-Jun-1993  
C;Accession: A37114  
R;Yuan, L.; Craig, R.; McKerrow, J.H.; Wang, C.C.  
J. Biol. Chem. 265, 13528-13532, 1990  
A;Title: The hypoxanthine-guanine phosphoribosyltransferase of Schistosoma mansoni. Fur  
A;Reference number: A37114; MUID:90337955; PMID:2199439

A:Accession: A37114  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-5 <YUA>  
 C:Keywords: glycosyltransferase; pentosyltransferase

Query Match 8.7%; Score 2; DB 2; Length 5;  
 Best Local Similarity 0.0%; Pred. No. 2.8e+05;  
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 L 4  
 :  
 Db 1 M 1

## RESULT 64

I50385

myosin light chain 2 - chicken (fragment)

C:Species: Gallus gallus (chicken)

C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 28-Feb-1997

C:Accession: I50385

R:Shen, R.; Goswami, S.K.; Mascareno, E.; Kumar, A.; Siddiqui, M.A.Q.

Mol. Cell. Biol. 11, 1676-1685, 1991

A:Title: Tissue-specific transcription of the cardiac myosin light-chain 2 gene is regulated by myosin light chain 2

A:Reference number: I50385; PMID:1996116

A:Accession: I50385

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-5 &lt;SHE&gt;

A:Cross-references: GB:M63969; NID:G212332

C:Genetics:

A:Gene: MLC2

Query Match 8.7%; Score 2; DB 2; Length 5;  
 Best Local Similarity 0.0%; Pred. No. 2.8e+05;  
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 L 4  
 :  
 Db 1 M 1

## RESULT 65

S62883

seminal plasma protein II - pig (fragment)

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 17-Mar-1999

C:Accession: S62883

R:Romero, A.; Varela, P.F.; Sanz, L.; Toepfer-Petersen, E.; Calvete, J.J.

FEBS Lett. 382, 15-17, 1996

A:Title: Crystallization and preliminary X-ray diffraction analysis of boar seminal plasma protein II

A:Reference number: S62883; PMID:8612739

A:Accession: S62883

A:Molecule type: protein

A:Residues: 1-5 &lt;ROM&gt;

A:Complex: heterodimer; seminal plasma protein I and seminal plasma protein II

C:Keywords: glycoprotein; heterodimer; semen

Query Match 8.7%; Score 2; DB 2; Length 5;  
 Best Local Similarity 0.0%; Pred. No. 2.8e+05;  
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 L 4  
 :  
 Db 3 I 3

## RESULT 66

B44823

synaptosomal-associated protein SNAP-25 peptide 10A - rabbit (fragment)

N:Alternate names: superprotein peptide 10A

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 31-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 15-Jun-1996

C:Accession: B44823  
 R:Loewy, A.; Liu, W.S.; Baitinger, C.; Willard, M.B.  
 J. Neurosci. 11, 3412-3421, 1991

A:Title: The major 35S-methionine-labeled rapidly transported protein (superprotein) is a novel protein

A:Reference number: A44823; PMID:92044785; PMID:1941090

A:Accession: B44823

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-5 &lt;LOE&gt;

A:Experimental source: visual tissue

A:Note: sequence extracted from NCBI backbone (NCBIP:64255)

C:Keywords: membrane trafficking

Query Match 8.7%; Score 2; DB 2; Length 5;  
 Best Local Similarity 0.0%; Pred. No. 2.8e+05;  
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 L 4  
 :  
 Db 3 M 3

## RESULT 67

PT0597

T-cell receptor beta chain V-D-J region (111-1B) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997

C:Accession: PT0597

R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A:Reference number: PT0509; PMID:91277601; PMID:1711558

A:Accession: PT0597

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-5 &lt;FEE&gt;

A:Experimental source: newborn thymus, strain BALB/c

C:Keywords: T-cell receptor

Query Match 8.7%; Score 2; DB 2; Length 5;  
 Best Local Similarity 0.0%; Pred. No. 2.8e+05;  
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 L 4  
 :  
 Db 4 I 4

## RESULT 68

PT0590

T-cell receptor beta chain V-D-J region (141-1B) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997

C:Accession: PT0590

R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A:Reference number: PT0509; PMID:91277601; PMID:1711558

A:Accession: PT0590

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-5 &lt;FEE&gt;

A:Experimental source: day 19 fetal thymus, strain BALB/c

C:Keywords: T-cell receptor

Query Match 8.7%; Score 2; DB 2; Length 5;  
 Best Local Similarity 0.0%; Pred. No. 2.8e+05;  
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 L 4  
 :  
 Db 3 M 3

## RESULT 69

PT0572  
T-cell receptor beta chain V-D-J region (141-100) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C/Accession: PT0572  
R/Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A/Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A/Reference number: PT0509; MUID:91277601; PMID:1711558  
A/Accession: PT0572  
A/Status: translation not shown  
A/Molecule type: mRNA  
A/Residues: 1-5 <PEE>  
A/Experimental source: day 19 fetal thymus, strain BALB/c  
C/Keywords: T-cell receptor

Query Match 8.7%; Score 2; DB 2; Length 5;  
Best Local Similarity 0.0%; Pred. No. 2.8e+05;  
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 L 4  
Db 4 I 4

## RESULT 70

H44817  
34.5K structural protein - Leuconostoc oenos phase P32 (fragment)  
C/Species: Leuconostoc oenos phase P32  
C/Date: 31-Mar-1993 #sequence\_revision 22-May-1998 #text\_change 22-May-1998  
C/Accession: H44817  
R/Arendt, E.K.; Lonvaud, A.; Hammes, W.P.  
J. Gen. Microbiol. 137, 2135-2139, 1991  
A/Title: Lysogeny in Leuconostoc oenos.  
A/Reference number: A44817; MUID:92085033; PMID:1748868  
A/Accession: H44817  
A/Molecule type: protein  
A/Residues: 1-5 <ARE>  
A/Note: sequence extracted from NCBI backbone (NCBIP:70332)

Query Match 8.7%; Score 2; DB 2; Length 5;  
Best Local Similarity 0.0%; Pred. No. 2.8e+05;  
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 L 4  
Db 1 M 1

## RESULT 71

F44817  
34.5K structural protein - Leuconostoc oenos phase P54 (fragment)  
C/Species: Leuconostoc oenos phase P54  
C/Date: 31-Mar-1993 #sequence\_revision 22-May-1998 #text\_change 22-May-1998  
C/Accession: F44817  
R/Arendt, E.K.; Lonvaud, A.; Hammes, W.P.  
J. Gen. Microbiol. 137, 2135-2139, 1991  
A/Title: Lysogeny in Leuconostoc oenos.  
A/Reference number: A44817; MUID:92085033; PMID:1748868  
A/Accession: F44817  
A/Molecule type: protein  
A/Residues: 1-5 <ARE>  
A/Note: sequence extracted from NCBI backbone (NCBIP:70335)

Query Match 8.7%; Score 2; DB 2; Length 5;  
Best Local Similarity 0.0%; Pred. No. 2.8e+05;  
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 L 4  
Db 1 M 1

## RESULT 72

S11127  
phosphoprotein, bone - chicken (fragment)  
C/Species: Gallus gallus (chicken)  
C/Date: 21-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 04-Mar-2000  
C/Accession: S11127; S11128  
R/Mikuni-Takagaki, Y.; Glincher, M.J.  
Biochem. J. 288, 585-591, 1990  
A/Title: Post-translational processing of chicken bone phosphoproteins. Identification of  
A/Reference number: S11127; MUID:90303246; PMID:2363696  
A/Accession: S11127  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-5 <MIK1>  
A/Accession: S11128  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 'X', 2-5 <MIK2>  
C/Keywords: phosphoprotein

Query Match 4.3%; Score 1; DB 2; Length 5;  
Best Local Similarity 0.0%; Pred. No. 2.8e+05;  
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 L 4  
Db 3 V 3

## RESULT 73

C23751  
spinal cord peptide SCP-6 - pig  
C/Species: Sus scrofa domestica (domestic pig)  
C/Date: 28-Sep-1987 #sequence\_revision 28-Sep-1987 #text\_change 18-Aug-2000  
C/Accession: C23751  
R/Hsi, K.L.; Chen, R.L.; Chen, Z.G.; Zhang, H.L.; Lu, Y.A.; Guo, S.Y.; Wu, S.X.; Tsou, K.  
Arch. Biochem. Biophys. 240, 178-183, 1995  
A/Reference number: A23751; MUID:85250425; PMID:4015098  
A/Accession: C23751  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-5 <HSI>  
C/Supfamily: unassigned animal peptides

Query Match 0.0%; Score 0; DB 2; Length 5;  
Best Local Similarity 0.0%; Pred. No. 2.8e+05;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 X 2  
Db 2 A 2

## RESULT 74

A26830  
mitosis inhibiting peptide - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 19-Nov-1988 #sequence\_revision 18-Aug-2000 #text\_change 18-Aug-2000  
C/Accession: A26830  
R/Reichelt, K.; Elgjo, K.; Edminson, P.D.  
Biochem. Biophys. Res. Commun. 146, 1493-1501, 1987  
A/Title: Isolation and structure of an epidermal mitosis inhibiting pentapeptide.  
A/Reference number: A26830; MUID:87298602; PMID:3619940  
A/Accession: A26830  
A/Molecule type: protein  
A/Residues: 1-5 <REI>  
C/Supfamily: unassigned animal peptides  
C/Keywords: blocked amino end; pyroglutamic acid  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 0.0%; Score 0; DB 2; Length 5;

Best Local Similarity 0.0%; Pred. No. 2.8e+05;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 X 2

Db 4 S 4

#### RESULT 75

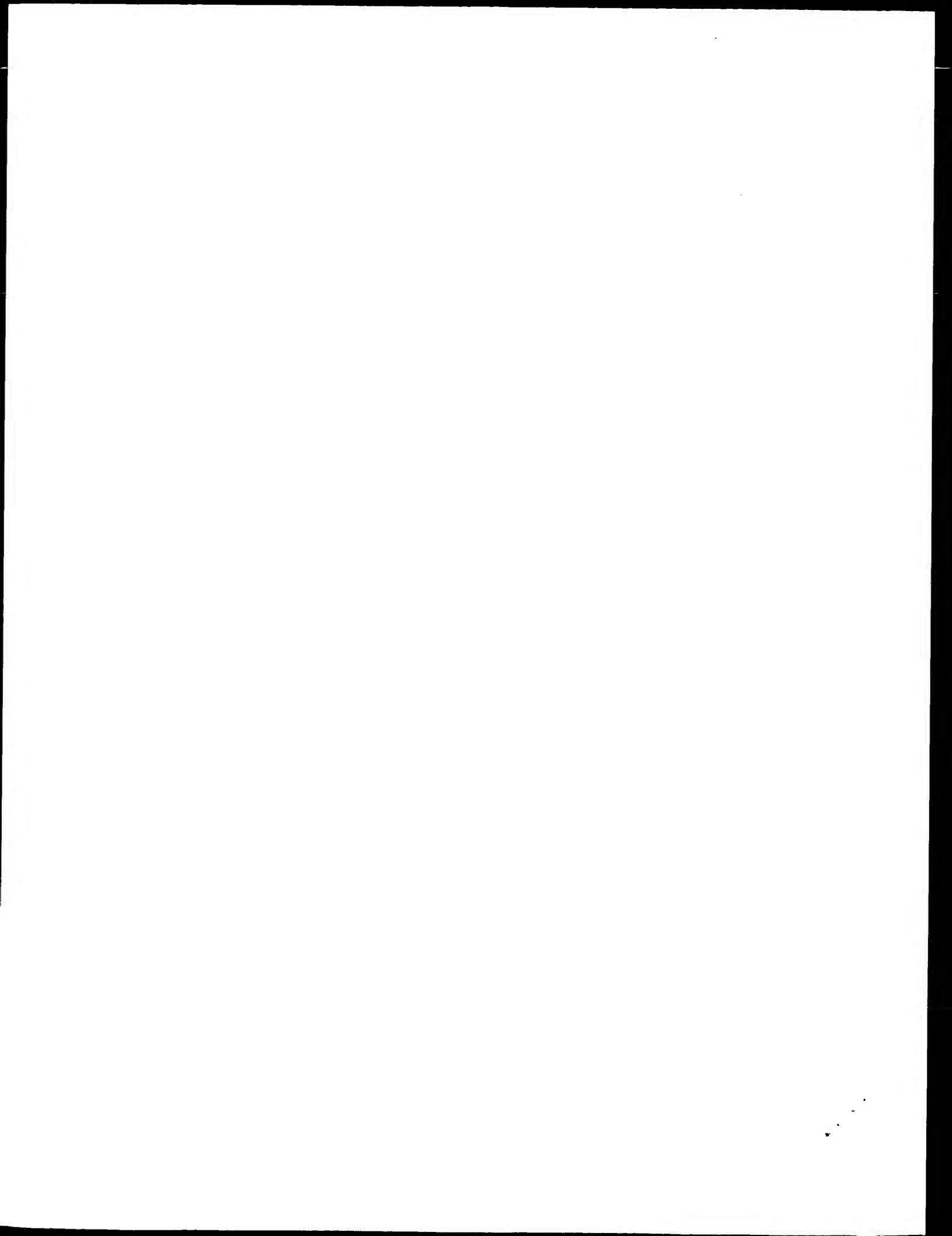
A41225  
copper resistance protein A - Pseudomonas syringae pv. tomato (fragment)  
C;Species: Pseudomonas syringae pv. tomato  
C;Date: 19-Jun-1992 #sequence\_revision 19-Jun-1992 #text\_change 24-Jun-1993  
C;Accession: A41225  
R;Cha, J.S.; Cooksey, D.A.  
Proc. Natl. Acad. Sci. U.S.A. 88, 8915-8919, 1991  
A;Title: Copper resistance in Pseudomonas syringae mediated by periplasmic and outer mem  
A;Reference number: A41225; MUID:92020961; PMID:1924351  
A;Accession: A41225  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-5 <CHA>

Query Match 0.0%; Score 0; DB 2; Length 5;  
Best Local Similarity 0.0%; Pred. No. 2.8e+05;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 X 2

Db 1 A 1

Search completed: February 12, 2003, 10:52:50  
Job time : 17 secs





GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 12, 2003, 10:46:33 ; Search time 11 Seconds  
(without alignments)  
18.853 Million cell updates/sec

Title: US-09-403-440A-1

Perfect score: 23  
Sequence: 1 FXLLW 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 20

Minimum DB seq length: 5  
Maximum DB seq length: 5

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	11	47.8	5	1 BPP7 BOTIN	P30425 bothrops in
2	11	47.8	5	1 UF01 MOUSE	P38639 mus musculu
3	6	26.1	5	1 AL14 CARMA	P81817 carcinus ma
4	6	26.1	5	1 EI03 LITRU	P82099 litoria rub
5	6	26.1	5	1 EI04 LITRU	P82100 litoria rub
6	6	26.1	5	1 FARP ARTTR	P41853 artiopeathi
7	6	26.1	5	1 PAP2 PARMA	P81864 pardachirus
8	6	26.1	5	1 RE11 LITRU	P82070 litoria rub
9	6	26.1	5	1 RE21 LITRU	P82071 litoria rub
10	6	26.1	5	1 RE31 LITRU	P82072 litoria rub
11	6	26.1	5	1 RE32 LITRU	P82073 litoria rub
12	6	26.1	5	1 SUGA ACHDO	P19991 acheta dome
13	6	26.1	5	1 TPIS CANPA	P54714 canis fami
14	6	26.1	5	1 UC22 MAIZE	P80628 zea mays (m
15	4	17.4	5	1 PRCT PERAM	P01373 periplaneta
16	4	17.4	5	1 PSK DAUCA	P58261 daucus caro
17	2	8.7	5	1 BIOA CITFR	P13071 citrobacter
18	2	8.7	5	1 BIOB CITFR	P12997 citrobacter
19	0	0.0	5	1 TRM3 ECOLI	P13973 escherichia
20	0	0.0	5	1 UXA4 CHLTR	P38005 chlamydia t

#### ALIGNMENTS

RESULT 1  
BPP7 BOTIN  
ID BPP7 BOTIN STANDARD; PRT; 5 AA.  
AC P30425;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 01-FEB-1994 (Rel. 28, Last annotation update)  
DE Bradykinin-potentiating peptide S5,2 (5A) (Angiotensin-converting

DE enzyme inhibitor).  
OS Bothrops insularis (Island jararaca) (Queimada jararaca).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;  
OC Viperidae; Crotalinae; Bothrops.  
OX NCBI\_TaxID=8723;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Venom;  
RX MEDLINE=90351557; PubMed=2386615;  
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;  
RT "Primary structure and biological activity of bradykinin potentiating  
peptides from Bothrops insularis snake venom.";  
RL J. Protein Chem. 9:221-227(1990).  
CC -!- FUNCTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE  
ANGIOTENSIN-CONVERTING ENZYME AND ENHANCES THE ACTION OF  
BRADYKININ BY INHIBITING THE KINASES THAT INACTIVATE IT.  
CC IT ACTS AS AN INDIRECT HYPOTENSIVE AGENT.  
DR PIR; G37196; G37196.  
KW Hypotensive agent; Venom.  
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
SQ SEQUENCE 5 AA; 629 MW; 776DC37326B00000 CRC64;

Query Match 47.8%; Score 11; DB 1; Length 5;

Best Local Similarity 100.0%; Pred. No. 1.1e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5

DB 3 W 3

#### RESULT 2

UF01 MOUSE  
ID UF01 MOUSE STANDARD; PRT; 5 AA.

AC P38639;

DT 01-OCT-1994 (Rel. 30, Created)

DT 01-OCT-1994 (Rel. 30, Last sequence update)

DT 01-FEB-1995 (Rel. 31, Last annotation update)

DE Unknown protein from 2D-page of fibroblasts (P19) (Fragment).

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE

RC TISSUE=Fibroblast;

MEDLINE=95009907; PubMed=7523108;

RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;

RT "Separation and sequencing of familial and novel murine proteins

using preparative two-dimensional gel electrophoresis.";

RL Electrophoresis 15:735-745(1994).

CC -!- MISCELLANEOUS: ON THE 2D-GEL, THE DETERMINED PI OF THIS UNKNOWN

PROTEIN IS: 6.6, ITS MW IS: 19 KDa.

FT NON TER 5

SQ SEQUENCE 5 AA; 717 MW; 7364087043100000 CRC64;

Query Match 47.8%; Score 11; DB 1; Length 5;

Best Local Similarity 100.0%; Pred. No. 1.1e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5

DB 1 W 1

#### RESULT 3

AL14 CARMA

ID AL14 CARMA STANDARD; PRT; 5 AA.

AC P81817;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Carcinustatin 14.  
 OS Carcinus maenas (Common shore crab) (Green crab).  
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea;  
 OC Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata;  
 OC Brachyura; Eubrachyura; Portunoidae; Portunidae; Carcinus.  
 OX NCBI\_TaxID=6759;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;  
 RX MEDLINE=98121193; PubMed=9461299;  
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,  
 RA Thorpe A.;  
 RT "Isolation and identification of multiple neuropeptides of the  
 RT allatostatin superfamily in the shore crab Carcinus maenas.";  
 RL Eur. J. Biochem. 250:727-734(1997).  
 CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.  
 CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
 KW Neuropeptide; Amidation; Multigene family.  
 FT MOD RES 5 5  
 FT AMIDATION (POTENTIAL).  
 SQ SEQUENCE 5 AA; 586 MW; 672879DSAB300000 CRC64;

Query Match 26.1%; Score 6; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 F 1  
 |  
 Db 3 F 3

RESULT 4  
 E103\_LITRU  
 ID E103\_LITRU STANDARD; PRT; 5 AA.  
 AC P82039;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Electrin 3  
 OS Litoria rubella (Desert tree frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;  
 OC Pelodyadinae; Litoria.  
 OX NCBI\_TaxID=104895;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;  
 RT "Peptides from the skin glands of the Australian buzzing tree frog  
 RT Litoria electrica. Comparison with the skin peptides from Litoria  
 RT rubella.";  
 RL Aust. J. Chem. 52:639-645(1999).  
 CC -1- SUBCELLULAR LOCATION: SECRETED.  
 CC Amphibian skin; Amidation.  
 KW Neuropeptide; Amidation.  
 FT MOD RES 5 5  
 FT AMIDATION.  
 SQ SEQUENCE 5 AA; 630 MW; 668761F2C9A00000 CRC64;

Query Match 26.1%; Score 6; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 F 1  
 |  
 Db 1 F 1

RESULT 5  
 E104\_LITRU  
 ID E104\_LITRU STANDARD; PRT; 5 AA.  
 AC P82100;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Electrin 4.

OS Litoria rubella (Desert tree frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;  
 OC Pelodyadinae; Litoria.  
 OX NCBI\_TaxID=104895;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;  
 RT "Peptides from the skin glands of the Australian buzzing tree frog  
 RT Litoria electrica. Comparison with the skin peptides from Litoria  
 RT rubella.";  
 RL Aust. J. Chem. 52:639-645(1999).  
 CC -1- SUBCELLULAR LOCATION: SECRETED.  
 CC Amphibian skin; Amidation.  
 KW Neuropeptide; Amidation.  
 FT MOD RES 5 5  
 FT AMIDATION.  
 SQ SEQUENCE 5 AA; 616 MW; 61F2D1A059A00000 CRC64;

Query Match 26.1%; Score 6; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 F 1  
 |  
 Db 1 F 1

RESULT 6  
 FARP\_ARTTR  
 ID FARP\_ARTTR STANDARD; PRT; 5 AA.  
 AC P41853;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE FMRFamide-like neuropeptide RYIRF-amide.  
 OS Actinosthia triangulata.  
 OC Eukaryota; Metazoa; Platyhelminthes; Turbellaria; Sericata; Tricladida;  
 OC Terricola; Geoplanidae; Arthurdendyus.  
 OX NCBI\_TaxID=132421;  
 RN [1]  
 RP SEQUENCE, AND SYNTHESIS.  
 RX MEDLINE=94211927; PubMed=7909164;  
 RA Maule A.G., Shaw C., Halton D.W., Curry W.J., Thim L.;  
 RT "RYIRFamide: a turbellarian FMRFamide-related peptide (FARP).";  
 RL Regul. Pept. 50:37-43(1994).  
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 KW Neuropeptide; Amidation.  
 FT MOD RES 5 5  
 FT AMIDATION.  
 SQ SEQUENCE 5 AA; 754 MW; 69D4004B4600000 CRC64;

Query Match 26.1%; Score 6; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 F 1  
 |  
 Db 5 F 5

RESULT 7  
 PAP2\_PARMA  
 ID PAP2\_PARMA STANDARD; PRT; 5 AA.  
 AC P81864;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Pardaxin II (PXII) (Fragment).  
 OS Pardachirus marmoratus (Red sea moles sole).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;  
 OC Soleioidae; Soleidae; Pardachirus.

OX NCBI\_TaxID=31087;  
 RP [1]  
 RN SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=87057369; PubMed=3782138;  
 RA Lazarovici P., Primor N., Loew L.M.;  
 RT "Purification and pore-forming activity of two hydrophobic  
 RT polypeptides from the secretion of the Red sea moose sole (*Pardachirus  
 RT marmoratus*).";  
 RL J. Biol. Chem. 261:16704-16713(1986).  
 CC -!- FUNCTION: EXHIBITS UNUSUAL SHARK REPELLENT AND SURFACTANT  
 CC PROPERTIES. FORMS VOLTAGE-DEPENDENT, ION-PERMEABLE CHANNELS  
 CC IN MEMBRANES. AT HIGH CONCENTRATION CAUSES CELL MEMBRANE LYSIS.  
 CC -!- SUBUNIT: MONOMER. IN AQUEOUS SOLUTION EXISTS AS A TETRAMER.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: BELONGS TO THE PARDAXIN FAMILY.  
 KW Toxin.  
 FT NON TER  
 SQ SEQUENCE 5 AA; 614 MW; 7769C9C8100000 CRC64;  
 Query Match 26.1%; Score 6; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 F 1  
 DB 2 F 2  
 RESULT 8  
 RE11\_LITRU  
 ID RE11\_LITRU STANDARD; PRT; 5 AA.  
 AC P82070;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Rubellidin 1.1.  
 OS Litoria rubella (Desert tree frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;  
 OC Pelodyadinae; Litoria.  
 OX NCBI\_TaxID=104895;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Skin secretion;  
 RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,  
 RA Tyler M.J., Wallace J.C.;  
 RT "The structure of new peptides from the Australian red tree frog  
 RT 'Litoria rubella', the skin peptide profile as a probe for the study  
 RT of evolutionary trends of amphibians.";  
 RL Aust. J. Chem. 49:955-963(1996).  
 CC -!- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC  
 CC ACTIVITY.  
 CC -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.  
 CC -!- MASS SPECTROMETRY: MW=598; METHOD=FAB.  
 KW Amphibian skin.  
 SQ SEQUENCE 5 AA; 598 MW; 6DD9C9C82A000000 CRC64;  
 Query Match 26.1%; Score 6; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 F 1  
 DB 3 F 3  
 RESULT 9  
 RE21\_LITRU  
 ID RE21\_LITRU STANDARD; PRT; 5 AA.  
 AC P82071;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DB Rubellidin 2.1.  
 OS Litoria rubella (Desert tree frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;  
 OC Pelodyadinae; Litoria.  
 OX NCBI\_TaxID=104895;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Skin secretion;  
 RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,  
 RA Tyler M.J., Wallace J.C.;  
 RT "The structure of new peptides from the Australian red tree frog  
 RT 'Litoria rubella', the skin peptide profile as a probe for the study  
 RT of evolutionary trends of amphibians.";  
 RL Aust. J. Chem. 49:955-963(1996).  
 CC -!- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC  
 CC ACTIVITY.  
 CC -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.  
 CC -!- MASS SPECTROMETRY: MW=626; METHOD=FAB.  
 KW Amphibian skin.  
 SQ SEQUENCE 5 AA; 626 MW; 6DD9C9C810300000 CRC64;  
 Query Match 26.1%; Score 6; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 F 1  
 DB 3 F 3

RESULT 10  
 RE31\_LITRU  
 ID RE31\_LITRU STANDARD; PRT; 5 AA.  
 AC P82072;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Rubellidin 3.1.  
 OS Litoria rubella (Desert tree frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;  
 OC Pelodyadinae; Litoria.  
 OX NCBI\_TaxID=104895;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Skin secretion;  
 RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,  
 RA Tyler M.J., Wallace J.C.;  
 RT "The structure of new peptides from the Australian red tree frog  
 RT 'Litoria rubella', the skin peptide profile as a probe for the study  
 RT of evolutionary trends of amphibians.";  
 RL Aust. J. Chem. 49:955-963(1996).  
 CC -!- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC  
 CC ACTIVITY.  
 CC -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.  
 CC -!- MASS SPECTROMETRY: MW=655; METHOD=FAB.  
 KW Amphibian skin.  
 FT MOD\_RES 5 AMIDATION.  
 SQ SEQUENCE 5 AA; 656 MW; 71A9C9C810300000 CRC64;  
 Query Match 26.1%; Score 6; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 F 1  
 DB 3 F 3

RESULT 11  
 RE32\_LITRU

ID RE32 LITRU STANDARD; PRT; 5 AA.  
 AC P82073;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Rubellidin 3.2.  
 OS Litoria rubella (Desert tree frog).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;  
 OC Pelodyadinae; Litoria.  
 OX NCBI\_TaxID=104895;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;  
 RT "Peptides from the skin glands of the Australian buzzing tree frog  
 RT Litoria electrica. Comparison with the skin peptides from Litoria  
 RT rubella.";  
 RL Aust. J. Chem. 52:639-645(1999).  
 CC -1- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC  
 CC ACTIVITY.  
 CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.  
 KW Amphibian skin.  
 SQ SEQUENCE 5 AA; 570 MW; 71A9C9C862A00000 CRC64;  
 Query Match 26.1%; Score 6; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
 DB 3 F 3

RESULT 12  
 SUGA\_ACHDO STANDARD; PRT; 5 AA.  
 AC P19931;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE Subesophageal ganglion pentapeptide.  
 OS Acheta domesticus (House cricket).  
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
 OC Insecta; Pterygota; Neoptera; Orthopteroidea; Orthoptera; Ensifera;  
 OC Gryllidae; Gryllinae; Acheta.  
 OX NCBI\_TaxID=6997;  
 RN [1]  
 RP SEQUENCE.  
 RA Wicker C.;  
 RT "Isolation and structure of a peptide isolated from the  
 RT subesophageal ganglion of Acheta domesticus (orthoptera).";  
 RL Comp. Biochem. Physiol. 88C:185-187(1987).  
 CC -1- SUBCELLULAR LOCATION: MAIN PEPTIDE FROM THE SUBESOPHAGEAL  
 CC GANGLIA.  
 DR PIR; JS0319.  
 SQ SEQUENCE 5 AA; 476 MW; 69D76DDDDDB00000 CRC64;

Query Match 26.1%; Score 6; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
 DB 5 F 5

RESULT 13  
 TPIS\_CANFA STANDARD; PRT; 5 AA.  
 ID TPIS\_CANFA  
 AC P54714;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE Triosephosphate isomerase (EC 5.3.1.1) (TIM) (Fragment).  
 GN TPI1.  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 OX NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Heart;  
 RX MEDLINE=98163340; PubMed=9504812;  
 RA Dunn M.J., Corbett J.M., Wheeler C.H.;  
 RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of  
 RT dog heart proteins.";  
 RL Electrophoresis 18:2795-2802(1997).  
 CC -1- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate = glycero-  
 CC phosphate.  
 CC -1- PATHWAY: PLAYS AN IMPORTANT ROLE IN SEVERAL METABOLIC PATHWAYS.  
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE TRIOSEPHOSPHATE ISOMERASE FAMILY.  
 DR HSC-2DPAGE; P54714; DOG.  
 DR InterPro; IPR000652; Triophos\_ismrse.  
 DR PROSITE; PS00171; TIM; PARTIAL.  
 KW Isomerase; Glycolysis; Gluconeogenesis; Fatty acid biosynthesis;  
 KW Pentose shunt.  
 FT NON\_TER 1 1  
 FT NON\_TER 5 5  
 SQ SEQUENCE 5 AA; 550 MW; 64444862C9A00000 CRC64;

Query Match 26.1%; Score 6; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
 DB 1 F 1

RESULT 14  
 UC22\_MAIZE STANDARD; PRT; 5 AA.  
 ID UC22\_MAIZE  
 AC P80628;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Unknown protein from 2D-page of etiolated coleoptile (Spot 474)  
 DE (Fragment).  
 DE Zea mays (Maize).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;  
 OC Panicoideae; Andropogoneae; Zea.  
 OX NCBI\_TaxID=4577;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Coleoptile;  
 RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,  
 RA Pernollet J.-C., Zivy M., de Vienne D.;  
 RT "The maize two dimensional gel protein database: towards an integrated  
 RT genome analysis program.";  
 RL Theor. Appl. Genet. 93:997-1005(1996).  
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 6.1, ITS MW IS: 30.4 kDa.  
 DR Maize-2DPAGE; P80628; COLEOPTILE.  
 DR MaizeDB; 123954; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 5 5  
 SQ SEQUENCE 5 AA; 654 MW; 72CB19C9C0300000 CRC64;

Query Match 26.1%; Score 6; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1

```

Db          4 |
            2 F 2

RESULT 15
PCT_PERAM
ID_PCT_PERAM  STANDARD;  PRT;  5 AA.
AC  F01373;
DT  21-JUL-1986 (Rel. 01, Created)
DT  21-JUL-1986 (Rel. 01, Last sequence update)
DT  01-FEB-1995 (Rel. 31, Last annotation update)
DE  Proctolin.
OS  Periplaneta americana (American cockroach),
OS  Limulus polyphemus (Atlantic horseshoe crab), and
OS  Carcinus maenas (Common shore crab) (Green crab).
OC  Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC  Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC  Blattoidea; Blattidae; Periplaneta.
OX  NCBI_TaxID=6978, 6850, 6759;
RN  [1]
RP  SEQUENCE.
RC  SPECIES=P.americana;
RC  MEDLINE=76074708; PubMed=576;
RA  Starratt A.N., Brown B.E.;
RT  "Structure of the pentapeptide proctolin, a proposed neurotransmitter
RT  in insects.";
RL  Life Sci. 17:1253-1256(1975).
RN  [2]
RP  BIOLOGICAL SOURCE.
RC  SPECIES=P.americana;
RC  MEDLINE=81225865; PubMed=6113690;
RA  O'Shea M., Adams M.E.;
RT  "Pentapeptide (proctolin) associated with an identified neuron.";
RL  Science 213:567-569(1981).
RN  [3]
RP  SEQUENCE.
RC  SPECIES=L.polyphemus;
RC  MEDLINE=90287800; PubMed=2356151;
RA  Groomer J.R., Tillinghast E.K., Townley M.A., Vetrovs A.,
RA  Watson W.H. III, Hunt D.F., Griffin P.R., Alexander J.E.,
RA  Shabanowitz J.;
RT  "Identification of proctolin in the central nervous system of the
RT  horseshoe crab, Limulus polyphemus.";
RL  Peptides 11:205-211(1990).
RN  [4]
RP  SEQUENCE.
RC  SPECIES=C.maenas;
RC  MEDLINE=86232789; PubMed=2872661;
RA  Stangier J., Bircksen H., Keller R.;
RT  "Identification and immunocytochemical localization of proctolin in
RT  pericardial organs of the shore crab, Carcinus maenas.";
RL  Peptides 7:67-72(1986).
CC  -!- FUNCTION: STIMULATES CARDIAC OUTPUT AND HINDGUT MOTILITY.
CC  MODULATES VISCERAL AND SKELETAL MUSCLE IN MANY ARTHROPODS.
CC  -!- TISSUE SPECIFICITY: FOUND IN THE LATERAL WHITE NEURONS AND IN
CC  THE CRAB PERICARDIAL ORGANS.
DR  PIR; A01644; HOROHA.
DR  PIR; A60411; A60411.
KW  Neuropeptide.
SQ  SEQUENCE  5 AA;  649 MW;  71B7673B44600000 CRC64;

Query Match      17.4%; Score 4; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY          4 L 4
            3 L 3

Db

RESULT 16
PSK_DAUCA
ID_PSK_DAUCA  STANDARD;  PRT;  5 AA.

```

```

AC  P58261;
DT  16-OCT-2001 (Rel. 40, Created)
DT  16-OCT-2001 (Rel. 40, Last sequence update)
DT  16-OCT-2001 (Rel. 40, Last annotation update)
DE  Phytosulfokine-alpha (PSK-alpha) [Contains: Phytosulfokine-beta (PSK-
DE  beta)].
OS  Daucus carota (Carrot).
OC  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC  Asteridae; euasterids II; Apiales; Apiaceae; Daucus.
OX  NCBI_TaxID=4039;
RN  [1]
RP  SEQUENCE, AND IDENTIFICATION BY MASS SPECTROMETRY.
RC  STRAIN=cv. US-Harumakigosun;
RC  MEDLINE=20212743; PubMed=10750705;
RA  Hanai H., Matsuno T., Yamamoto M., Matsubayashi Y., Kobayashi T.,
RA  Kanada H., Sakagami Y.;
RT  "A secreted peptide growth factor, phytosulfokine, acting as a
RT  stimulatory factor of carrot somatic embryo formation.";
RL  Plant Cell Physiol. 41:27-32(2000).
CC  -!- FUNCTION: IN PRESENCE OF 2,4-D, STIMULATES PROLIFERATION OF THE
CC  CELLS, BUT DOES NOT STIMULATE DIFFERENTIATION INTO THE SOMATIC
CC  EMBRYOS.
CC  -!- SUBCELLULAR LOCATION: Secreted.
CC  -!- PTM: SULFATION IS IMPORTANT FOR ACTIVITY AND FOR THE BINDING TO A
CC  PUTATIVE MEMBRANE RECEPTOR (BY SIMILARITY).
CC  -!- SIMILARITY: BELONGS TO THE PHYTOSULFOKINE FAMILY.
KW  Growth factor; Sulfation.
FT  PEPTIDE 1 4 PHYTOSULFOKINE-BETA.
FT  MOD_RES 1 1 SULFATION.
FT  MOD_RES 3 3 SULFATION.
SQ  SEQUENCE  5 AA;  687 MW;  76C1BB504B300000 CRC64;

Query Match      17.4%; Score 4; DB 1; Length 5;
Best Local Similarity 0.0%; Pred. No. 1.1e+05;
Matches 0; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY          4 LW 5
            2 IY 3
            2 IY 3

Db

RESULT 17
BIOA_CITFR
ID_BIOA_CITFR  STANDARD;  PRT;  5 AA.
AC  P13071;
DT  01-JAN-1990 (Rel. 13, Created)
DT  01-JAN-1990 (Rel. 13, Last sequence update)
DT  16-OCT-2001 (Rel. 40, Last annotation update)
DE  Adenosylmethionine-8-amino-7-oxononanoate aminotransferase
DE  (EC 2.6.1.62) (7,8-diamino-pelargonic acid aminotransferase) (DAPA
DE  aminotransferase) (Fragment).
GN  BIOA.
OS  Citrobacter freundii.
OC  Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC  Citrobacter.
OX  NCBI_TaxID=546;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  MEDLINE=89006280; PubMed=2971595;
RA  Shivan D., Campbell A.;
RT  "Transcriptional regulation and gene arrangement of Escherichia coli,
RT  Citrobacter freundii and Salmonella typhimurium biotin operons.";
RL  Gene 67:203-211(1988).
CC  -!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 8-amino-7-
CC  oxononanoate = S-adenosyl-4-methylthio-2-oxobutanoate + 7,8-
CC  diaminononanoate.
CC  -!- COFACTOR: PYRIDOXAL PHOSPHATE.
CC  -!- PATHWAY: Biotin biosynthesis.
CC  -!- SUBUNIT: HOMODIMER.
CC  -!- SIMILARITY: BELONGS TO CLASS-III OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC  AMINOTRANSFERASES.

```

CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC -----  
 CC EMBL; M21922; -; NOT ANNOTATED CDS.  
 CC InterPro; IPR000954; AminoTran\_3.  
 CC PROSITE; PS00600; AA\_TRANSFER\_CLASS\_3; PARTIAL.  
 CC Biotin biosynthesis; Transferase; AminoTransferase;  
 CC Pyridoxal phosphate. 5  
 CC NON\_TER 5  
 CC SEQUENCE 5 AA; 582 MW; 6AAAB1B1A6F00000 CRC64;

Query Match 8.7%; Score 2; DB 1; Length 5;  
 Best Local Similarity 0.0%; Pred. No. 1.1e+05; Indels 0; Gaps 0;  
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 L 4  
 Db 1 M 1

## RESULT 18

ID\_BIOB\_CITFR STANDARD; PRT; 5 AA.  
 AC P12997;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Biotin synthase (EC 2.8.1.6) (Biotin synthetase) (Fragment).  
 GN BIOB.  
 OS Citrobacter freundii.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Citrobacter.  
 OX NCBI\_TaxID=546;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89006280; PubMed=2971595;  
 RA Shuan D., Campbell A.;  
 RT "Transcriptional regulation and gene arrangement of Escherichia coli,  
 RT Citrobacter freundii and Salmonella typhimurium biotin operons.";  
 RL Gene 67:203-211(1988).  
 CC -|- CATALYTIC ACTIVITY: Dethiobiotin + sulfur = biotin.  
 CC -|- PATHWAY: Biotin biosynthesis; last step.  
 CC -|- SIMILARITY: BELONGS TO THE BIOTIN AND LIPOIC ACID SYNTHETASES  
 CC FAMILY.

CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC EMBL; M21922; -; NOT ANNOTATED CDS.  
 CC Biotin biosynthesis; Iron-sulfur; Transferase.  
 CC NON\_TER 5  
 CC SEQUENCE 5 AA; 532 MW; 75A5B1EDD6F00000 CRC64;

Query Match 8.7%; Score 2; DB 1; Length 5;  
 Best Local Similarity 0.0%; Pred. No. 1.1e+05; Indels 0; Gaps 0;  
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 L 4  
 Db 1 M 1

## RESULT 19

Query Match 0.0%; Score 0; DB 1; Length 5;

TRM3\_ECOLI STANDARD; PRT; 5 AA.  
 ID TRM3\_ECOLI  
 AC P13973;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE TrmM protein (Fragment).  
 GN TRAM.  
 OS Escherichia coli.  
 OG Plasmid IncFII R100.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Escherichia.  
 OX NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88227859; PubMed=2836369;  
 RA Inamoto S., Yoshioka Y., Ohtsubo E.;  
 RT "Identification and characterization of the products from the traJ  
 RT and traY genes of plasmid R100.";  
 RL J. Bacteriol. 170:2749-2757(1988).  
 CC -|- FUNCTION: TRANSFER GENE PROTEIN. IS INVOLVED IN THE CONJUGATION  
 CC PROCESS OF BACTERIAL CELLS FOR THE EXCHANGE OF PLASMID DNA.  
 CC -|- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -|- SIMILARITY: TO TRAM PROTEIN OF OTHER PLASMIDS.

CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC EMBL; M20941; -; NOT ANNOTATED\_CDS.  
 CC PIR; A32014; A32014.  
 CC Conjugation; Plasmid; DNA-binding.  
 CC NON\_TER 1  
 CC SEQUENCE 5 AA; 634 MW; 6B1B1AA443500000 CRC64;

Query Match 0.0%; Score 0; DB 1; Length 5;  
 Best Local Similarity 0.0%; Pred. No. 1.1e+05; Indels 0; Gaps 0;  
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 X 2  
 Db 1 K 1

## RESULT 20

ID\_UXAA4\_CHLTR STANDARD; PRT; 5 AA.  
 AC P38005;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Unknown protein from 2D-page from elementary body (Fragment).  
 OS Chlamydia trachomatis.  
 OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.  
 OX NCBI\_TaxID=813;  
 RN [1]  
 RP SEQUENCE.

CC STEAIN=L2/434/Bu;  
 CC Bini L., Santucci A., Magi B., Marzocchi B., Sanchez-Campillo M.,  
 CC Comanducci M., Christianen G., Birkelund S., Vitreou E., Ratti G.,  
 CC Pallini V.;  
 CC Submitted (SEP-1994) to the SWISS-PROT data bank.  
 CC -|- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 4.5, ITS MW IS: 28 kDa.  
 CC Sienaa-2DPAGE; P38005; -.  
 CC NON\_TER 5  
 CC SEQUENCE 5 AA; 474 MW; 75BAA865AA800000 CRC64;

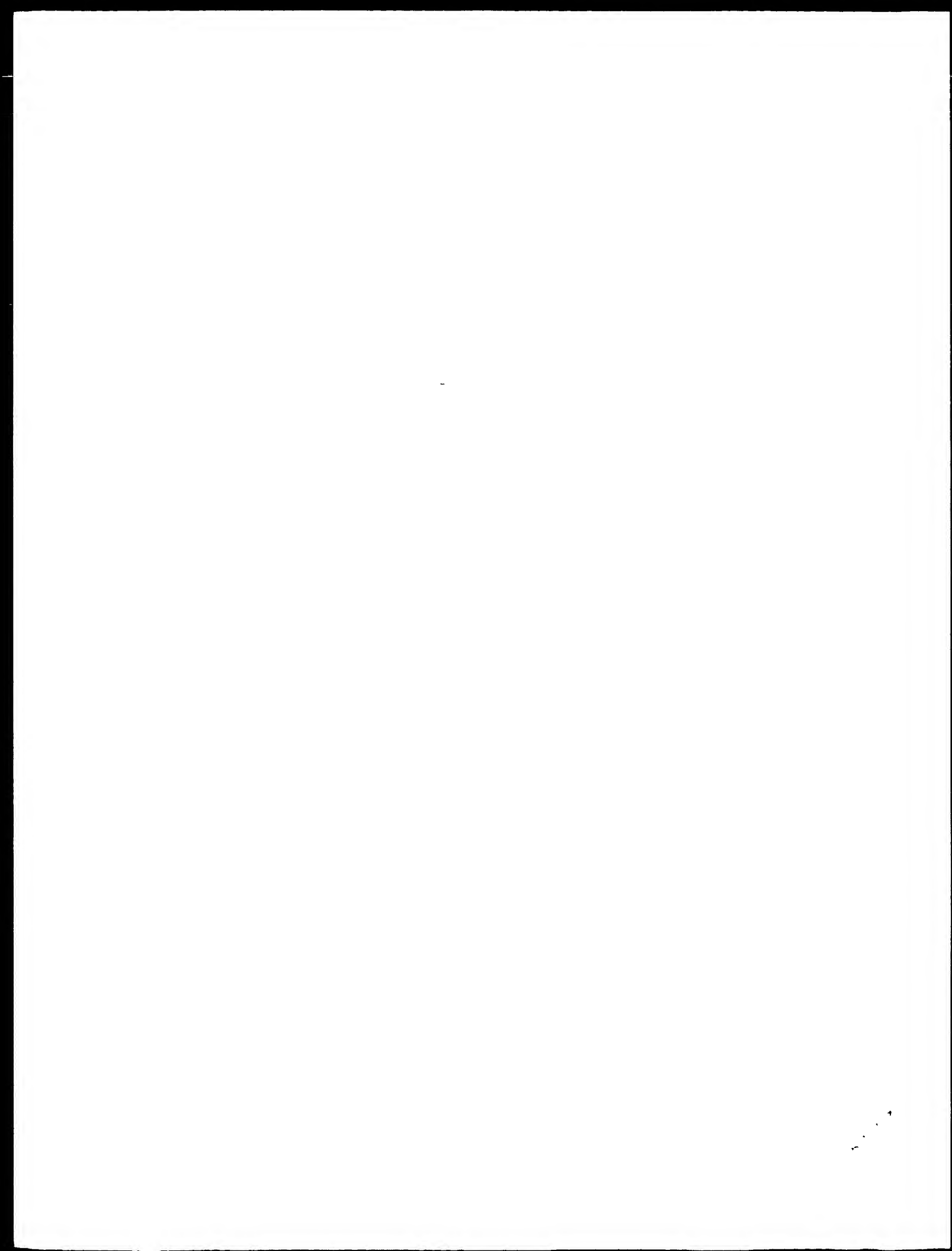
Query Match 0.0%; Score 0; DB 1; Length 5;

Best Local Similarity 0.0%; Pred. No. 1.1e+05;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 X 2

Db 2 S 2

Search completed: February 12, 2003, 10:51:53  
Job time : 12 secs





GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 12, 2003, 10:48:54 ; Search time 28 Seconds  
(without alignments)  
36.794 Million cell updates/sec

Title: US-09-403-440A-1  
Perfect score: 23  
Sequence: 1 FXXLW 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 3

Minimum DB seq length: 5  
Maximum DB seq length: 5

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database :

SPTREMBL\_21.\*  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phase.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_virus.\*  
16: sp\_bacteriap.\*  
17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6	26.1	5	13 P83308	P83308 gallus gall
2	2	8.7	5	2 P83073	P83073 bacillus ce
3	2	8.7	5	10 Q99007	Q99007 hordeum vul

#### ALIGNMENTS

RESULT 1  
ID P83308 PRELIMINARY; PRT; 5 AA.  
AC P83308;  
DT 01-JUN-2002 (TREMREL. 21, Created)  
DT 01-JUN-2002 (TREMREL. 21, Last sequence update)  
DT 01-JUN-2002 (TREMREL. 21, Last annotation update)  
DE FMRamide-like neuropeptide (LPLRF-amide).

OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE, AND SYNTHESIS.  
RC TISSUE=BRAIN;  
RX PubMed=6137771;  
RA Dockray G.J., Reeve J.R. Jr., Shively J., Gayton R.J., Barnard C.S.;  
RT "A novel active pentapeptide from chicken brain identified by  
RT antibodies to FMRamide."  
RL Nature 305:328-330(1983).  
CC -|- FUNCTION: MAY FUNCTION AS A NEUROTRANSMITTER OR MODULATOR.  
CC -|- SIMILARITY: BELONGS TO THE FARP (FMRAMIDE RELATED PEPTIDE)  
CC FAMILY.  
KW Neuropeptide.  
SQ SEQUENCE 5 AA; 645 MW; 69D4073767400000 CRC64;

Query Match 26.1%; Score 6; DB 13; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6.7e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 F 1  
Db 5 F 5

#### RESULT 2

ID P83073 PRELIMINARY; PRT; 5 AA.  
AC P83073;  
DT 01-OCT-2001 (TREMREL. 18, Created)  
DT 01-OCT-2001 (TREMREL. 18, Last sequence update)  
DT 01-OCT-2001 (TREMREL. 18, Last annotation update)  
DE 88 kDa protein (Fragment).  
OS Bacillus cereus.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;  
OC Bacillaceae; Bacillus.  
OX NCBI\_TaxID=1396;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=NCIMB 11796;  
RA Browne N., Dows B.C.A.;  
RL Submitted (JUL-2001) to the SWISS-PROT data bank.  
FT NON\_TER 5 5  
SQ SEQUENCE 5 AA; 623 MW; 6B01AAA336F00000 CRC64;

Query Match 8.7%; Score 2; DB 2; Length 5;  
Best Local Similarity 0.0%; Pred. No. 6.7e+05;  
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 L 4  
Db 1 M 1

#### RESULT 3

ID Q99007 PRELIMINARY; PRT; 5 AA.  
AC Q99007;  
DT 01-NOV-1996 (TREMREL. 01, Created)  
DT 01-NOV-1996 (TREMREL. 01, Last sequence update)  
DT 01-NOV-1998 (TREMREL. 08, Last annotation update)  
DE Alpha-amylase (EC 3.2.1.1) (Fragment).  
GN AMY1.  
OS Hordeum vulgare (Barley).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;  
OC Triticeae; Hordeum.  
OX NCBI\_TaxID=4513;  
RN [1]  
RP SEQUENCE FROM N.A.

RC STRAIN=HIMALAYA; TISSUE=ALEURONE LAYER;  
 RX MEDLINE=91329704; PubMed=1831055;  
 RA Jacobsen J.V., Close T.J.;  
 RT "Control of transient expression of chimaeric genes by gibberellic  
 RT acid and abscisic acid in protoplasts prepared from mature barley  
 RT aleurone layers.";  
 RL Plant Mol. Biol. 16:713-721 (1991).  
 CC -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-ALPHA-GLUCOSIDIC  
 CC LINKAGES IN OLIGOSACCHARIDES AND POLYASACCHARIDES.  
 CC -!- COPACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.  
 CC -!- MISCELLANEOUS: THERE ARE AT LEAST 4 TYPES OF ALPHA-AMYLASE IN  
 CC BARLEY.  
 DR ENBL; X54643; CAA38455.1; --  
 KW Hydrolase; Glycosidase; Carbohydrate metabolism; Seed; Germination;  
 KW Calcium; Multigene family.  
 FT NON TER 5 5  
 SQ SEQUENCE 5 AA; 600 MW; 61E3344DD6F00000 CRC64;

Query Match 8.7%; Score 2; DB 10; Length 5;  
 Best Local Similarity 0.0%; Pred. No. 6.7e+05;  
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 L 4  
 Db 1 M 1

Search completed: February 12, 2003, 10:52:27  
 Job time : 28 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 12, 2003, 10:45:58 ; Search time 80 Seconds  
(without alignments)  
8.328 Million cell updates/sec

Title: US-09-403-440A-1

Perfect score: 23

Sequence: 1 FXLWM 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 13629

Minimum DB seq length: 5

Maximum DB seq length: 5

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : A\_Geneseq 101002.\*

	1:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
	2:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
	3:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
	4:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
	5:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
	6:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
	7:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
	8:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
	9:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
	10:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
	11:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
	12:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
	13:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
	14:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
	15:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
	16:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
	17:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
	18:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
	19:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
	20:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
	21:	/SID22/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
	22:	/SID22/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
	23:	/SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	87.0	5	20	AA1933038
2	20	87.0	5	21	AA1933038
3	19	82.6	5	17	AA197808
4	19	82.6	5	17	AA198911
5	19	82.6	5	17	AA199912
6	19	82.6	5	21	AA1958280
7	19	82.6	5	23	AA1958280
8	17	73.9	5	13	AA1929438
9	17	73.9	5	13	AA1929438
10	17	73.9	5	15	AA1929438

11	73.9	5	15	AA1929438	Endothelin C-termi
12	73.9	5	15	AA1929438	Endothelin C-termi
13	65.2	5	12	AA193339	Endothelin antag
14	65.2	5	12	AA194025	Endothelin antag
15	65.2	5	12	AA193909	Endothelin antag
16	65.2	5	14	AA1938437	Endothelin recepto
17	65.2	5	14	AA1938438	Endothelin recepto
18	65.2	5	14	AA1938436	Endothelin recepto
19	65.2	5	14	AA1938436	Endothelin recepto
20	65.2	5	14	AA1938436	Endothelin recepto
21	65.2	5	14	AA1938436	Endothelin recepto
22	65.2	5	14	AA1938436	Endothelin recepto
23	65.2	5	14	AA1938436	Endothelin recepto
24	65.2	5	14	AA1938436	Endothelin recepto
25	65.2	5	14	AA1938436	Endothelin recepto
26	65.2	5	14	AA1938436	Endothelin recepto
27	65.2	5	14	AA1938436	Endothelin recepto
28	65.2	5	14	AA1938436	Endothelin recepto
29	65.2	5	15	AA1938436	Endothelin metal c
30	65.2	5	15	AA1938436	Cyclic peptide whi
31	65.2	5	15	AA1938436	Monomeric peptide
32	65.2	5	15	AA1938436	TAN-1462A - cyclic
33	65.2	5	15	AA1938436	TAN-1462B - cyclic
34	65.2	5	15	AA1938436	TAN-1477K - cyclic
35	65.2	5	15	AA1938436	TAN-1477K - cyclic
36	65.2	5	15	AA1938436	CENP-B protein res
37	65.2	5	15	AA1938436	Endothelin cyclic
38	65.2	5	15	AA1938436	Cyclic pentapeptid
39	65.2	5	15	AA1938436	Cyclic pentapeptid
40	65.2	5	15	AA1938436	Cyclic pentapeptid
41	65.2	5	15	AA1938436	Cyclic pentapeptid
42	65.2	5	15	AA1938436	Cyclic pentapeptid
43	65.2	5	15	AA1938436	Endothelin cyclic
44	65.2	5	15	AA1938436	Endothelin cyclic
45	65.2	5	15	AA1938436	Cyclic peptide lig
46	65.2	5	16	AA1938436	DP-118 homologue 3
47	65.2	5	16	AA1938436	Melanin pigmentati
48	65.2	5	16	AA1938436	Melanin pigmentati
49	65.2	5	16	AA1938436	Melanin pigmentati
50	65.2	5	16	AA1938436	Cyclic endothelin
51	65.2	5	16	AA1938436	Cyclic endothelin
52	65.2	5	16	AA1938436	Cyclic endothelin
53	65.2	5	16	AA1938436	Cyclic endothelin
54	65.2	5	16	AA1938436	Endothelin antag
55	65.2	5	16	AA1938436	Endothelin antag
56	65.2	5	16	AA1938436	Endothelin sequenc
57	65.2	5	17	AA1938436	Cyclic pentapeptid
58	65.2	5	18	AA1938436	Targetting conjuga
59	65.2	5	18	AA1938436	Targetting conjuga
60	65.2	5	18	AA1938436	Targetting conjuga
61	65.2	5	18	AA1938436	Targetting conjuga
62	65.2	5	18	AA1938436	Targetting conjuga
63	65.2	5	18	AA1938436	Conjugating cyclic
64	65.2	5	18	AA1938436	Low density lipopr
65	65.2	5	18	AA1938436	Low density lipopr
66	65.2	5	18	AA1938436	Low density lipopr
67	65.2	5	19	AA1938436	Human microtubule
68	65.2	5	19	AA1938436	Endothelin recepto
69	65.2	5	19	AA1938436	Cyclic peptide whi
70	65.2	5	19	AA1938436	Cyclic peptide whi
71	65.2	5	20	AA1938436	Non-crosslinked pr
72	65.2	5	20	AA1938436	Acetyl choline (mu
73	65.2	5	20	AA1938436	Antigenic peptide
74	65.2	5	20	AA1938436	Fibrinogen peptide
75	65.2	5	21	AA1938436	T20/DP178 peptide
76	65.2	5	21	AA1938436	T20/DP178 peptide
77	65.2	5	21	AA1938436	Protein encoded by
78	65.2	5	21	AA1938436	HIV-1 isolate LAI
79	65.2	5	21	AA1938436	EGIII-like cellula
80	65.2	5	21	AA1938436	Endothelin recepto
81	65.2	5	21	AA1938436	Endothelin recepto
82	65.2	5	21	AA1938436	Endothelin recepto
83	65.2	5	21	AA1938436	Hepatitis GB virus

84 15 65.2 5 21 AAY97920 Endothelin recepto  
 85 15 65.2 5 21 AAY97921 Endothelin recepto  
 86 15 65.2 5 21 AAY97922 Endothelin recepto  
 87 15 65.2 5 21 AAY97935 Endothelin recepto  
 88 15 65.2 5 21 AAY97936 Endothelin recepto  
 89 15 65.2 5 21 AAY97937 Endothelin recepto  
 90 15 65.2 5 21 AAY97950 Endothelin recepto  
 91 15 65.2 5 21 AAY97951 Endothelin recepto  
 92 15 65.2 5 21 AAY97952 Endothelin recepto  
 93 15 65.2 5 21 AAY85099 HBV surface antige  
 94 15 65.2 5 21 AAY85100 HBV surface antige  
 95 15 65.2 5 21 AAY85101 HBV surface antige  
 96 15 65.2 5 21 AAY85102 HBV surface antige  
 97 15 65.2 5 21 AAY85103 HBV surface antige  
 98 15 65.2 5 21 AAY89380 Core polypeptide f  
 99 15 65.2 5 22 AAM47406 Peptide #36 for il  
 100 15 65.2 5 22 ABB00788 Viral DPI78/107-11

## ALIGNMENTS

RESULT 1  
 AAY33038  
 ID AAY33038 standard; peptide; 5 AA.

XX AC AAY33038;  
 XX 03-NOV-1999 (first entry)  
 XX DE Carbohydrate antigen peptide mimotope 11.  
 XX Mimotope; antigen; carbohydrate; antibody; mimic; vaccine; adjuvant;  
 KW tumour immunity; cancer therapy; antibacterial; immune response;  
 KW immunogenicity; anti-idiotype; T cell response manipulation.  
 XX Synthetic.  
 XX WO9940433-A1.  
 XX 12-AUG-1999.  
 XX 04-FEB-1999; 99WO-US02405.  
 XX 04-FEB-1998; 98US-0073690.  
 XX (UYPE-) UNIV PENNSYLVANIA.  
 XX Kieber-Emmons T;  
 XX WPI; 1999-527317/44.

XX Peptides and recombinant antibody mimics of carbohydrate antigens,  
 PT used for, e.g. treatment of cancer and infection

XX Claim 21; Page 72; 88pp; English.  
 XX This invention describes a novel method for preparing a peptide or  
 CC recombinant antibody, which mimics an antigenic carbohydrate. The  
 CC peptides and recombinant antibodies prepared to mimic antigenic  
 CC carbohydrates can be used to enhance binding of anti-antigenic  
 CC carbohydrate antibodies to the antigenic carbohydrate, e.g. as vaccine  
 CC adjuvants. The peptides can be used to inhibit binding of a ligand to a  
 CC receptor, which is an antigenic carbohydrate. The methods are used to  
 CC prepare the peptides and antigenic antibodies, which mimic the antigenic  
 CC carbohydrates. Carbohydrate-conjugate vaccines could be used in tumour  
 CC immunity and cancer therapy. The peptides and antibodies can also be  
 CC used as antibacterials. Peptides that mimic carbohydrate antigens can be  
 CC formulated to develop a longer lasting immune response. Other advantages  
 CC of the peptide mimics are; (1) the chemical composition and purity of  
 CC synthesized peptides can be precisely defined; (2) the immunogenicity  
 CC of the peptides can be significantly enhanced by polymerization or  
 CC addition of relatively small carrier molecules that reduce the total

CC amount of antigen required for immunization; (3) peptide synthesis may  
 CC be more practical than synthesis of carbohydrate-protein conjugates or  
 CC the production of anti-idiotypes; (4) peptide mimicking sequences can  
 CC be engineered into DNA plasmids for DNA vaccination to further  
 CC manipulate T cell responses. AAY33028-Y33087 represent the carbohydrate  
 CC antigen peptide mimotopes described in the invention.

XX SQ Sequence 5 AA;

Query Match 87.0%; Score 20; DB 20; Length 5;  
 Best Local Similarity 60.0%; Pred. No. 7.8e+05;  
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 FXLW 5  
 | |  
 Db 1 FSLW 5

RESULT 2  
 AAB07280  
 ID AAB07280 standard; peptide; 5 AA.

XX AC AAB07280;  
 XX 17-OCT-2000 (first entry)  
 XX DE Motif binding to anti-Lewis antigen antibody BR55-2.  
 XX Human; peptide-mimetic; tumour metastasis; E-selectin;  
 KW adhesion molecule; Lewis antigen; anti-adhesion therapy.  
 XX Unidentified.  
 OS WO200027420-A1.  
 XX 18-MAY-2000.  
 XX 05-NOV-1999; 99WO-US26277.  
 XX 06-NOV-1998; 98US-0107478.  
 XX (WIST-) WISTAR INST ANATOMY & BIOLOGY.  
 XX (UYPE-) UNIV PENNSYLVANIA.  
 XX Blaszczyk-Thurin M, Kieber-Emmons T;  
 XX WPI; 2000-376309/32.  
 XX Peptidomimetics of carbohydrate Lewis ligands useful for modulating  
 PT inflammation, metastasis and angiogenesis -  
 XX Example 5; Page 37; 107pp; English.

XX Tumour metastasis requires detachment of malignant cells from the primary  
 CC tumour, penetration of blood or lymph vessels and attachment to the  
 CC endothelium of distant organs, ultimately resulting in the formation of  
 CC new tumours. The selectin family of adhesion molecules is implicated in  
 CC this process. E-selectin is a calcium-dependent molecule expressed by  
 CC activated vascular endothelium. E-selectins bind to glycoconjugates  
 CC carrying a terminal tetrasaccharide Lewis antigen, which are found on  
 CC tumour cell surfaces. One such Lewis antigen is Lewis Y (LeY). The  
 CC binding of selectin molecules to their ligands is thought to be an  
 CC important step in metastasis. Therefore, inhibition of  
 CC E-selectin-dependent carbohydrate-mediated interactions is thought to  
 CC be a target for anti-cancer therapy. The present sequence is a non  
 CC planar-X-planar type motif. This motif is thought to bind to anti-LeY  
 CC antibody BR55-2. BR55-2 is a peptide-mimetic of E-selectins. Peptides  
 CC that block E-selectin-LeY binding and therefore adhesion of tumour cells  
 CC and leukocytes to endothelial cells inhibit metastasis.

XX SQ Sequence 5 AA;

Query Match 87.0%; Score 20; DB 21; Length 5;

```

Best Local Similarity 60.0%; Pred. No. 7.8e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXLW 5
   |  |  |
Db 1 FSLWL 5

RESULT 3
AAW17808
ID AAW17808 standard; peptide; 5 AA.
XX
AC AAW17808;
XX
DT 07-JUL-1997 (first entry)
XX
DE Cyclic pentapeptide #24 used in LH-RH receptor antagonist.
XX
KW Luteinising hormone releasing hormone receptor; LH-RH; antagonist;
KW sex-hormone; human; veterinary medicine; cancer; prostate; uterus;
KW breast; pituitary; prostatic; endometriosis; hysteromyoma;
KW precocious puberty; amenorrhoea; premenstrual syndrome; cyclic;
KW multilocular ovarian syndrome; comedo; pregnancy; contraception;
KW ovulation; menstrual cycle; oestrus; meat quality; growth; spawning;
KW fish; testosterone; superagonist; leuprorelin acetate.
XX
FH Key Location/Qualifiers
FT Modified-site 1 /note= "Joined via a peptide linkage to Trp5"
FT Modified-site 2 /note= "N-pToluenesulphonylarginine, D-form residue"
FT Misc-difference 4 /note= "D-form residue"
FT Modified-site 5 /note= "Joined via a peptide linkage to Phe1"
FT
FT
XX Synthetic.
XX
PN WO9634012-A1.
XX
PD 31-OCT-1996.
XX
PF 25-APR-1996; 96WO-JP01140.
XX
PR 09-MAY-1995; 95JP-0110933.
PR 28-APR-1995; 95JP-0106775.
XX
PA (TAKE ) TAKEDA CHEM IND LTD.
XX
PI Furuya S, Kato K, Kitada C;
XX
XX WPI; 1996-497569/49.
XX
Cyclic penta-peptide(s), some new, as LH-RH receptor antagonists -
used to treat or prevent sex hormone dependent disorders, e.g.
cancer, also for control of pregnancy and menstruation and to
improve meat quality in animals
XX
Example 44; Page 172; 198pp; English.
XX
CC This peptide represents a cyclic peptide which is included in the
CC luteinising hormone releasing hormone (LH-RH) receptor antagonist
CC composition of the invention. Peptides such as this are used to
CC prevent or treat sex-hormone dependent disorders in human or veterinary
CC medicine, esp. cancers (of the prostate, uterus, breast or pituitary),
CC prostatic, endometriosis, hysteromyoma or precocious puberty, but
CC also amenorrhoea, premenstrual syndrome, multilocular ovarian syndrome,
CC comedo, etc.; also to control pregnancy (contraception for men or women,
CC also to induce ovulation) and the menstrual cycle. They are also used
CC to control oestrus in animals, to improve meat quality and control
CC growth, and to promote spawning in fish. They may also inhibit the
CC transient increase in testosterone blood levels caused by admin. of
CC superagonists such as leuprorelin acetate.

```

---

```

XX
SQ Sequence 5 AA;
Query Match 82.6%; Score 19; DB 17; Length 5;
Best Local Similarity 60.0%; Pred. No. 7.8e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXLW 5
   |  |  |
Db 1 FFLWL 5

RESULT 4
AAR89911
ID AAR89911 standard; peptide; 5 AA.
XX
AC AAR89911;
XX
DT 10-SEP-1996 (first entry)
XX
DE p53/MDM2 binding inhibitor #1.
XX
KW Interference; binding; p53; tumour suppressor; MDM2; oncogene; cancer;
KW inhibition; diagnosis; treatment; malignancy; consensus.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 2 /note= Any amino acid
FT Misc-difference 3 /note= Any amino acid
FT
FT
XX WO9602642-A1.
XX
PD 01-FEB-1996.
XX
PF 20-JUL-1995; 95WO-GB01719.
XX
PR 19-APR-1995; 95US-0424957.
PR 20-JUL-1994; 94US-0277660.
XX
PA (UYDU-) UNIV DUNDEE.
XX
PI Lane DP, Pickesley SM;
XX
XX WPI; 1996-105905/11.
XX
New cpds. which interfere with binding of MDM2 and p53 - used to
develop prods. for use in the diagnosis and treatment of cancer and
other malignancies
XX
Claim 4; Page 29; 46pp; English.
XX
CC New peptides of the invention which interfere with the binding of the
CC p53 tumour suppressor protein and the MDM2 oncogene protein contain
CC the peptide sequences AAR89911-3 which form part of the p53 protein
CC binding motif between amino acids 16-33 (AAR89914). The peptides were
CC identified by modifying the p53 consensus binding sequence by
CC substitution of an Alanine at each pos. and identifying which amino
CC acid changes altered binding to expressed MDM2. The peptides and
CC methods of identifying similar inhibitory peptides can be used to
CC diagnose and treat e.g. cancer and other malignancies.
XX
SQ Sequence 5 AA;
Query Match 82.6%; Score 19; DB 17; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXLW 5
   |  |  |
Db 1 FXXLW 5

```

<p> <b>RESULT 5</b>  <b>AAR89912</b>  ID AAR89912 standard; peptide; 5 AA.  XX AC AAR89912;  XX DT 10-SEP-1996 (first entry)  XX  XX p53/MDM2 binding inhibitor #2.  XX  XX Interference; binding; p53; tumour suppressor; MDM2; oncogene; cancer;  KW inhibition; diagnosis; treatment; malignancy; consensus.  XX  XX Synthetic.  XX  XX Key Location/Qualifiers  FT Misc-difference 2 /note= Any amino acid  FT  XX WO9602642-A1.  XX  XX 01-FEB-1996.  XX  XX 20-JUL-1995; 95WO-CB01719.  XX  XX 19-APR-1995; 95US-0424957.  PR 20-JUL-1994; 94US-0277660.  XX  XX (UYDU-) UNIV DUNDEE.  XX  XX Lane DP, Picksley SM;  PI  XX WPI; 1996-105905/11.  XX  XX New cpds. which interfere with binding of MDM2 and p53 - used to  PT develop prods. for use in the diagnosis and treatment of cancer and  PT other malignancies  PT  XX Claim 5; Page 29; 46pp; English.  PS  XX  XX New peptides of the invention which interfere with the binding of the  CC p53 tumour suppressor protein and the MDM2 oncogene protein contain  CC the peptide sequences AAR89911-3 which form part of the p53 protein  CC binding motif between amino acids 16-33 (AAR89914). The peptides were  CC identified by modifying the p53 consensus binding sequence by  CC substitution of an Alanine at each pos. and identifying which amino  CC acid changes altered binding to expressed MDM2. The peptides and  CC methods of identifying similar inhibitory peptides can be used to  CC diagnose and treat e.g. cancer and other malignancies.  XX  XX Sequence 5 AA;  SQ </p>	<p> Nuclear receptor; p160 coactivator; NR-box; coactivator binding domain;  NR; AF2 transactivation domain; wild-type; thyroid hormone receptor; TR;  KW retinoid receptor; RAR; RXR; peroxisome receptor; PPAR;  KW vitamin D receptor; VDR; oestrogen receptor; ER; glucocorticoid receptor;  KW GR; progesterin receptor; PR; mineralocorticoid receptor; MR;  KW androgen receptor; AR; Grip-1; Tif2; NcoA-2; RAC3; AIB1; TRAM-1; p/CIP;  KW SRC1; breast cancer; prostate cancer; cardiac arrhythmia; infertility;  KW osteoporosis; hyperthyroidism; hypercholesterolaemia; obesity;  KW protein_coordiates.  XX  XX Homo sapiens.  OS  XX Key Location/Qualifiers  FH Misc-difference 2 /label= Xaa  FT /note= "Xaa = any amino acid"  FT  FT Misc-difference 3 /label= Xaa  FT /note= "Xaa = any amino acid"  XX  XX WO9960014-A2.  XX  XX 25-NOV-1999.  XX  XX 30-MAR-1999; 99WO-US06899.  XX  XX 30-MAR-1998; 98US-0079956.  PR 16-DEC-1998; 98US-0113146.  XX  XX (REGC ) UNIV CALIFORNIA.  XX  XX Baxter JD, Darimont B, Feng W, Fletterick R, Kushner PJ;  PI Wagner RL, West BL, Yamamoto KR;  XX  XX WPI; 2000-072429/06.  XX  XX Identifying modulators of nuclear receptor coactivator binding useful  PT for generating new compounds which distinguish nuclear receptor  PT isoforms -  XX  XX Example 14B; Page 12; 281pp; English.  PS  XX  XX The invention relates a method of identification of a compound that  CC modulates coactivator binding to a nuclear receptor. The method  CC comprises modelling test compounds that fit spatially into a nuclear  CC receptor (NR) coactivator binding site of interest using an atomic  CC structural model of a nuclear receptor coactivator binding site. The  CC test compounds are screened by their ability to bind to an NR  CC coactivator binding site, leading to the identification of a compound  CC which modulates coactivator binding. Nuclear receptors are a superfamily  CC of hormone/ligand activated transcription factors, and includes thyroid  CC hormone receptors (TRs), retinoid receptors (RARs and RXRs), peroxisome  CC receptors (PPARs and XPARs), vitamin D receptors (VDRs), oestrogen  CC receptors (ERs), glucocorticoid receptors (GRs), progesterin receptors  CC (PRs), mineralocorticoid receptors (MRs), androgen receptors (ARs) and  CC isooctanoic acid receptors (IRs). These receptors, in addition to binding their  CC cognate ligand, also bind coactivator proteins that are involved in  CC receptor function, for example NRs can stimulate transcription in  CC response to hormone binding by recruiting coactivator proteins to the  CC promoters of responsive genes. Coactivators of the p160 family mediate  CC activity of a transcriptional activation domain, AF2, that is part of the  CC nuclear receptor's ligand binding domain. The method may be used to  CC identify an agonist or antagonist of coactivator binding to a nuclear  CC receptor. The methods can also be used to identify residues which  CC comprise a coactivator binding site of a nuclear receptor of interest.  CC The methods are applicable to generating new compounds that distinguish  CC nuclear receptor isoforms. This can facilitate generation of either  CC tissue-specific or function-specific compounds. Nuclear receptors have  CC been implicated in a variety of medical disorders, including breast  CC cancer, prostate cancer, cardiac arrhythmia, infertility, osteoporosis,  CC hyperthyroidism, hypercholesterolaemia and obesity. Sequences AAY58282-  CC AAY58302 represent the regions (NR-boxes 1-3) of p160 coactivator  CC proteins which interact with the nuclear receptor coactivator binding </p>
---	---

CC sites (AAV58307-Y58328). The NR coactivator binding sites comprise two  
 CC regions of the NR; Helices 3-6 (H3-H6), and helix 12 (H12). The  
 CC coactivator NR-boxes all share a consensus sequence LXLL (AAV58278),  
 CC with the NR-box 2 motifs sharing the consensus motif ILXLL (AAV58279).  
 CC Sequences AAV58280-Y58281 represent the hydrophobic interaction motifs of  
 CC p53 and Vp16 used in an exemplification of the invention. Sequences  
 CC AAV58329-Y58240 represent mutant versions of the human Grip-1 NR-box 2  
 CC sequence (AAV58283), and sequences AAV58341-Y58353 represent mutant  
 CC versions of NR coactivator binding sites, used in exemplifications of the  
 CC invention.

XX Sequence 5 AA;

Query Match 82.6%; Score 19; DB 21; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXLW 5  
 |||||  
 DB 1 FXXLW 5

RESULT 7  
 AAO20822  
 ID AAO20822 standard; Peptide; 5 AA.

XX AC AAO20822;

XX DT 08-JUL-2002 (first entry)

XX DE Hydrophobic interaction FxxLW motif of p53.

XX KW Cytostatic; cardiovascular; antiarrhythmic; vasotropic; osteopathic;  
 KW endocrinal; antilipaeamic; anorectic; coactivator binding; lead compound;  
 KW nuclear receptor; NR; BS; peptidomimetic; scaffold; breast cancer;  
 KW nuclear receptor-based disorder; prostate cancer; cardiac arrhythmia;  
 KW infertility; osteoporosis; hyperthyroidism; hypercholesterolaemia;  
 KW obesity; FxxLW motif; p53; Glucocorticoid; GR; protein co-ordinate data.  
 XX Unidentified.

XX Key Location/Qualifiers

FT Misc-difference 2 /label= unknown

FT /note= "Xaa is unknown"

FT Misc-difference 3

FT /label= unknown

FT /note= "Xaa is unknown"

XX WO200202488-A2.

XX 10-JAN-2002.

XX 29-JUN-2001; 2001WO-US20969.

XX 30-JUN-2000; 2000US-0609361.

XX (REGC ) UNIV CALIFORNIA.

XX PI Guy RK, Baxter JD, Darimont B, Feng W, Fletterick RJ, Kushner PJ;  
 PI Wagner RL, West BL, Yamamoto KK, Geistlinger TR, Arnold JR;  
 PI Kuntz ID;

XX WPI; 2002-315164/35.

XX Method for identifying agonist and antagonist compounds used for  
 PT modulating nuclear receptor coactivator binding, which are useful in  
 PT treating nuclear receptor-based disorders e.g. breast cancer,  
 PT infertility, or hyperthyroidism -

XX Example 14; Page 15; 307pp; English.

XX The invention relates to a method for identifying a compound that

CC modulates coactivator binding to a nuclear receptor (NR). The method  
 CC comprises modelling test compounds that fit electrostatically into an NR  
 CC coactivator binding site (BS) using an appropriate atomic structural  
 CC model of (BS); screening the test compounds in an assay characterised by  
 CC binding of a test compound to (BS); and identifying a library or test  
 CC compound that modulates coactivator binding to the NR. The methods of the  
 CC invention are useful for identifying peptides, peptidomimetics, or small  
 CC natural or synthetic organic molecules that modulate nuclear receptor  
 CC activity, particularly new lead compounds, scaffolds and combinatorial  
 CC libraries. The methods are used in selecting and characterising structure  
 CC /function relationships of natural or synthetic coactivator compounds,  
 CC which are useful in treating nuclear receptor-based disorders e.g. breast  
 CC cancer, prostate cancer, cardiac arrhythmia, infertility, osteoporosis,  
 CC hyperthyroidism, hypercholesterolaemia or obesity. This sequence  
 CC represents the hydrophobic interaction FxxLW motif of p53. The  
 CC glucocorticoid (GR) nuclear receptor of the invention is able to interact  
 CC with peptides containing this motif.

XX SQ Sequence 5 AA;

Query Match 82.6%; Score 19; DB 23; Length 5;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXLW 5  
 |||||  
 DB 1 FXXLW 5

RESULT 8

AAAR29438

ID AAR29438 standard; peptide; 5 AA.

XX AC AAR29438;

XX DT 13-APR-1993 (first entry)

XX DE Endothelin antagonist peptide.

XX KW Hypertension; myocardial infarction; congestive heart failure;  
 KW endotoxic shock; subarachnoid haemorrhage; asthma; arrhythmias;  
 KW acute renal failure; preclampsia; diabetes; metabolic;  
 KW endocrinological; neurological; disorders.

XX OS Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1

FT /note= " (Ac- or 1-adamantyl acetic acid) - D-Phe"

XX WO9220706-A.

XX 26-NOV-1992.

XX 24-APR-1992; 92WO-US03408.

XX 16-MAY-1991; 91US-0701274.

XX 18-DEC-1991; 91US-0809746.

XX (WARN ) WARNER LAMBERT CO.

XX Cody WL, Depue P, Doherty AM, Taylor MD;

XX WPI; 1992-415706/50.

XX New peptide(s) used as endothelin antagonists - for treating  
 PT hypertension, metabolic and endocrine disorders, heart failure,  
 PT diabetes, asthma, neurological disorders, etc.

XX Claim 5; Page 94; 116pp; English.

XX The peptide is an endothelin antagonist useful in controlling  
 CC hypertension, myocardial infarction, congestive heart failure,

CC endotoxemic shock, subarachnoid haemorrhage, asthma, arrhythmias,  
CC acute renal failure, pre-eclampsia, diabetes and metabolic,  
CC endocrinological and neurological disorders. Administration is oral  
CC parenteral or by inhalation in doses of 0.01-20 (esp. 0.01-10) mg/kg/  
CC day. It may be prepared by conventional peptide synthesis.  
XX  
SQ Sequence 5 AA;  
  
Query Match 73.9%; Score 17; DB 13; Length 5;  
Best Local Similarity 40.0%; Pred. No. 7.8e+05;  
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 FXXLM 5  
Db 1 FDIW 5  
  
RESULT 9  
AAR29448  
ID AAR29448 standard; peptide; 5 AA.  
XX  
AC AAR29448;  
XX  
DT 13-APR-1993 (first entry)  
XX  
DE Endothelin antagonist peptide.  
XX  
KW Hypertension; myocardial infarction; congestive heart failure;  
KW endotoxemic shock; subarachnoid haemorrhage; asthma; arrhythmias;  
KW acute renal failure; pre-eclampsia; diabetes; metabolic;  
KW endocrinological; neurological; disorders.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 1 /note= "Ac-D-Phe"  
XX  
XX WO9220706-A.  
XX  
PD 26-NOV-1992.  
XX  
PF 24-APR-1992; 92WO-US03408.  
XX  
PR 16-MAY-1991; 91US-0701274.  
PR 18-DEC-1991; 91US-0809746.  
XX  
XX (WARN ) WARNER LAMBERT CO.  
XX  
XX Cody WL, Depue P, Doherty AM, Taylor MD;  
XX WPI; 1992-415706/50.  
XX  
XX New peptide(s) used as endothelin antagonists - for treating  
XX hypertension, metabolic and endocrine disorders, heart failure,  
XX diabetes, asthma, neurological disorders, etc.  
XX  
XX Claim 5; Page 95; 116pp; English.  
XX  
XX The peptide is an endothelin antagonist useful in controlling  
XX hypertension, myocardial infarction, congestive heart failure,  
XX endotoxemic shock, subarachnoid haemorrhage, asthma, arrhythmias,  
XX acute renal failure, pre-eclampsia, diabetes and metabolic,  
XX endocrinological and neurological disorders. Administration is oral  
XX parenteral or by inhalation in doses of 0.01-20 (esp. 0.01-10) mg/kg/  
XX day. It may be prepared by conventional peptide synthesis.  
XX  
SQ Sequence 5 AA;  
  
Query Match 73.9%; Score 17; DB 13; Length 5;  
Best Local Similarity 40.0%; Pred. No. 7.8e+05;  
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 FXXLM 5  
Db 1 FDIW 5  
  
RESULT 10  
AAR69220  
ID AAR69220 standard; peptide; 5 AA.  
XX  
AC AAR69220;  
XX  
DT 06-MAR-1995 (first entry)  
XX  
DE Endothelin C-terminal peptide analog, useful as antagonist.  
XX  
KW Endothelin; ET-1; receptor; antagonist.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 1 /note= "Ac-D-Phe"  
XX  
XX WO9414843-A.  
XX  
PD 07-JUL-1994.  
XX  
PF 17-DEC-1993; 93WO-US12377.  
PR 21-DEC-1992; 92US-0995480.  
XX  
XX (WARN ) WARNER LAMBERT CO.  
XX  
XX Cody WL, Depue P, Doherty AM, He JX, Taylor MD;  
XX WPI; 1994-234617/28.  
XX  
XX New hexapeptide derivs. inhibiting endothelin - for treatment of  
XX e.g. renal failure, hypertension, asthma, restenosis, angina,  
XX cancer etc.  
XX  
XX Claim 5; Page 119; 146pp; English.  
XX  
XX Novel antagonists of endothelin are claimed which are C-terminal  
XX hexapeptides and analogs of ET-1. The first (N-terminal) amino acid  
XX of the new peptides has D-configuration. The peptides are claimed  
XX generically. The present peptide is a specifically claimed example  
XX of the generic compounds.  
XX The peptides are useful for treating hypertension, metabolic and  
XX endocrine disorders, congestive heart failure, myocardial infarction,  
XX endotoxemic shock, subarachnoid haemorrhage, arrhythmia, asthma, acute  
XX and chronic renal failure, pre-eclampsia, diabetes, neurological  
XX disorders, pulmonary hypertension, ischaemic disease, ischaemic bowel  
XX disease, gastric mucosal damage, Raynaud's disease, restenosis,  
XX percutaneous transluminal coronary angioplasty, angina and cancer.  
XX  
SQ Sequence 5 AA;  
  
Query Match 73.9%; Score 17; DB 15; Length 5;  
Best Local Similarity 40.0%; Pred. No. 7.8e+05;  
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 FXXLM 5  
Db 1 FDIW 5  
  
RESULT 11  
AAR69260  
ID AAR69260 standard; peptide; 5 AA.  
XX  
AC AAR69260;  
XX



DT 07-MAR-1995 (first entry)  
 XX Endothelin C-terminal peptide analog, useful as antagonist.  
 XX Endothelin; ET-1; receptor; antagonist.  
 KW Synthetic.  
 OS  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 1  
 FT /note= "Ac-D-Phe"  
 XX  
 PN WO9414843-A.  
 XX  
 PD 07-JUL-1994.  
 XX  
 PF 17-DEC-1993; 93WO-US12377.  
 XX  
 PR 21-DEC-1992; 92US-0995480.  
 XX  
 PA (WARN ) WARNER LAMBERT CO.  
 XX  
 PI Cody WL, Depue P, Doherty AM, He JX, Taylor MD;  
 XX WPI; 1994-234617/28.  
 DR  
 XX New hexa:peptide derivs. inhibiting endothelin - for treatment of  
 FT e.g. renal failure, hypertension, asthma, restenosis, angina,  
 PT cancer etc.  
 FT  
 XX Claim 5; Page 120; 146pp; English.  
 PS  
 XX Novel antagonists of endothelin are claimed which are C-terminal  
 CC hexapeptides and analogs of ET-1. The first (N-terminal) amino acid  
 CC of the new peptides has D-configuration. The peptides are claimed  
 CC generically. The present peptide is a specifically claimed example  
 CC of the generic compounds.  
 CC The peptides are useful for treating hypertension, metabolic and  
 CC endocrine disorders, congestive heart failure, myocardial infarction,  
 CC endotoxic shock, subarachnoid haemorrhage, arrhythmia, asthma, acute  
 CC and chronic renal failure, preclampsia, diabetes, neurological  
 CC disorders, pulmonary hypertension, ischaemic disease, ischaemic bowel  
 CC disease, gastric mucosal damage, Raynaud's disease, restenosis,  
 CC percutaneous transluminal coronary angioplasty, angina and cancer.  
 XX  
 SQ Sequence 5 AA;  
 Query Match 73.9%; Score 17; DB 15; Length 5;  
 Best Local Similarity 40.0%; Pred. No. 7.8e+05;  
 Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 Qy 1 FXXLW 5  
 Db 1 FDFIW 5  
 RESULT 12  
 AAR69210  
 XX AAR69210 standard; peptide; 5 AA.  
 AC  
 XX  
 DT 06-MAR-1995 (first entry)  
 XX Endothelin C-terminal peptide analog, useful as antagonist.  
 DE Endothelin; ET-1; receptor; antagonist.  
 KW Synthetic.  
 OS  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 1  
 FT /note= "Ac-D-Phe or Ada-D-Phe, where Ada is

FT 1-adamantyl-acetyl"  
 XX WO9414843-A.  
 XX 07-JUL-1994.  
 XX 17-DEC-1993; 93WO-US12377.  
 XX 21-DEC-1992; 92US-0995480.  
 XX (WARN ) WARNER LAMBERT CO.  
 XX Cody WL, Depue P, Doherty AM, He JX, Taylor MD;  
 PI WPI; 1994-234617/28.  
 DR  
 XX New hexa:peptide derivs. inhibiting endothelin - for treatment of  
 FT e.g. renal failure, hypertension, asthma, restenosis, angina,  
 PT cancer etc.  
 FT  
 XX Claim 5; Page 118; 146pp; English.  
 PS  
 XX Novel antagonists of endothelin are claimed which are C-terminal  
 CC hexapeptides and analogs of ET-1. The first (N-terminal) amino acid  
 CC of the new peptides has D-configuration. The peptides are claimed  
 CC generically. The present peptide is a specifically claimed example  
 CC of the generic compounds.  
 CC The peptides are useful for treating hypertension, metabolic and  
 CC endocrine disorders, congestive heart failure, myocardial infarction,  
 CC endotoxic shock, subarachnoid haemorrhage, arrhythmia, asthma, acute  
 CC and chronic renal failure, preclampsia, diabetes, neurological  
 CC disorders, pulmonary hypertension, ischaemic disease, ischaemic bowel  
 CC disease, gastric mucosal damage, Raynaud's disease, restenosis,  
 CC percutaneous transluminal coronary angioplasty, angina and cancer.  
 XX  
 SQ Sequence 5 AA;  
 Query Match 73.9%; Score 17; DB 15; Length 5;  
 Best Local Similarity 40.0%; Pred. No. 7.8e+05;  
 Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 Qy 1 FXXLW 5  
 Db 1 FDFIW 5  
 RESULT 13  
 AAR13339  
 ID AAR13339 standard; peptide; 5 AA.  
 XX  
 AC AAR13339;  
 XX  
 DT 22-OCT-1991 (first entry)  
 XX Endothelin antagonist peptide WS 7338.  
 DE  
 XX  
 KW Cyclic.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 1  
 FT /label= D-allo, D-Val  
 FT Modified-site 3  
 FT /label= D-Trp  
 FT Modified-site 4  
 FT /label= D-Glu  
 XX  
 PN JP03130299-A.  
 XX  
 PD 04-JUN-1991.  
 XX  
 FT 08-AUG-1990; 90JP-0212952.

```

XX PR 31-AUG-1989; 89GB-0019726.
XX PA (FUJI ) FUJISAWA PHARM KK.
XX DR WPI; 1991-241129/33.
XX PT New peptide prepd. by culturing Streptomyces spp - used as
XX PT endothelin antagonist.
XX PS Claim 1; page 1; 15pp; Japanese.
XX CC The peptide is prepd. by cyclisation of the synthetic peptide.
CC CC The Trp residue at posn. 3 may be side chain protected with a lower
CC CC alkanoyl gp; the Glu residue at posn. 4 may be protected with an
CC CC al (lower) alkyl gp. An analogous natural peptide, WS 7338, may be
CC CC isolated from cultures of Streptomyces sp. no. 7338.
XX CC See also AAR13909 and AAR14025.
XX SQ Sequence 5 AA;
Query Match 65.2%; Score 15; DB 12; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 LW 5
DB 2 LW 3
RESULT 14
AAR14025
ID AAR14025 standard; peptide; 5 AA.
XX AC AAR14025;
XX XX 22-OCT-1991 (first entry)
XX DE Endothelin antagonist peptide.
XX CC Cyclic.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT Modified-site 1 /label= D-Val
FT Modified-site 3 /label= D-Trp
FT Modified-site 4 /label= D-Glu
XX PN JP03130299-A.
XX PD 04-JUN-1991.
XX PF 08-AUG-1990; 90JP-0212952.
XX PR 31-AUG-1989; 89GB-0019726.
XX PA (FUJI ) FUJISAWA PHARM KK.
XX DR WPI; 1991-241129/33.
XX PT New peptide prepd. by culturing Streptomyces spp - used as
XX PT endothelin antagonist.
XX PS Claim 1; page 1; 15pp; Japanese.
XX CC The peptide is prepd. by cyclisation of the synthetic peptide.
CC CC The Trp residue at posn. 3 may be side chain protected with a lower
CC CC alkanoyl gp; the Glu residue at posn. 4 may be protected with an
CC CC al (lower) alkyl gp. An analogous natural peptide, WS 7338, may be
CC CC isolated from cultures of Streptomyces sp. no. 7338.
XX CC See also AAR13909 and AAR14025.
XX SQ Sequence 5 AA;
Query Match 65.2%; Score 15; DB 12; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 LW 5
DB 2 LW 3
RESULT 15
AAR13909
ID AAR13909 standard; peptide; 5 AA.
XX AC AAR13909;
XX XX 22-OCT-1991 (first entry)
XX DE Endothelin antagonist peptide.
XX CC Cyclic.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT Modified-site 1 /label= D-Val
FT Modified-site 3 /label= D-Trp
FT Modified-site 4 /label= D-Glu
XX PN JP03130299-A.
XX PD 04-JUN-1991.
XX PF 08-AUG-1990; 90JP-0212952.
XX PR 31-AUG-1989; 89GB-0019726.
XX PA (FUJI ) FUJISAWA PHARM KK.
XX DR WPI; 1991-241129/33.
XX PT New peptide prepd. by culturing Streptomyces spp - used as
XX PT endothelin antagonist.
XX PS Claim 1; page 1; 15pp; Japanese.
XX CC The peptide is prepd. by cyclisation of the synthetic peptide.
CC CC The Trp residue at posn. 3 may be side chain protected with a lower
CC CC alkanoyl gp; the Glu residue at posn. 4 may be protected with an
CC CC al (lower) alkyl gp. An analogous natural peptide, WS 7338, may be
CC CC isolated from cultures of Streptomyces sp. no. 7338.
XX CC See also AAR13909 and AAR14025.
XX SQ Sequence 5 AA;
Query Match 65.2%; Score 15; DB 12; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 LW 5
DB 2 LW 3
RESULT 16
AAR38437

```



PF 30-JUN-1992; 92JP-0173065.  
 XX  
 PR 31-JUL-1991; 91JP-0191454.  
 XX  
 XX (TAKE ) TAKEDA CHEM IND LTD.  
 XX  
 DR WPI; 1993-282913/36.  
 XX  
 XX Novel cyclic peptide(s) used as endothelin receptor antagonists -  
 PT for treating cardiac diseases, e.g. myocardial infarction, acute  
 PT renal insufficiency or asthma  
 XX  
 PS Example 1-3; Page 6; 8pp; Japanese.  
 XX  
 CC The sequences given in AAR38436-38 are cyclic peptides which act as  
 CC endothelin receptor antagonists. They may be used in the treatment  
 CC of cardiac disease, acute renal insufficiency or asthma.  
 XX  
 SQ Sequence 5 AA;  
 Query Match 65.2%; Score 15; DB 14; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 LW 5  
 DB 4 LW 5  
 RESULT 19  
 AAR35418  
 ID AAR35418 standard; peptide; 5 AA.  
 XX  
 AC AAR35418;  
 XX  
 DT 03-AUG-1993 (first entry)  
 XX  
 DE Endothelin receptor inhibitor peptide #1.  
 XX  
 KW Cyclic; endothelin; inhibitor; vasoconstriction; drug; circulation;  
 KW mammal; myocardial infarction; renal dysfunction; asthma.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 1 /note= "D-form residue"  
 FT Misc-difference 3 /note= "D-form residue"  
 FT Misc-difference 5 /note= "D-form residue"  
 FT Misc-difference 5 /note= "D-form residue"  
 XX  
 PN JP05059098-A.  
 XX  
 PD 09-MAR-1993.  
 XX  
 PF 30-AUG-1991; 91JP-0220610.  
 XX  
 PR 30-AUG-1991; 91JP-0220610.  
 XX  
 PA (TAKE ) TAKEDA CHEM IND LTD.  
 XX  
 DR WPI; 1993-128388/16.  
 XX  
 XX New cyclic penta:peptide derivs. contg. one L-aminoacid - inhibit  
 PT endothelin receptor activity, vasoconstriction etc.; useful for  
 PT treating myocardial infarction, acute renal dysfunction and  
 PT asthma, etc.  
 XX  
 PS Example 1; Page 6; 8pp; Japanese.  
 XX  
 CC The sequences given in AAR35418-28 are cyclic peptides which act as  
 CC endothelin inhibitors. They strongly inhibit the vasoconstrictive

CC action of endothelin. They are useful as drugs for improving  
 CC circulatory function in mammals, in treatment of myocardial  
 CC infarction, acute renal dysfunction or asthma. These peptides may  
 CC be prepared by conventional methods of solid or aqueous phase  
 CC synthesis.  
 XX  
 SQ Sequence 5 AA;  
 Query Match 65.2%; Score 15; DB 14; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 LW 5  
 DB 3 LW 4  
 RESULT 20  
 AAR35419  
 ID AAR35419 standard; peptide; 5 AA.  
 XX  
 AC AAR35419;  
 XX  
 DT 03-AUG-1993 (first entry)  
 XX  
 DE Endothelin receptor inhibitor peptide #2.  
 XX  
 KW Cyclic; endothelin; inhibitor; vasoconstriction; drug; circulation;  
 KW mammal; myocardial infarction; renal dysfunction; asthma.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 1 /note= "D-form residue"  
 FT Misc-difference 3 /note= "D-form residue"  
 FT Misc-difference 5 /note= "D-form residue"  
 FT Misc-difference 5 /note= "D-form residue"  
 XX  
 PN JP05059098-A.  
 XX  
 PD 09-MAR-1993.  
 XX  
 PF 30-AUG-1991; 91JP-0220610.  
 XX  
 PR 30-AUG-1991; 91JP-0220610.  
 XX  
 PA (TAKE ) TAKEDA CHEM IND LTD.  
 XX  
 DR WPI; 1993-128388/16.  
 XX  
 XX New cyclic penta:peptide derivs. contg. one L-aminoacid - inhibit  
 PT endothelin receptor activity, vasoconstriction etc.; useful for  
 PT treating myocardial infarction, acute renal dysfunction and  
 PT asthma, etc.  
 XX  
 PS Example 2; Page 7; 8pp; Japanese.  
 XX  
 CC The sequences given in AAR35418-28 are cyclic peptides which act as  
 CC endothelin inhibitors. They strongly inhibit the vasoconstrictive  
 CC action of endothelin. They are useful as drugs for improving  
 CC circulatory function in mammals, in treatment of myocardial  
 CC infarction, acute renal dysfunction or asthma. These peptides may  
 CC be prepared by conventional methods of solid or aqueous phase  
 CC synthesis.  
 XX  
 SQ Sequence 5 AA;  
 Query Match 65.2%; Score 15; DB 14; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 4 LW 5  
||  
Db 3 LW 4

## RESULT 21

AAR35421  
ID AAR35421 standard; peptide; 5 AA.

AC AAR35421;

XX 03-AUG-1993 (first entry)

XX Endothelin receptor inhibitor peptide #4.

KW Cyclic; endothelin; inhibitor; vasoconstriction; drug; circulation;  
KW mammal; myocardial infarction; renal dysfunction; asthma.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1 /note= "D-form residue"

FT Misc-difference 3 /note= "D-form residue"

FT Misc-difference 5 /note= "D-form residue"

FT Misc-difference 5 /note= "D-form residue"

XX JP05059098-A.

XX 09-MAR-1993.

XX 30-AUG-1991; 91JP-0220610.

XX 30-AUG-1991; 91JP-0220610.

XX (TAKE ) TAKEDA CHEM IND LTD.

XX WPI; 1993-128388/16.

XX New cyclic penta:peptide derivs. contg. one L-aminoacid - inhibit  
XX endothelin receptor activity, vasoconstriction etc., useful for  
XX treating myocardial infarction, acute renal dysfunction and  
XX asthma, etc.

XX Example 4; Page 8; 8pp; Japanese.

XX The sequences given in AAR35418-28 are cyclic peptides which act as  
XX endothelin inhibitors. They strongly inhibit the vasoconstrictive  
XX action of endothelin. They are useful as drugs for improving  
XX circulatory function in mammals, in treatment of myocardial  
XX infarction, acute renal dysfunction or asthma. These peptides may  
XX be prepared by conventional methods of solid or aqueous phase  
XX synthesis.

XX Sequence 5 AA;

Query Match 65.2%; Score 15; DB 14; Length 5;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5

||

Db 3 LW 4

## RESULT 22

AAR35422

ID AAR35422 standard; peptide; 5 AA.

XX AAR35422;

XX 03-AUG-1993 (first entry)

XX

DE

XX

KW

XX

OS

XX

PH

FT

FT

FT

FT

FT

FT

XX

XX

PN

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

```

FT      /note= "D-form residue"
FT      /note= "D-form residue"
PN      JP05059098-A.
PD      09-MAR-1993.
XX      30-AUG-1991; 91JP-0220610.
XX      30-AUG-1991; 91JP-0220610.
XX      (TAKE ) TAKEDA CHEM IND LTD.
XX      WPI; 1993-128388/16.
XX      New cyclic penta-peptide derivs. contg. one L-aminoacid -inhibit
PT      endothelin receptor activity, vasoconstriction etc., useful for
PT      treating myocardial infarction, acute renal dysfunction and
PT      asthma, etc.
XX      Example 6; Page 8; 8pp; Japanese.
XX      The sequences given in AAR35418-28 are cyclic peptides which act as
CC      endothelin inhibitors. They strongly inhibit the vasoconstrictive
CC      action of endothelin. They are useful as drugs for improving
CC      circulatory function in mammals, in treatment of myocardial
CC      infarction, acute renal dysfunction or asthma. These peptides may
CC      be prepared by conventional methods of solid or aqueous phase
CC      synthesis.
XX      Sequence 5 AA;
SQ      Query Match 65.2%; Score 15; DB 14; Length 5;
          Best Local Similarity 100.0%; Pred. No. 7.8e+05;
          Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 LW 5
Db      3 LW 4

RESULT 25
AAR35425
ID      AAR35425 standard; peptide; 5 AA.
XX      AC AAR35425;
XX      DT 03-AUG-1993 (first entry)
XX      DE Endothelin receptor inhibitor peptide #7.
XX      KW Cyclic; endothelin; inhibitor; vasoconstriction; drug; circulation;
XX      KW mammal; myocardial infarction; renal dysfunction; asthma.
XX      OS Synthetic.
XX      PH Key Location/Qualifiers
FT      Misc-difference 1 /note= "D-form residue"
FT      Misc-difference 3 /note= "D-form residue"
FT      Misc-difference 5 /note= "D-form residue"
XX      JP05059098-A.
XX      PN 09-MAR-1993.
XX      PF 30-AUG-1991; 91JP-0220610.
XX      PR 30-AUG-1991; 91JP-0220610.
XX      PA (TAKE ) TAKEDA CHEM IND LTD.
XX      PT WPI; 1993-128388/16.
XX      New cyclic penta-peptide derivs. contg. one L-aminoacid - inhibit
PT      endothelin receptor activity, vasoconstriction etc., useful for
PT      treating myocardial infarction, acute renal dysfunction and
PT      asthma, etc.
XX      Example 8; Page 8; 8pp; Japanese.
XX      The sequences given in AAR35418-28 are cyclic peptides which act as

```

CC endothelin inhibitors. They strongly inhibit the vasoconstrictive  
 CC action of endothelin. They are useful as drugs for improving  
 CC circulatory function in mammals, in treatment of myocardial  
 CC infarction, acute renal dysfunction or asthma. These peptides may  
 CC be prepared by conventional methods of solid or aqueous phase  
 CC synthesis.  
 XX  
 SQ Sequence 5 AA;

Query Match 65.2%; Score 15; DB 14; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 LW 5  
 ||  
 Db 3 LW 4

RESULT 26  
 AAR35426  
 ID AAR35426 standard; peptide; 5 AA.

XX AAR35426;  
 XX  
 DT 03-AUG-1993 (first entry)

Endothelin receptor inhibitor peptide #9.

Cyclic; endothelin; inhibitor; vasoconstriction; drug; circulation;  
 KW mammal; myocardial infarction; renal dysfunction; asthma.

XX Synthetic.

Key Location/Qualifiers  
 FT Misc-difference 1 /note= "D-form residue"  
 FT Misc-difference 3 /note= "D-form residue"  
 FT Misc-difference 5 /note= "D-form residue"  
 FT Misc-difference 5 /note= "D-form residue"

XX JP05059098-A.

XX 09-MAR-1993.

XX 30-AUG-1991; 91JP-0220610.

XX 30-AUG-1991; 91JP-0220610.

XX (TAKE ) TAKEDA CHEM IND LTD.

XX WPI; 1993-128388/16.

XX New cyclic penta-peptide derivs. contg. one L-aminoacid - inhibit  
 PT endothelin receptor activity, vasoconstriction etc., useful for  
 PT treating myocardial infarction, acute renal dysfunction and  
 PT asthma, etc.

XX Example 9; Page 8; 8pp; Japanese.

XX The sequences given in AAR35418-28 are cyclic peptides which act as  
 CC endothelin inhibitors. They strongly inhibit the vasoconstrictive  
 CC action of endothelin. They are useful as drugs for improving  
 CC circulatory function in mammals, in treatment of myocardial  
 CC infarction, acute renal dysfunction or asthma. These peptides may  
 CC be prepared by conventional methods of solid or aqueous phase  
 CC synthesis.

XX Sequence 5 AA;

Query Match 65.2%; Score 15; DB 14; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 LW 5  
 ||  
 Db 3 LW 4

RESULT 27  
 AAR35427  
 ID AAR35427 standard; peptide; 5 AA.

XX AAR35427;

XX 03-AUG-1993 (first entry)

XX Endothelin receptor inhibitor peptide #10.

Cyclic; endothelin; inhibitor; vasoconstriction; drug; circulation;  
 KW mammal; myocardial infarction; renal dysfunction; asthma.

XX Synthetic.

Key Location/Qualifiers  
 FT Misc-difference 1 /note= "D-form residue"  
 FT Misc-difference 3 /note= "D-form residue"  
 FT Misc-difference 5 /note= "D-form residue"  
 FT Misc-difference 5 /note= "D-form residue"

XX JP05059098-A.

XX 09-MAR-1993.

XX 30-AUG-1991; 91JP-0220610.

XX 30-AUG-1991; 91JP-0220610.

XX (TAKE ) TAKEDA CHEM IND LTD.

XX WPI; 1993-128388/16.

XX New cyclic penta-peptide derivs. contg. one L-aminoacid - inhibit  
 PT endothelin receptor activity, vasoconstriction etc., useful for  
 PT treating myocardial infarction, acute renal dysfunction and  
 PT asthma, etc.

XX Example 10; Page 8; 8pp; Japanese.

XX The sequences given in AAR35418-28 are cyclic peptides which act as  
 CC endothelin inhibitors. They strongly inhibit the vasoconstrictive  
 CC action of endothelin. They are useful as drugs for improving  
 CC circulatory function in mammals, in treatment of myocardial  
 CC infarction, acute renal dysfunction or asthma. These peptides may  
 CC be prepared by conventional methods of solid or aqueous phase  
 CC synthesis.

XX Sequence 5 AA;

Query Match 65.2%; Score 15; DB 14; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 LW 5  
 ||  
 Db 3 LW 4

RESULT 28  
 AAR35428  
 ID AAR35428 standard; peptide; 5 AA.

XX AAR35428;  
 XX

DT 03-AUG-1993 (first entry)  
 XX Endothelin receptor inhibitor peptide #11.  
 DE Cyclic; endothelin; inhibitor; vasoconstriction; drug; circulation;  
 XX mammal; myocardial infarction; renal dysfunction; asthma.  
 KW Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 FH Misc-difference 1 /note= "D-form residue"  
 FT Misc-difference 3 /note= "D-form residue"  
 FT Misc-difference 5 /note= "D-form residue"  
 FT Misc-difference 5 /note= "D-form residue"  
 FT JP05059098-A.  
 XX  
 XX 09-MAR-1993.  
 XX 30-AUG-1991; 91JP-0220610.  
 XX 30-AUG-1991; 91JP-0220610.  
 XX (TAKE ) TAKEDA CHEM IND LTD.  
 XX WPI; 1993-128388/16.  
 XX  
 XX New cyclic penta-peptide derivs. contg. one L-aminoacid - inhibit  
 FT endothelin receptor activity, vasoconstriction etc., useful for  
 FT treating myocardial infarction, acute renal dysfunction and  
 PT asthma, etc.  
 XX  
 XX Example 11; Page 8; 8pp; Japanese.  
 XX  
 CC The sequences given in AAR35418-28 are cyclic peptides which act as  
 CC endothelin inhibitors. They strongly inhibit the vasoconstrictive  
 CC action of endothelin. They are useful as drugs for improving  
 CC circulatory function in mammals, in treatment of myocardial  
 CC infarction, acute renal dysfunction or asthma. These peptides may  
 CC be prepared by conventional methods of solid or aqueous phase  
 CC synthesis.  
 XX  
 SQ Sequence 5 AA;  
 Query Match 65.2%; Score 15; DB 14; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 LW 5  
 DB 3 LW 4  
 RESULT 29  
 AAY08516  
 ID AAY08516 standard; peptide; 5 AA.  
 XX  
 AC AAY08516;  
 XX  
 DT 30-JUL-1999 (first entry)  
 XX  
 DE Endothelin metal conjugate peptide 15.  
 XX  
 KW Endothelin; metal conjugate; complex; diagnostic; contrast agent;  
 KW x-ray imaging; NMR imaging; pathological vascular change; stenotic;  
 KW atherosclerosis; radiopharmaceutical; non-invasive diagnosis;  
 KW arterial wall lesion; pharmacokinetic.  
 XX  
 OS Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 FH

FT Misc-difference 1 /note= "D-form residue"  
 FT Misc-difference 3 /note= "Residue is alloDile"  
 FT Misc-difference 5 /note= "D-form residue"  
 XX  
 XX DE4301871-A1.  
 XX  
 XX 14-JUL-1994.  
 XX  
 XX 13-JAN-1993; 93DE-4301871.  
 XX  
 XX 13-JAN-1993; 93DE-4301871.  
 XX  
 XX (DIAG-) INST DIAGNOSTIKFORSCHUNG GMBH.  
 XX (DINK/) DINKELBORG L.  
 XX (UYBE-) UNIV BERLIN INST DIAGNOSTIKFORSCHUNG.  
 XX  
 XX Dinkelborg L, Erber S, Gries H, Hilger CS, Kramp W;  
 XX Platzeck J, Schier H, Speck U, Reiser JH;  
 XX WPI; 1994-226321/28.  
 XX  
 XX New complexes of derivatised endothelin or related cpds. - with  
 FT radioactive or paramagnetic metal ions, useful as diagnostic agents  
 FT for imaging pathological changes in blood vessels  
 PT  
 XX  
 XX Claim 6; Page 31; 40pp; German.  
 XX  
 CC This invention describes novel complexes of compounds which have the  
 CC formula E-L-(K)b with metal ions of atomic number 21-32, 37-39, 42-51  
 CC and 57-83 where E = residue of an endothelin (or its derivative, partial  
 CC sequence, analogue or antagonist), including forms with free SH groups  
 CC that bind directly to metal, optionally labelled with radioactive iodine  
 CC isotopes, L = bond, Zi-R-z2 or a group (i), R = 1-20C, optionally  
 CC unsaturated alkyl, optionally substituted by OH and/or epoxy, and  
 CC optionally interrupted by 1 or more O, S, CO, NCO or NH (the last 2  
 CC optionally N substituted by 1-6C alkyl), Zi and Z = O, S, COO, NH, CS,  
 CC NH, CO, CSO, NH, NHCN or NHCS, s and t = 0-3, B = phenyl or cyclohexyl  
 CC ring, b = 0 or 1, K is a chelating residue. The compounds of the  
 CC invention are useful as diagnostic agents, including contrast agents for  
 CC x-ray and NMR imaging of pathological vascular changes e.g. The  
 CC atherosclerosis. They can also be used as radiopharmaceuticals. The  
 CC invention allows the marking of possible early non-invasive diagnosis  
 CC of vascular changes before these become stenotic. The E component  
 CC provides strong localisation to arterial wall lesions without significant  
 CC accumulation in other tissues or organs. Compared with known diagnostic  
 CC agents they have better pharmacokinetic properties and provide improved  
 CC contrast. They have excellent in vitro and in vivo stability (no  
 CC significant release or exchange of bound radionuclides). This sequence  
 CC is a specific claimed example of a peptide used in the construction of  
 CC the metalcomplex-conjugates of the invention.  
 XX  
 SQ Sequence 5 AA;  
 Query Match 65.2%; Score 15; DB 15; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0.  
 QY 4 LW 5  
 DB 4 LW 5  
 RESULT 30  
 AAR47438  
 ID AAR47438 standard; peptide; 5 AA.  
 XX  
 AC AAR47438;  
 XX  
 DT 30-JUN-1994 (first entry)  
 XX





```

OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1 /note= "D-form residue"
FT Modified-site 3 /label= alle
FT FT /note= "D-form residue"
FT Misc-difference 5 /note= "D-form residue"
FT
XX JP06192293-A.
XX
XX 12-JUL-1994.
XX
XX 20-JUN-1991; 91JP-0148807.
XX
XX 20-JUN-1991; 91JP-0148807.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
XX
XX WPI; 1994-260512/32.
XX
XX Cyclic penta:peptide(s) - useful as endothelin receptor
XX antagonists for treatment of myocardial infarction, etc.
XX
XX Disclosure; Page 7; 13pp; Japanese.
XX
XX The sequences of ET-1, ET-2 and ET-3 are given in AAR60076-78. Cyclic
XX pentapeptides, useful as endothelin receptor antagonists are given
XX in AAR60079-88. They are useful in the treatment or prophylaxis of
XX hypertension, myocardial infarction, acute renal insufficiency or
XX asthma.
XX
XX Sequence 5 AA;
XX
XX Query Match 65.2%; Score 15; DB 15; Length 5;
XX Best Local Similarity 100.0%; Pred. No. 7.8e+05;
XX Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 4 LW 5
XX Db 4 LW 5
XX
XX RESULT 34
XX AAR60082
XX ID AAR60082 standard; Protein; 5 AA.
XX
XX AC AAR60082;
XX
XX 21-MAR-1995 (first entry)
XX
XX TAN-1477D - cyclic ET receptor antagonist.
XX
XX Endothelin; ET; ET-1; ET-2; ET-3; pentapeptide; receptor;
XX antagonist; myocardial infarction; hypertension;
XX acute renal insufficiency; asthma; cyclic.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX FT Misc-difference 1 /note= "D-form residue"
XX FT Modified-site 3 /note= "D-form residue"
XX FT Misc-difference 5 /note= "D-form residue"
XX
XX JP06192293-A.
XX
XX 12-JUL-1994.
XX
XX 20-JUN-1991; 91JP-0148807.
XX
XX 20-JUN-1991; 91JP-0148807.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
XX
XX WPI; 1994-260512/32.
XX
XX Cyclic penta:peptide(s) - useful as endothelin receptor
XX antagonists for treatment of myocardial infarction, etc.
XX
XX Disclosure; Page 7; 13pp; Japanese.
XX
XX The sequences of ET-1, ET-2 and ET-3 are given in AAR60076-78. Cyclic
XX pentapeptides, useful as endothelin receptor antagonists are given
XX in AAR60079-88. They are useful in the treatment or prophylaxis of
XX hypertension, myocardial infarction, acute renal insufficiency or
XX asthma.
XX
XX Sequence 5 AA;
XX
XX Query Match 65.2%; Score 15; DB 15; Length 5;
XX Best Local Similarity 100.0%; Pred. No. 7.8e+05;
XX Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 4 LW 5
XX Db 4 LW 5
XX
XX RESULT 33
XX AAR60080
XX ID AAR60080 standard; Protein; 5 AA.
XX
XX AC AAR60080;
XX
XX 21-MAR-1995 (first entry)
XX
XX TAN-1462B - cyclic ET receptor antagonist.
XX
XX Endothelin; ET; ET-1; ET-2; ET-3; pentapeptide; receptor;
XX antagonist; myocardial infarction; hypertension;
XX acute renal insufficiency; asthma; cyclic.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX FT Misc-difference 1 /note= "D-form residue"
XX FT Modified-site 3 /note= "D-form residue"
XX FT Misc-difference 5 /note= "D-form residue"
XX
XX JP06192293-A.
XX
XX 12-JUL-1994.
XX
XX

```

CC in AAR60079-88. They are useful in the treatment or prophylaxis of  
 CC hypertension, myocardial infarction, acute renal insufficiency or  
 CC asthma.

SQ Sequence 5 AA;

Query Match 65.2%; Score 15; DB 15; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 LW 5  
 ||  
 Db 4 LW 5

RESULT 35

AAR60088  
 ID AAR60088 standard; Protein; 5 AA.

XX AAR60088;

XX 21-MAR-1995 (first entry)

XX TAN-1477K - cyclic ET receptor antagonist.

XX Endothelin; ET; ET-1; ET-2; ET-3; pentapeptide; receptor;  
 KW antagonist; myocardial infarction; hypertension;  
 KW acute renal insufficiency; asthma; cyclic.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1 /note= "D-form residue"

FT Modified-site 3 /label= alle

FT Modified-site 5 /note= "D-form residue"

FT Modified-site 5 /note= "D-5-methyltryptophan"

XX JP06192293-A.

XX 12-JUL-1994.

XX 20-JUN-1991; 91JP-0148807.

XX 20-JUN-1991; 91JP-0148807.

XX (TAKE ) TAKEDA CHEM IND LTD.

XX WPI; 1994-260512/32.

XX Cyclic pentapeptide(s) - useful as endothelin receptor  
 PT antagonists for treatment of myocardial infarction, etc.

XX Disclosure; Page 7; 13pp; Japanese.

XX The sequences of ET-1, ET-2 and ET-3 are given in AAR60076-78. Cyclic  
 CC pentapeptides, useful as endothelin receptor antagonists are given  
 CC in AAR60079-88. They are useful in the treatment or prophylaxis of  
 CC hypertension, myocardial infarction, acute renal insufficiency or  
 CC asthma.

SQ Sequence 5 AA;

Query Match 65.2%; Score 15; DB 15; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 LW 5  
 ||  
 Db 4 LW 5

RESULT 36

AAR62195  
 ID AAR62195 standard; Protein; 5 AA.

XX AAR62195;

XX 03-MAY-1995 (first entry)

XX CENP-B protein residues 191-195, homologous to SRV-1 protease motif.  
 DE CENP-B protein; centromere protein; epitope;  
 KW autoantibody; immunoinfective cluster virus; nuclear protein antigen;  
 KW systemic rheumatic disorder; SRV-1 viral protease;  
 KW systemic lupus erythematosus; scleroderma.

XX Homo sapiens.

XX WO9420141-A.

XX 15-SBP-1994.

XX 10-MAR-1994; 94WO-US02631.

XX 11-MAR-1993; 93US-0029850.

XX (UYSC-) UNIV SOUTHERN CALIFORNIA.

XX Douvas A, Ehresmann G, Takehana Y;

XX WPI; 1994-302689/37.

XX Methods for treating immunoinfective cluster virus infections -  
 PT utilise antibodies or fragments characteristic of auto antibodies  
 PT produced by patients with rheumatic disorders

XX Disclosure; Page 71; 106pp; English.

XX A comparison of the CENP-B centromere protein sequence with proteins  
 CC from immunoinfective cluster viruses revealed widespread  
 CC homologues. The importance of these homologous motifs is that they  
 CC are epitopes for autoantibodies occurring in high titres in systemic  
 CC rheumatic disorders. Sera from such patients could be used for  
 CC treatment of immunoinfective cluster virus infections, e.g. HIV-1,  
 CC immunoinfective adenoviruses, human lymphotropic retroviruses,  
 CC rubella virus, CMV and EBV infections.

SQ Sequence 5 AA;

Query Match 65.2%; Score 15; DB 15; Length 5;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 LW 5  
 ||  
 Db 4 LW 5

RESULT 37

AAR71907  
 ID AAR71907 standard; peptide; 5 AA.

XX AAR71907;

XX 19-MAY-1995 (first entry)

XX Endothelin cyclic peptide conjugated to chalcogen-contg. ligand.  
 DE Chalcogen; ligand; complex; endothelin; non-invasive imaging;  
 KW technetium; rhenium; in vivo imaging; cyclic.

XX Synthetic.

XX

FF	Key	Location/Qualifiers	
FT	Peptide	1..5	
FT		/label= cyclic	
FT		/note= "attached to chalcogen-contg. ligand,	
FT		see comments"	
FT	Misc-difference 1		
FT		/note= "D-form residue"	
FT	Modified-site 3		
FT		/label= aile	
FT		/note= "D-form residue"	
FT	Misc-difference 5		
FT		/note= "D-form residue"	
XX			
XX	DE4311022-A.		
PN			
XX			
XX	06-OCT-1994.		
PD			
XX			
XX	31-MAR-1993; 93DE-4311022.		
PP			
XX			
XX	31-MAR-1993; 93DE-4311022.		
PR			
XX			
XX	(UYBE-) UNIV BERLIN INST DIAGNOSTIKFORSCHUNG.		
PA			
XX			
XX	Dinkelborg L, Hilger C, Kramp W, Schier H;		
PI			
XX	WPI; 1994-311304/39.		
DR			
XX			
XX	Bis-(N-(mercapto-ethyl- or -propyl) amino:carbonyl:methyl) oxide,		
PT	sulphide or selenide and derivs. - are ligands for radioactive		
PT	technetium or rhenium for diagnosis and therapy, e.g. for		
PT	non-invasive in-vivo visualisation of receptors		
PT			
XX			
XX	Claim 9; Page 14; 15pp; German.		
PS			
XX			
XX	This peptide is one of 14 endothelin derivatives which are		
CC	preferred for use in conjugates with novel bis-(N-(mercapto-ethyl-		
CC	or -propyl) aminocarbonylmethyl) oxide, sulphide or selenide		
CC	compounds. The chalcogen-containing compounds are ligands which are		
CC	complexed with a technetium or rhenium radioisotope. The		
CC	ligand-peptide conjugates are useful for non-invasive, in vivo		
CC	imaging, e.g. of receptors.		
XX			
XX	Sequence 5 AA;		
SQ			
	Query Match	65.2%; Score 15; DB 15; Length 5;	
	Best Local Similarity	100.0%; Pred. No. 7.8e+05;	
	Matches 2; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
OY	4 LW 5		
Db	4 LW 5		
	RESULT 38		
	AAR69266		
ID	AAR69266 standard; peptide; 5 AA.		
XX			
XX	AAR69266;		
AC			
XX			
XX	22-MAY-1995 (first entry)		
DT			
XX			
XX	Cyclic pentapeptide having beta-turn and gamma-turn.		
DE			
XX			
XX	Beta-turn; gamma-turn; NK2; neurokinin; endothelin; receptor;		
KW	antiasthmatic; antiinflammatory; antiarthritic;		
KW	affinity purification; cyclic.		
KW			
XX			
OS	Synthetic.		
XX			
Key	Location/Qualifiers		
FT	Misc-difference 1		
FT		/note= "D-Glu; and this amino acid is part of a	
FT		cyclic structure formed by condensation	
FT			

FT	Modified-site	2	with the C-terminal amino acid"
FT	FT	/note=	"Ser(Bzl)"
FT	Misc-difference	3	
FT	FT	/note=	"D-Leu"
FT	Misc-difference	5	
FT	FT	/note=	"D-Trp; and this amino acid is condensed onto the N-terminal to form a cyclic peptide"
FT	FT		
XX	EP606881-A.		
PN	XX		
XX	20-JUL-1994.		
PD	XX		
XX	11-JAN-1994;	94EP-0100276.	
PF	XX		
PR	13-JAN-1993;	93JP-0004125.	
XX	(TAKE )	TAKEDA CHEM IND LTD.	
PA	XX		
XX	Endo S, Inooka H, Kikuchi T, Wakimasu M;		
PI	XX		
XX	WPI; 1994-226821/28.		
DR	XX		
XX	New cyclic penta:peptide(s) having a gamma-turn and a beta-turn -		
PT	used as NK2 receptor antagonists for treating asthma,		
PT	inflammation or arthritis		
PT	Claim 10; Page 16; 29pp; English.		
XX	PS		
XX	New cyclic pentapeptides are disclosed which have a gamma-turn and a		
CC	beta-turn and which are of formula Cyclo(-A1-A2-A3-A4-A5-) where the		
CC	amino acids in positions 1-2-3 form a gamma-turn and the amino acids		
CC	in positions 3-4-5-1 form a beta-turn in combination with the gamma-		
CC	turn. Either D-amino acid residues are chosen for A1, A3 and A5 and		
CC	L-amino acids for A2 and A4; or L-amino acid residues are chosen for		
CC	A1, A3 and A5 and D-residues for A2 and A5. The peptides are		
CC	antagonists against the NK2 receptor or endothelin receptor. They		
CC	can be used as antiasthmatic, antiinflammatory or antiarthritic		
CC	agents or as assay or affinity purification reagents for the		
CC	receptors.		
CC	The present sequence is a specifically claimed example of the		
CC	cyclic pentapeptides.		
XX	XX		
SQ	Sequence	5 AA;	
	Query Match	65.2%; Score 15; DB 15; Length 5;	
	Best Local Similarity	100.0%; Pred. No. 7.8e+05;	
	Matches	2; Conservative 0; Mismatches 0; Indels 0; Gaps	
QY	4	LW 5	
DB	4	LW 5	
	RESULT 39		
	AAR69267		
	ID	AAR69267 standard; peptide; 5 AA.	
XX	XX		
AC	AAR69267;		
XX	XX		
DT	22-MAY-1995	(first entry)	
DE	XX		
XX	Cyclic pentapeptide having beta-turn and gamma-turn.		
XX	Beta-turn; gamma-turn; NK2; neurokinin; endothelin; receptor;		
KW	antiasthmatic; antiinflammatory; antiarthritic;		
KW	affinity purification; cyclic.		
XX	XX		
OS	Synthetic.		
XX	XX		
FT	Key	Location/Qualifiers	
FT	Misc-difference	1	

FT	/note= "D-Glu; and this amino acid is part of a
FT	cyclic structure formed by condensation
FT	with the C-terminal amino acid"
FT	
FT	Modified-site    2                 /note= "Thr(Bzl) "
FT	Misc-difference   3               /note= "D-Leu"
FT	Misc-difference   5               /note= "D-Trp; and this amino acid is condensed
FT	onto the N-terminal to form a cyclic
FT	peptide"
XX	
XX	EP606881-A.
PN	
XX	20-JUL-1994.
PD	
XX	
XX	11-JAN-1994;    94EP-0100276.
PX	
XX	
PR	13-JAN-1993;    93JP-0004125.
XX	
PA	(TAKE ) TAKEDA CHEM IND LTD.
XX	
PI	Endo S, Inooka H, Kikuchi T, Wakimasu M;
DR	WPI; 1994-226821/28.
XX	
PT	New cyclic penta;peptide(s) having a gamma-turn and a beta-turn -
PT	used as NK2 receptor antagonists for treating asthma,
PT	inflammation or arthritis
XX	
PS	Claim 11; Page 16; 29pp; English.
XX	
CC	New cyclic pentapeptides are disclosed which have a gamma-turn and a
CC	beta-turn and which are of formula Cyclo(-A1-A2-A3-A4-A5-) where the
CC	amino acids in positions 1-2-3 form a gamma-turn and the amino acids
CC	in positions 3-4-5-1 form a beta-turn in combination with the gamma-
CC	turn. Either D-amino acid residues are chosen for A1, A3 and A5 and
CC	L-amino acids for A2 and A4; or L-amino acid residues are chosen for
CC	A1, A3 and A5 and D-residues for A2 and A5. The peptides are
CC	antagonists against the NK2 receptor or endothelin receptor. They
CC	can be used as antisthmatic, antiinflammatory or antiarthritic
CC	agents or as assay or affinity purification reagents for the
CC	receptors.
CC	The present sequence is a specifically claimed example of the
CC	cyclic pentapeptides.
XX	
XX	Sequence    5 AA;
SQ	
	Query Match                  65.2%; Score 15; DB 15; Length 5;
	Best Local Similarity      100.0%; Pred.No. 7.8e+05;
	Matches    2; Conservative    0; Mismatches    0; Indels    0; Gaps    0;
Qy	4 LW 5
Dd	4 LW 5
RESULT 40	
AAR69268	
ID	AAR69268 standard; peptide; 5 AA.
XX	
AC	AAR69268;
XX	
DT	22-MAY-1995 (first entry)
XX	
DE	Cyclic pentapeptide having beta-turn and gamma-turn.
XX	
KW	Beta-turn; gamma-turn; NK2; neurokinin; endothelin; receptor;
KW	antasthmatic; antiinflammatory; antiarthritic;
KW	affinity purification; cyclic.
XX	
OS	Synthetic.
XX	

```

FH Key Location/Qualifiers
FT Misc-difference 1
FT /note= "D-Asp; and this amino acid is part of a
FT cyclic structure formed by condensation
FT with the C-terminal amino acid"
FT
FT Misc-difference 3
FT /note= "D-Leu"
FT Misc-difference 5
FT /note= "D-Trp; and this amino acid is condensed
FT onto the N-terminal to form a cyclic
FT peptide"
FT
XX EP606881-A.
XX
XX 20-JUL-1994.
XX
XX 11-JAN-1994; 94EP-0100276.
XX
XX 13-JAN-1993; 93JP-0004125.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
XX
XX Endo S, Inooka H, Kikuchi T, Wakimasu M;
XX WPI; 1994-226821/28.
XX
XX New cyclic penta-peptide(s) having a gamma-turn and a beta-turn -
PT used as NK2 receptor antagonists for treating asthma,
PT inflammation or arthritis
PT
XX Example 5; Page 15; 29pp; English.
XX
XX New cyclic pentapeptides are disclosed which have a gamma-turn and a
CC beta-turn and which are of formula Cyclo(-A1-A2-A3-A4-A5-) where the
CC amino acids in positions 1-2-3 form a gamma-turn and the amino acids
CC in positions 3-4-5-1 form a beta-turn in combination with the gamma-
CC turn. Either D-amino acid residues are chosen for A1, A3 and A5 and
CC L-amino acids for A2 and A4; or L-amino acid residues are chosen for
CC A1, A3 and A5 and D-residues for A2 and A5. The peptides are
CC antagonists against the NK2 receptor or endothelin receptor. They
CC can be used as antiasthmatic, antiinflammatory or antiarthritic
CC agents or as assay or affinity purification reagents for the
CC receptors.
CC The present sequence is a specific example of the cyclic
CC pentapeptides.
XX
XX Sequence 5 AA;
SQ
Query Match 65.2%; Score 15; DB 15; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 LW 5
DB 4 LW 5
||
||
RESULT 42
AAR65742
ID AAR65742 standard; peptide; 5 AA.
XX
XX AAR65742;
XX
XX 09-JUN-1995 (first entry)
XX
XX Endothelin cyclic peptide conjugated to chalcogen-contg. ligand.
XX
XX Chalcogen; ligand; complex; endothelin; non-invasive imaging;
XX technetium; rhenium; in vivo imaging; atherosclerotic plaque;
XX bifunctional chalcogen-interrupted chelate former; cyclic.
XX
XX Synthetic.
XX

```

```

FH Key Location/Qualifiers
FT Peptide
FT 1..5
FT /label= cyclic
FT /note= "attached to chalcogen-contg. ligand,
FT see comments"
FT
FT Misc-difference 1
FT /note= "D-form residue"
FT Modified-site 3
FT /label= alle
FT /note= "D-form residue"
FT Misc-difference 5
FT /note= "D-form residue"
FT Modified-site 1
FT /note= "the amino group of D-Glu forms a peptide
FT linkage with the carboxy group of D-Trp"
FT Modified-site 5
FT /note= "the amino group of D-Glu forms a peptide
FT linkage with the carboxy group of D-Trp"
XX
XX DE4311023-A.
XX
XX 06-OCT-1994.
XX
XX 31-MAR-1993; 93DE-4311023.
XX
XX 31-MAR-1993; 93DE-4311023.
XX
XX (UYBE-) UNIV BERLIN INST DIAGNOSTIKFORSCHUNG.
XX
XX Dinkelborg L, Hilger C, Kramp W, Schier H;
XX WPI; 1994-311305/39.
XX
XX Bifunctional chalcogen-atom interrupted chelate formers - for
XX radioactive isotopes, their prodn. and use in diagnostics and
XX therapy, e.g. for non-invasive in-vivo representation of
XX receptors
XX
XX Claim 9; Page 11; 13pp; German.
XX
XX This peptide is one of 14 endothelin derivatives which are
XX preferred for use in conjugates with novel, bifunctional chalcogen-
XX interrupted chelate forming compounds. The chalcogen-containing
XX compounds are ligands which are complexed with a technetium or
XX rhenium radioisotope. The ligand-peptide conjugates are useful
XX for non-invasive, in vivo imaging, e.g. of receptors or of
XX atherosclerotic plaques.
XX
XX Sequence 5 AA;
SQ
Query Match 65.2%; Score 15; DB 15; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
QY 4 LW 5
DB 4 LW 5
||
||
RESULT 43
AAR65728
ID AAR65728 standard; peptide; 5 AA.
XX
XX AAR65728;
XX
XX 02-JUN-1995 (first entry)
XX
XX Endothelin cyclic peptide conjugated to chalcogen-contg. ligand.
XX
XX Chalcogen; ligand; complex; endothelin; non-invasive imaging;
XX technetium; rhenium; in vivo imaging; atherosclerotic plaque;
XX bifunctional chalcogen-interrupted chelate former; cyclic.
XX
XX

```

OS Synthetic.  
 XX Key Location/Qualifiers  
 FH Peptide 1..5  
 FT /label= cyclic  
 FT /note= "attached to chalcogen-contg. ligand,  
 FT see comments"  
 FT Misc-difference 1 /note= "D-form residue"  
 FT Modified-site 3 /label= alle  
 FT /note= "D-form residue"  
 FT Misc-difference 5 /note= "D-form residue"  
 FT DE4310999-A.  
 PN 06-OCT-1994.  
 XX  
 XX 31-MAR-1993; 93DE-4310999.  
 XX 31-MAR-1993; 93DE-4310999.  
 XX (UYBE-) UNIV BERLIN INST DIAGNOSTIKFORSCHUNG.  
 PA Dinkelborg L, Hilger C, Kramp W, Schier H;  
 PI WPI; 1994-311297/39.  
 DR  
 XX Bifunctional, chalcogen-interrupted chelate former for  
 FT radioisotopes - used in diagnostics and therapy, e.g. for  
 FT non-invasive in-vivo representation of receptors  
 XX  
 PS Claim 9; Page 12; 13pp; German.  
 XX This peptide is one of 14 endothelin derivatives which are  
 CC preferred for use in conjugates with novel, bifunctional chalcogen-  
 CC interrupted chelate forming compounds. The chalcogen-containing  
 CC compounds are ligands which are complexed with a technetium or  
 CC rhodium radioisotope. The ligand-peptide conjugates are useful  
 CC for non-invasive, in vivo imaging, e.g. of receptors or of  
 CC atherosclerotic plaques.  
 XX  
 SQ Sequence 5 AA;  
 Query Match 65.2%; Score 15; DB 15; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 LW 5  
 Db 4 LW 5  
 RESULT 44  
 AAR63183  
 ID AAR63183 standard; peptide; 5 AA.  
 XX  
 AC AAR63183;  
 XX  
 DT 16-JUN-1995 (first entry)  
 XX  
 DE Cyclic peptide ligand #2 for radiopharmaceutical agent.  
 KW Peptide; ligand; radioactive; peptide complex; imaging; receptor;  
 KW steroid; hormone; atherosclerotic plaque; targeting; endothelin;  
 KW analogue; derivative; antagonist.  
 XX  
 OS Synthetic.  
 XX Key Location/Qualifiers  
 FH Modified-site 1 /note= "Forms peptide linkage with DTrp5"  
 FT

FT Misc-difference 1 /note= "D-form residue"  
 FT Misc-difference 3 /note= "alloDile"  
 FT Misc-difference 5 /note= "D-form residue"  
 FT Modified-site 5 /note= "Forms peptide linkage with DGIu1"  
 XX  
 XX WO9422491-A.  
 PN 13-OCT-1994.  
 XX  
 XX 29-MAR-1994; 94WO-DE00369.  
 XX 31-MAR-1993; 93DE-4311021.  
 XX (UYBE-) UNIV BERLIN INST DIAGNOSTIKFORSCHUNG.  
 PA Dinkelborg L, Erber S, Noll B, Rohlf G, Schulze P;  
 PI WPI; 1994-332837/41.  
 DR  
 XX New radio-pharmaceutical agents deriv. from peptide chelating  
 FT ligands - also the new ligands and complexes with tissue  
 FT targeting peptide(s), useful for imaging and treatment of e.g.  
 PT atherosclerosis or steroid dependent cancer  
 XX  
 PS Claim 14; Page 66; 81pp; German.  
 XX  
 CC The sequences given in AAR731170-83 represent peptide ligands which are  
 CC used with the radioactive peptide complex of the invention. The  
 CC complexes may be used to image receptors, specifically of steroid  
 CC hormones, receptor contg. tissue and/or atherosclerotic plaque.  
 CC These peptides allow the complex to be targeted to a specific  
 CC tissue. These peptides are pref. derived from endothelin, and  
 CC represent analogues, derivatives or antagonists.  
 XX  
 SQ Sequence 5 AA;  
 Query Match 65.2%; Score 15; DB 15; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 LW 5  
 Db 4 LW 5  
 RESULT 45  
 AAR64367  
 ID AAR64367 standard; Peptide; 5 AA.  
 XX  
 AC AAR64367;  
 XX  
 DT 25-AUG-1995 (first entry)  
 XX  
 DE DP-178 homologue 36 derived from HIV-1 has antiviral activity.  
 KW antiviral activity; DP-178; DP-107; diagnostic; HIV-1LAI;  
 KW human immunodeficiency virus; transmembrane protein; gp41;  
 KW alpha helix; leucine zipper; DP-185.  
 XX  
 OS Synthetic.  
 XX Key Location/Qualifiers  
 FH Modified-site 1 /note= "optionally has an amino, acetyl,  
 FT 9-fluorenylmethoxy-carbonyl, hydrophobic or  
 FT macromolecular carrier gp. attached"  
 FT Modified-site 5 /note= "optionally has a carboxyl, amido, hydrophobic  
 FT or macromolecular carrier gp. attached"  
 FT

```

XX WO9428920-A.
XX 22-DEC-1994.
XX 07-JUN-1994; 94WO-US05739.
XX 07-JUN-1993; 93US-0073028.
XX (UYDU-) UNIV DUKE.
XX Barney SO, Bolognesi DP, Lambert DM, Matthews TU;
XX Petteway SR, Wild CT;
XX WPI; 1995-036105/05.
XX Computer search generated synthetic peptides - are inhibitors of
XX HIV transmission
XX Claim 11; Page 133; 182pp; English.
XX AAR64365-97 are peptide derivs. Of DP-178 (AAR64364) which have been
XX truncated at the amino terminus. DP-178 corresponds to amino acids
XX 638 to 673 of the HIV-1 isolate LAI transmembrane protein gp41. It
XX forms a putative alpha helix at the C-terminal end of the gp41
XX ectodomain, and complexes with DP-107 (corresponds to amino acids
XX 558-595) which contains a leucine zipper motif. The peptides complex
XX via non-covalent protein-protein interactions, and possess anti-viral
XX activity. The peptide derivs. were identified by a computer assisted
XX peptide sequence search. The peptides inhibit transmission to
XX uninfected cells, and can also be used as type and/or subtype
XX specific diagnostic tools.
XX Sequence 5 AA;
QY Query Match 65.2%; Score 15; DB 16; Length 5;
DB Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 LW 5
DB 1 LW 2
RESULT 46
AAR59459
ID AAR59459 standard; peptide; 5 AA.
XX AC AAR59459;
XX DT 01-SEP-1995 (first entry)
XX DE Melanin pigmentation inhibiting cyclic pentapeptide.
XX KW Melanin pigmentation inhibition; skin whitening cosmetic;
XX OS cyclic peptide; sunburn fleck formation treatment.
XX Synthetic.
XX Key Location/Qualifiers
XX Modified-site 1 /note= "forms peptide bond with Xaa at position 5"
XX Misc-difference 2 /note= "D or L form residues"
XX Misc-difference 3 /label= Glu, Asp
XX Misc-difference 4 /note= "D or L form residues"
XX Misc-difference 4 /label= Ala, Pro, Hyp
XX Misc-difference 5 /note= "D or L form residues"
XX /label= Val, Asp

```

```

FT Modified-site 5 /note= "D or L form residues"
FT /note= "forms peptide bond with Leu at position 1"
XX JP06321755-A.
XX 22-NOV-1994.
XX 11-MAY-1993; 93JP-0109456.
XX 11-MAY-1993; 93JP-0109456.
XX (KAOS ) KAO CORP.
XX WPI; 1995-041168/06.
XX Skin whitening cosmetic contg. cyclic penta:peptide - e.g.
XX cyclo(L-Leu-D-Trp-D-Glu-L-Ala-D-Val), for inhibiting melanin
XX pigmentation
XX Claim 1; Page 2; 7pp; Japanese.
XX AAR59459-R59461 are cyclic pentapeptides which inhibit melanin
XX pigmentation. As part of a skin whitening cosmetic they can be
XX used for the prevention of fleck formation after sunburn.
XX Sequence 5 AA;
QY Query Match 65.2%; Score 15; DB 16; Length 5;
DB Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 LW 5
DB 1 LW 2
RESULT 47
AAR59460
ID AAR59460 standard; peptide; 5 AA.
XX AC AAR59460;
XX DT 01-SEP-1995 (first entry)
XX DE Melanin pigmentation inhibiting cyclic pentapeptide.
XX KW Melanin pigmentation inhibition; skin whitening cosmetic;
XX OS cyclic peptide; sunburn fleck formation treatment.
XX Synthetic.
XX Key Location/Qualifiers
XX Modified-site 1 /note= "forms peptide bond with Val at position 5"
XX Misc-difference 2 /note= "D-form residue"
XX Misc-difference 3 /note= "D-form residue"
XX Misc-difference 5 /note= "D-form residue"
XX Modified-site 5 /note= "forms peptide bond with Leu at position 1"
XX JP06321755-A.
XX 22-NOV-1994.
XX 11-MAY-1993; 93JP-0109456.
XX 11-MAY-1993; 93JP-0109456.
XX (KAOS ) KAO CORP.

```



XX WPI; 1995-041168/06.  
 XX Skin whitening cosmetic contg. cyclic penta:peptide - e.g.  
 PT cyclo(L-Leu-D-Trp-D-Glu-L-Ala-D-Val), for inhibiting melanin  
 PT pigmentation  
 XX Example 1; Page 3; 7pp; Japanese.  
 XX AAR59459-R59461 are cyclic pentapeptides which inhibit melanin  
 CC pigmentation. As part of a skin whitening cosmetic they can be  
 CC used for the prevention of fleck formation after sunburn.  
 XX SQ Sequence 5 AA;  
 Query Match 65.2%; Score 15; DB 16; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 LW 5  
 DB 1 LW 2  
 RESULT 48  
 AAR59461  
 ID AAR59461 standard; peptide; 5 AA.  
 XX  
 AC AAR59429;  
 XX  
 DT 18-JUL-1995 (first entry)  
 XX  
 DE Cyclic endothelin receptor peptide for treating organ hypofunction.  
 XX Endothelin receptor antagonist; organ hypofunction; liver; surgery;  
 KW transplant; cyclic.  
 KW  
 OS Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 FH Misc-difference 1 /note= "D-Asp, which is part of a cyclic peptide  
 FT formed by condensation with D-Trp(5)"  
 FT  
 FT Modified-site 2 /label= OTHER  
 FT /note= "alpha-amino acid with conformationally  
 FT restricted 4-16C side chain, preferably  
 FT 1,2,3,4-tetrahydro-2-carboline-3-carboxylic  
 FT acid"  
 FT  
 FT Misc-difference 3 /note= "D-Val"  
 FT  
 FT Misc-difference 5 /note= "D-Trp, which is part of a cyclic peptide  
 FT formed by condensation with D-Asp(1)"  
 FT  
 XX EP626174-A.  
 XX  
 XX 30-NOV-1994.  
 XX  
 XX 20-APR-1994; 94EP-0106093.  
 XX  
 XX 21-APR-1993; 93JP-0094332.  
 XX  
 XX (TAKE ) TAKEDA CHEM IND LTD.  
 XX  
 XX Kitada C, Wakimasu M, Watanabe T;  
 PI WPI; 1995-000740/01.  
 XX  
 XX Use of endothelin receptor antagonists - for prophylaxis or  
 PT treatment of organ hypofunction, partic. caused by surgery on or  
 PT transplant of the organ  
 XX  
 XX Claim 34; Page 106; 107pp; English.  
 XX  
 XX The invention relates to the new use of known endothelin receptor  
 CC antagonists for prophylaxis and/or therapy of hypofunction of organs  
 CC (particularly the liver) which occurs following their surgery or  
 CC transplant. The present sequence is a specific example of a suitable  
 CC antagonist listed in the Claims.  
 XX  
 XX SQ Sequence 5 AA;  
 Query Match 65.2%; Score 15; DB 16; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 LW 5  
 DB 1 LW 2  
 RESULT 48  
 AAR59461  
 ID AAR59461 standard; peptide; 5 AA.  
 XX  
 AC AAR59461;  
 XX  
 DT 01-SEP-1995 (first entry)  
 XX  
 DE Melanin pigmentation inhibiting cyclic pentapeptide.  
 XX  
 DE Melanin pigmentation inhibition; skin whitening cosmetic;  
 KW cyclic peptide; sunburn fleck formation treatment.  
 KW  
 OS Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 FH Modified-site 1 /note= "forms peptide bond with Asp at position 5"  
 FT /note= "D-form residue"  
 FT Misc-difference 2 /note= "D-form residue"  
 FT /note= "D-form residue"  
 FT Misc-difference 3 /note= "D-form residue"  
 FT /note= "D-form residue"  
 FT Misc-difference 5 /note= "forms peptide bond with Leu at position 1"  
 FT /note= "D-form residue"  
 FT  
 XX JP06321755-A.  
 XX  
 XX 22-NOV-1994.  
 XX  
 XX 11-MAY-1993; 93JP-0109456.  
 XX  
 XX 11-MAY-1993; 93JP-0109456.  
 XX  
 XX (KAOS ) KAO CORP.  
 XX  
 XX WPI; 1995-041168/06.  
 XX  
 XX Skin whitening cosmetic contg. cyclic penta:peptide - e.g.  
 PT cyclo(L-Leu-D-Trp-D-Glu-L-Ala-D-Val), for inhibiting melanin  
 PT pigmentation  
 XX Example 1; Page 3; 7pp; Japanese.  
 XX AAR59459-R59461 are cyclic pentapeptides which inhibit melanin  
 CC pigmentation. As part of a skin whitening cosmetic they can be  
 CC used for the prevention of fleck formation after sunburn.  
 XX

OY 4 LW 5  
DB 4 LW 5

## RESULT 50

AAR69430  
ID AAR69430 standard; peptide; 5 AA.

XX AC AAR69430;  
XX 18-JUL-1995 (first entry)  
XX DT  
XX DE

Cyclic endothelin receptor peptide for treating organ hypofunction.  
XX Endothelin receptor antagonist; organ hypofunction; liver; surgery;  
KW transplant; cyclic.  
XX Synthetic.

OS  
XX Key

## Location/Qualifiers

FT Misc-difference 1 /note= "D-Ser, which is part of a cyclic peptide  
formed by condensation with D-Trp(5)"

FT Modified-site 2 /label= OTHER  
FT /note= "alpha-amino acid with conformationally  
restricted side chain"

FT Misc-difference 3 /note= "D-Val"

FT Misc-difference 5 /note= "D-Trp, which is part of a cyclic peptide  
formed by condensation with D-Ser(1)"

XX EP626174-A.  
XX 30-NOV-1994.

XX 20-APR-1994; 94EP-0106093.

XX 21-APR-1993; 93JP-0094332.

XX (TAKE ) TAKEDA CHEM IND LTD.

XX Kitada C, Wakimasu M, Watanabe T;

XX WPI; 1995-000740/01.

XX Use of endothelin receptor antagonists - for prophylaxis or  
treatment of organ hypofunction, partic. caused by surgery on or  
transplant of the organ

XX Claim 34; Page 106; 107pp; English.

XX The invention relates to the new use of known endothelin receptor  
antagonists for prophylaxis and/or therapy of hypofunction of organs  
(particularly the liver) which occurs following their surgery or  
transplant. The present sequence is a specific example of a suitable  
antagonist listed in the Claims.

XX Sequence 5 AA;

Query Match 65.2%; Score 15; DB 16; Length 5;  
Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 LW 5  
DB 4 LW 5

## RESULT 51

AAR69414

XX AAR69414 standard; peptide; 5 AA.

XX AC AAR69414;  
XX 18-JUL-1995 (first entry)

XX DT  
XX DE

Cyclic endothelin receptor peptide for treating organ hypofunction.  
XX Endothelin receptor antagonist; organ hypofunction; liver; surgery;  
KW transplant; cyclic.  
XX Synthetic.

OS  
XX Key

## Location/Qualifiers

FT Misc-difference 1 /note= "D-Cys(03S), which is part of a cyclic peptide  
formed by condensation with D-Trp(5)"

FT Misc-difference 3 /note= "D-Val"

FT Misc-difference 5 /note= "D-Trp, which is part of a cyclic peptide  
formed by condensation with D-Cys(1)"

XX EP626174-A.  
XX 30-NOV-1994.

XX 20-APR-1994; 94EP-0106093.

XX 21-APR-1993; 93JP-0094332.

XX (TAKE ) TAKEDA CHEM IND LTD.

XX Kitada C, Wakimasu M, Watanabe T;

XX WPI; 1995-000740/01.

XX Use of endothelin receptor antagonists - for prophylaxis or  
treatment of organ hypofunction, partic. caused by surgery on or  
transplant of the organ

XX Claim 12; Page 86; 107pp; English.

XX The invention relates to the new use of known endothelin receptor  
antagonists for prophylaxis and/or therapy of hypofunction of organs  
(particularly the liver) which occurs following their surgery or  
transplant. The present sequence is a specific example of a suitable  
antagonist listed in the Claims.

XX Sequence 5 AA;

Query Match 65.2%; Score 15; DB 16; Length 5;  
Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 LW 5  
DB 4 LW 5

## RESULT 52

AAR69415  
ID AAR69415 standard; peptide; 5 AA.

XX AC AAR69415;  
XX 18-JUL-1995 (first entry)

XX DT  
XX DE

Cyclic endothelin receptor peptide for treating organ hypofunction.  
XX Endothelin receptor antagonist; organ hypofunction; liver; surgery;  
KW transplant; cyclic.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT FT Misc-difference 1 /note= "D-Trp, which is part of a cyclic peptide  
formed by condensation with D-Trp(5)"

FT FT Misc-difference 3 /label= OTHER

FT FT /note= "D-Thg(2) or D-Cpg, where Thg(2) is 2-(2-  
thienyl)glycine and Cpg is 2-cyclopentyl-  
glycine"

FT FT Misc-difference 5 /note= "D-Trp, which is part of a cyclic peptide  
formed by condensation with D-Asp(1)"

FT FT EP626174-A.

XX PN 30-NOV-1994.

XX PD 20-APR-1994; 94EP-0106093.

XX PF 21-APR-1993; 93JP-0094332.

XX PR (TAKE ) TAKEDA CHEM IND LTD.

XX PA Kitada C, Wakimasu M, Watanabe T;

XX PI WPI; 1995-000740/01.

XX DR Use of endothelin receptor antagonists - for prophylaxis or  
treatment of organ hypofunction, partic. caused by surgery on or  
transplant of the organ

XX PS Claim 12; Page 86; 107pp; English.

XX CC The invention relates to the new use of known endothelin receptor  
antagonists for prophylaxis and/or therapy of hypofunction of organs  
(particularly the liver) which occurs following their surgery or  
transplant. The present sequence is a specific example of a suitable  
antagonist listed in the Claims.

XX SQ Sequence 5 AA;

Query Match 65.2%; Score 15; DB 16; Length 5;  
Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5  
||  
Db 4 LW 5

RESULT 53

AAR69413

XX ID AAR69413 standard; peptide; 5 AA.

XX AC AAR69413;

XX DT 18-JUL-1995 (first entry)

XX DE Cyclic endothelin receptor peptide for treating organ hypofunction.

XX KW Endothelin receptor antagonist; organ hypofunction; liver; surgery;

XX KW transplant; cyclic.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT FT Misc-difference 1 /note= "D-Asp, which is part of a cyclic peptide  
formed by condensation with D-Trp(5)"

FT FT Misc-difference 3

FT FT Misc-difference 5 /note= "D-Val"

FT FT /note= "D-Trp, which is part of a cyclic peptide  
formed by condensation with D-Asp(1)"

XX PN EP626174-A.

XX PD 30-NOV-1994.

XX PF 20-APR-1994; 94EP-0106093.

XX PR 21-APR-1993; 93JP-0094332.

XX PA (TAKE ) TAKEDA CHEM IND LTD.

XX PI Kitada C, Wakimasu M, Watanabe T;

XX DR WPI; 1995-000740/01.

XX CC Use of endothelin receptor antagonists - for prophylaxis or  
treatment of organ hypofunction, partic. caused by surgery on or  
transplant of the organ

XX PS Claim 12; Page 86; 107pp; English.

XX CC The invention relates to the new use of known endothelin receptor  
antagonists for prophylaxis and/or therapy of hypofunction of organs  
(particularly the liver) which occurs following their surgery or  
transplant. The present sequence is a specific example of a suitable  
antagonist listed in the Claims.

XX SQ Sequence 5 AA;

Query Match 65.2%; Score 15; DB 16; Length 5;  
Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5  
||  
Db 4 LW 5

RESULT 54

AAR69392

XX ID AAR69392 standard; peptide; 5 AA.

XX AC AAR69392;

XX DT 16-JUL-1995 (first entry)

XX DE Endothelin antagonist peptide for treating organ hypofunction.

XX KW Endothelin receptor antagonist; organ hypofunction; liver; surgery;

XX KW transplant; cyclic.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT FT Modified-site 1 /note= "hexamethyleneimino-CO-Leu"

FT FT Misc-difference 2 /label= D-Trp

FT FT Misc-difference 3 /note= "D-Ala"

FT FT Modified-site 4 /label= bAla

FT FT Modified-site 5 /note= "Tyr-NH-Ind-OH, where Ind is  
1-carboxyindane-2-yl"

XX PN EP626174-A.

XX PD 30-NOV-1994.

XX 20-APR-1994; 94EP-0106093.  
 XX 21-APR-1993; 93JP-0094332.  
 XX (TAKE ) TAKEDA CHEM IND LTD.  
 XX  
 XX Kitada C, Wakimasu M, Watanabe T;  
 XX WPI; 1995-000740/01.  
 XX  
 XX Use of endothelin receptor antagonists - for prophylaxis or  
 PT treatment of organ hypofunction, partic. caused by surgery on or  
 PT transplant of the organ  
 XX  
 XX Claim 7; Page 83; 107pp; English.  
 XX  
 XX The invention relates to the new use of known endothelin receptor  
 CC antagonists for prophylaxis and/or therapy of hypofunction of organs  
 CC (particularly the liver) which occurs following their surgery or  
 CC transplant. The present sequence is a specific example of a suitable  
 CC antagonist listed in the Claims.  
 XX  
 XX Sequence 5 AA;  
 SQ  
 Query Match 65.2%; Score 15; DB 16; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 LW 5  
 ||  
 Db 1 LW 2  
 RESULT 55  
 AAR86453  
 ID AAR86453 standard; peptide; 5 AA.  
 XX  
 AC AAR86453;  
 XX  
 DT 05-FEB-1996 (first entry)  
 XX  
 DE Endothelin sequence for use as conjugate with Cys-free peptide.  
 XX  
 XX diagnostic imaging; atherosclerotic plaque; tumour; inflammation;  
 KW conjugate; radiotherapy; cysteine-free; metal-binding; endothelin;  
 KW cyclic.  
 XX  
 OS Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 FH Misc-difference 1 /note= "D-form residue; and this amino acid forms  
 FT part of a cyclic structure obtained by  
 FT condensation of D-Trp(5) onto the alpha-NH2"  
 FT Misc-difference 3 /label= alle  
 FT /note= "D-form residue"  
 FT Misc-difference 5 /note= "D-form residue; and this amino acid forms  
 FT part of a cyclic structure formed by  
 FT condensation of the COOH onto the NH2 group  
 FT of D-Glu(1)"  
 XX  
 XX DB4337599-A1.  
 XX  
 XX 04-MAY-1995.  
 PD  
 XX 01-NOV-1993; 93DE-4337599.  
 PF  
 XX 01-NOV-1993; 93DE-4337599.  
 PR  
 XX (UYBE-) UNIV BERLIN INST DIAGNOSTIKFORSCHUNG.  
 PA

XX Conrad J, Dinkelborg L, Erber S, Frommel C, Hohne W;  
 PI Kramp W, Kuttner G, Malin R, Schier HM, Schneider-Mergener J;  
 PI Steinbrecher R, Froemmel C, Hoehne W, Kuettner G, Schier H;  
 XX WPI; 1995-171400/23.  
 XX  
 XX New cysteine-free peptide(s) and their metal ion complexes - opt.  
 PT conjugated to targeting agent, useful for in vivo imaging of  
 PT tumours, atherosclerotic plaque etc. and for radiotherapy  
 XX  
 XX Claim 13; Page 20; 25pp; German.  
 XX  
 XX New peptides of formula R1-X-R2 are provided, together with their  
 CC conjugates with peptides, proteins, biomolecules and macromolecules,  
 CC their complexes with metal ions and their water-soluble salts; where  
 CC X is a chain of up to 20 alpha, beta, and/or gamma amino acid residues,  
 CC including at least one Met, Arg, Lys or Asn but no Cys; R1 is H or a  
 CC hydrocarbyl or acyl group, or a bond to a conjugate; and R2 is OH,  
 CC hydrocarbyl or an optionally substituted amine group (forming an  
 CC amide), or a bond to a conjugate. The peptides are useful when complexed  
 CC to a metal (e.g. 99m-Tc) for in-vivo diagnostic imaging and therapy of  
 CC tumours, organs and foci of inflammation. Conjugates of the peptides can  
 CC be targeted to specific tissues. A particular application is imaging of  
 CC atherosclerotic plaque. Metal is bound with good in-vivo stability;  
 CC unbound material is rapidly cleared; and there is no allergic reaction.  
 CC Since the peptides are free of Cys, they can be prepared simply and  
 CC rapidly and can be presented in the form of a kit for radio-  
 CC pharmaceutical production. Specific examples of the peptides are  
 CC given in AAR86424 - AAR86439.  
 CC The present sequence is a specific example of an endothelin peptide  
 CC which can be used as a conjugate with the new peptides.  
 XX  
 XX Sequence 5 AA;  
 SQ  
 Query Match 65.2%; Score 15; DB 16; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 LW 5  
 ||  
 Db 4 LW 5  
 RESULT 56  
 AAW17809  
 ID AAW17809 standard; peptide; 5 AA.  
 XX  
 AC AAW17809;  
 XX  
 DT 07-JUL-1997 (first entry)  
 XX  
 DE Cyclic pentapeptide #25 used in LH-RH receptor antagonist.  
 XX  
 KW Lutetising hormone releasing hormone receptor; LH-RH; antagonist;  
 KW sex-hormone; human; veterinary medicine; cancer; prostate; uterus;  
 KW breast; pituitary; prostatic; endometriosis; hysterioma;  
 KW precocious puberty; amenorrhoea; premenstrual syndrome; cyclic;  
 KW multilocular ovarian syndrome; comedo; pregnancy; contraception;  
 KW ovulation; menstrual cycle; oestrus; meat quality; growth; spawning;  
 KW fish; testosterone; superagonist; leuporelin acetate.  
 XX  
 XX Key Location/Qualifiers  
 FH Modified-site 1 /note= "Joined via a peptide linkage to Trp5"  
 FT Modified-site 2 /note= "N-pToluenesulphonylarginine, D-form residue"  
 FT Modified-site 4 /note= "D-form residue"  
 FT Modified-site 5 /note= "Joined via a peptide linkage to Phe1"  
 XX  
 XX Synthetic.

XX PN W09634012-AL.  
 XX XX  
 XX PD 31-OCT-1996.  
 XX XX  
 XX PF 25-APR-1996; 96WO-JP01140.  
 XX XX  
 XX PR 09-MAY-1995; 95JP-0110933.  
 XX PR 28-APR-1995; 95JP-0106775.  
 XX XX  
 XX PA (TAKE ) TAKEDA CHEM IND LTD.  
 XX XX  
 XX PI Furuya S, Kato K, Kitada C;  
 XX XX  
 XX DR WPI; 1996-497569/49.  
 XX XX  
 XX PT Cyclic penta;peptide(s), some new, as LH-RH receptor antagonists -  
 XX PT used to treat or prevent sex hormone dependent disorders, e.g.  
 XX PT cancer, also for control of pregnancy and menstruation and to  
 XX PT improve meat quality in animals  
 XX PS Example 45; Page 173; 198pp; English.  
 XX XX  
 XX CC This peptide represents a cyclic peptide which is included in the  
 XX CC luteinising hormone releasing hormone (LH-RH) receptor antagonist  
 XX CC composition of the invention. Peptides such as this are used to  
 XX CC prevent or treat sex-hormone dependent disorders in human or veterinary  
 XX CC medicine, esp. cancers (of the prostate, uterus, breast or pituitary),  
 XX CC prostatically, endometriosis, hysteromyoma or precocious puberty, but  
 XX CC also amenorrhoea, premenstrual syndrome, multilocular ovarian syndrome,  
 XX CC comedo, etc.; also to control pregnancy (contraction for men or women,  
 XX CC also to induce ovulation) and the menstrual cycle. They are also used  
 XX CC to control oestrus in animals, to improve meat quality and control  
 XX CC growth, and to promote spawning in fish. They may also inhibit the  
 XX CC transient increase in testosterone blood levels caused by admin. of  
 XX CC superagonists such as leuprolerin acetate.  
 XX SQ  
 SQ Sequence 5 AA;  
 Query Match 65.2%; Score 15; DB 17; Length 5;  
 Best Local Similarity 40.0%; Pred. No. 7.8e+05;  
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 FXXLW 5  
 Db 1 FRFFW 5  
 RESULT 57  
 AAR86236  
 ID AAR86236 standard; peptide; 5 AA.  
 XX AC  
 XX AC AAR86236;  
 XX DT 27-JUN-1996 (first entry)  
 XX XX  
 XX DE Anti-ELAM-1 binding peptide #213.  
 XX KW Peptide mimetic; endothelial leukocyte adhesion molecule; ELAM; selectin;  
 KW KW receptor; leukocyte; vascular wall; endothelium; extravasation;  
 KW KW inflammation; sialyl Lewis; cell surface glycoprotein; HL60 cell.  
 XX OS Synthetic.  
 XX XX  
 XX FH Key Location/Qualifiers  
 XX FT Modified-site 1 /note= "Ac-Leu"  
 XX FT Modified-site 5 /note= "amidated C-terminus"  
 XX FT  
 XX XX W09531210-AL.  
 XX XX  
 XX PD 23-NOV-1995.

XX 11-MAY-1995; 95WO-US06315.  
 XX PR 11-MAY-1994; 94US-0241054.  
 XX XX  
 XX PA (AFFY-) AFFYMAX TECHNOLOGIES NV.  
 XX XX  
 XX PI Barrett RW, Cwirila SE, Dower WJ, Koller KJ, Lee J;  
 XX PI Martens CL, Ruhland-fritsch B;  
 XX DR WPI; 1996-010687/01.  
 XX XX  
 XX PT New peptide(s) that bind to endothelial leukocyte adhesion molecule  
 XX PT 1 - useful for treating inflammation and other E-selectin mediated  
 XX PT diseases  
 XX PS Claim 3; Page 73; 85pp; English.  
 XX XX  
 XX CC Peptides AAR86024-R86236 are examples of peptides and their mimetics  
 XX CC that bind to endothelial leukocyte adhesion molecule (ELAM)-1. This  
 XX CC molecule is a member of the selectin family of receptors and is involved  
 XX CC in binding of leukocytes to the vascular endothelial wall prior to  
 XX CC extravasation of the leukocyte, e.g. to a site of inflammation.  
 XX CC The peptides bind pref. to E-selectin but may also bind L- or  
 XX CC P-selectin, and can be used to treat conditions mediated by E-selectin,  
 XX CC e.g. inflammatory conditions. The peptides have strong affinity for the  
 XX CC selectin receptors and inhibit the binding of the sialyl Lewis (SLe-x)  
 XX CC part of cell surface glycoproteins to E-selectin. The peptide are  
 XX CC small, generally less than 2 KD, have an IC50 of up to 100 micromole  
 XX CC against binding of HL60 cells to ELAM-1, have one or more peptide  
 XX CC linkages replaced by CH2OC(O)NR, phosphonate, CH2SO2NR, CH2NR, CON(R6),  
 XX CC or NHC(=O)NH linkages where R = H or a lower alkyl and R6 = a lower alkyl.  
 XX CC The peptides may also have substituted N- and C-termini e.g.  
 XX CC succinimido, N-benzoyloxycarbonyl or N-lower alkyl cpds.  
 XX SQ  
 SQ Sequence 5 AA;  
 Query Match 65.2%; Score 15; DB 17; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 LW 5  
 Db 1 LW 2  
 RESULT 58  
 AAW33328  
 ID AAW33328 standard; peptide; 5 AA.  
 XX AC  
 XX AC AAW33328;  
 XX DT 05-FEB-1998 (first entry)  
 XX XX  
 XX DE Targetting conjugate for bis-nicotinamide bifunctional chelator.  
 XX XX  
 XX KW Bifunctional; bis-nicotinamide; chelator; radioactive; technetium;  
 KW KW rhodium; conjugate; endothelin; angiotensin; targeting agent;  
 KW KW organ; in vivo imaging; receptor; tissue; atherosclerotic plaque;  
 KW KW diagnosis; breast; prostatic; carcinoma; cytostatic agent;  
 KW KW delivery; cyclic.  
 XX OS Synthetic.  
 XX OS Homo sapiens.  
 XX XX  
 XX FH Key Location/Qualifiers  
 XX FT Misc-difference 1 /note= "D-form residue"  
 XX FT Misc-difference 3 /note= "allo-D-form residue"  
 XX FT Misc-difference 5 /note= "D-form residue"  
 XX FT

[illegible]

PA (UYBE-) UNIV BERLIN INST DIAGNOSTIKFORSCHUNG.  
 XX Dinkelborg L, Erber S, Hilger CS, Kramp W, Platzek J;  
 PI Raduechel B;  
 XX WPI; 1997-193894/18.  
 XX Bifunctional sulphonamide type ligands for radioactive technetium or  
 PT rhenium - and their chelates and conjugates, useful for imaging  
 PT carcinoma or atherosclerosis  
 XX Claim 9; Page 12; 12pp; German.  
 XX Novel bifunctional sulphonamide type ligands for radioactive  
 CC technetium and rhenium, when conjugated to an endothelin or  
 CC angiotensin derived targeting agent, e.g. the present peptide, can  
 CC be used for the in vivo imaging of organs, receptors and receptor  
 CC containing tissues and/or atherosclerotic plaques, e.g. for the  
 CC diagnosis of breast or prostatic carcinoma. They can also be used  
 CC for cytostatic agent delivery.  
 XX Sequence 5 AA;  
 SQ Query Match 65.2%; Score 15; DB 18; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5  
 ||  
 Db 4 LW 5

RESULT 61  
 AAW11213  
 ID AAW11213 standard; peptide; 5 AA.  
 XX AAW11213;  
 XX 26-JAN-1998 (first entry)  
 DE Targetting conjugate for bifunctional sulphonamide type ligand.  
 XX Bifunctional sulphonamide; ligand; radioactive; technetium;  
 KW rhenium; conjugate; endothelin; angiotensin; targeting agent;  
 KW organ; in vivo imaging; receptor; tissue; atherosclerotic plaque;  
 KW diagnosis; breast; prostatic; carcinoma; cytostatic agent;  
 KW delivery; cyclic.  
 XX Homo sapiens.  
 OS Synthetic.  
 XX Key Location/Qualifiers  
 FT Misc-difference 1 /note= "D-form residue"  
 FT Misc-difference 3 /note= "D-form residue"  
 FT Misc-difference 5 /note= "allo D-form residue"  
 FT Misc-difference 5 /note= "D-form residue"  
 XX DE19536780-A1.  
 XX 27-MAR-1997.  
 XX 21-SEP-1995; 95DE-1036780.  
 XX 21-SEP-1995; 95DE-1036780.  
 XX (UYBE-) UNIV BERLIN INST DIAGNOSTIKFORSCHUNG.  
 XX Dinkelborg L, Erber S, Hilger CS, Kramp W, Platzek J;  
 PI Raduechel B;  
 XX WPI; 1997-193892/18.

XX Bifunctional sulphonamide type ligands for radioactive technetium  
 PT and rhenium - and their chelates and conjugates with targeting  
 agents, useful for imaging carcinoma, atherosclerotic plaque, etc.  
 XX Claim 11; Page 19; 19pp; German.

XX Novel bifunctional sulphonamide type ligands for radioactive  
 CC technetium and rhenium, when conjugated to an endothelin or  
 CC angiotensin derived targeting agent, e.g. the present peptide, can  
 CC be used for the in vivo imaging of organs, receptors and receptor  
 CC containing tissues and/or atherosclerotic plaques, e.g. for the  
 CC diagnosis of breast or prostatic carcinoma. They can also be used  
 CC for cytostatic agent delivery.  
 XX Sequence 5 AA;  
 SQ Query Match 65.2%; Score 15; DB 18; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5  
 ||  
 Db 4 LW 5

RESULT 62  
 AAW11212  
 ID AAW11212 standard; peptide; 5 AA.  
 XX AAW11212;  
 XX 26-JAN-1998 (first entry)  
 DE Targetting conjugate for bifunctional sulphonamide type ligand.  
 XX Bifunctional sulphonamide; ligand; radioactive; technetium;  
 KW rhenium; conjugate; endothelin; angiotensin; targeting agent;  
 KW organ; in vivo imaging; receptor; tissue; atherosclerotic plaque;  
 KW diagnosis; breast; prostatic; carcinoma; cytostatic agent;  
 KW delivery; cyclic.  
 XX Homo sapiens.  
 OS Synthetic.  
 XX Key Location/Qualifiers  
 FT Misc-difference 1 /note= "D-form residue"  
 FT Misc-difference 2 /note= "D-form residue"  
 FT Misc-difference 4 /note= "D-form residue"  
 FT Misc-difference 4 /note= "D-form residue"  
 XX DE19536780-A1.  
 XX 27-MAR-1997.  
 XX 21-SEP-1995; 95DE-1036780.  
 XX 21-SEP-1995; 95DE-1036780.  
 XX (UYBE-) UNIV BERLIN INST DIAGNOSTIKFORSCHUNG.  
 XX Dinkelborg L, Erber S, Hilger CS, Kramp W, Platzek J;  
 PI Raduechel B;  
 XX WPI; 1997-193892/18.  
 XX Bifunctional sulphonamide type ligands for radioactive technetium  
 PT and rhenium - and their chelates and conjugates with targeting  
 PT agents, useful for imaging carcinoma, atherosclerotic plaque, etc.  
 XX Claim 11; Page 19; 19pp; German.

XX Novel bifunctional sulphonamide type ligands for radioactive  
 CC technetium and rhenium, when conjugated to an endothelin or  
 CC angiotensin derived targeting agent, e.g. the present peptide, can  
 CC be used for the in vivo imaging of organs, receptors and receptor  
 CC containing tissues and/or atherosclerotic plaques, e.g. for the  
 CC diagnosis of breast or prostatic carcinoma. They can also be used  
 CC for cytostatic agent delivery.

XX SQ Sequence 5 AA;  
 Query Match 65.2%; Score 15; DB 18; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5  
 Db 4 LW 5

RESULT 63  
 AAW14986  
 ID AAW14986 standard; peptide; 5 AA.  
 XX AC AAW14986;  
 XX 28-NOV-1997 (first entry)  
 DT  
 DE Conjugating cyclic peptide for radio-therapeutic/diagnostic agent.  
 XX Conjugate; diseased tissue; endothelin; angiotensin; chemotactic;  
 KW radiodiagnostic; radiotherapeutic; diagnosis; tumour; ischaemia;  
 KW atherosclerosis; vascular disorder; ischemia; circular; cyclic.  
 XX Synthetic.  
 OS  
 XX Key Location/Qualifiers  
 FH Misc-difference 1 /note= "D-form residue"  
 FT Misc-difference 3  
 FT Misc-difference 5 /note= "D-form residue"  
 FT Misc-difference 5 /note= "D-form residue"  
 XX WO9710852-A2.  
 XX 27-MAR-1997.  
 XX 19-SEP-1996; 96WO-DR01821.  
 XX 21-SEP-1995; 95DE-4036781.  
 XX (UYBE-) UNIV BERLIN INST DIAGNOSTIKFORSCHUNG.  
 XX Dinkelborg L, Erber S, Hilger CS, Kramp W, Platzek J;  
 PI Raduechel B;  
 XX WPI; 1997-202627/18.  
 XX New sulphide-sulphonamide bi:functional chelating agents - forming  
 PT new, stable technetium or rhenium complexes and conjugates useful as  
 PT radiodiagnostic and radio-therapeutic agents  
 XX Claim 13; Page 45; 50pp; German.  
 XX XSNS-type bifunctional sulphide containing sulphonamide chelating  
 CC agents and their technetium or rhenium complexes, can form  
 CC covalently bonded conjugates with substances selectively enriched  
 CC in diseased tissue, e.g. the present peptide. The substance is an  
 CC endothelin or angiotensin peptide, or a partial sequence, analogue,  
 CC derivative or antagonist, or a chemotactic peptide.  
 CC The conjugates are radiodiagnostic or radiotherapeutic agents,  
 CC useful in the diagnosis of tumours, ischaemia or atherosclerotic

CC vascular disorders.  
 XX SQ Sequence 5 AA;  
 Query Match 65.2%; Score 15; DB 18; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5  
 Db 4 LW 5

RESULT 64  
 AAW22915  
 ID AAW22915 standard; peptide; 5 AA.  
 XX AC AAW22915;  
 XX 02-OCT-1997 (first entry)  
 DT  
 DE Low density lipoprotein binding peptide.  
 XX Low density; lipoprotein; LDL; binding; absorbent; removal;  
 KW body fluid; reagent.  
 XX Synthetic.  
 OS  
 XX Key Location/Qualifiers  
 FH Modified-site 5 /note= "amidated"  
 FT WO9700889-A1.  
 XX 09-JAN-1997.  
 XX 21-JUN-1996; 96WO-JP01734.  
 XX 21-JUN-1995; 95JP-0176904.  
 XX (ASAH ) ASAH KASEI KOGYO KK.  
 XX (ASAH ) ASAH MEDICAL CO LTD.  
 XX Aritomi M, Hatanaka Y;  
 XX WPI; 1997-087320/08.  
 XX Peptide binding to low density lipoprotein - useful in removing LDL  
 PT from body fluids and as carrier peptide(s) for drugs  
 XX Example 11; Page 50; 61pp; Japanese.  
 XX The present low density lipoprotein (LDL) binding peptide can be  
 CC used as an absorbent to remove LDL from body fluids, or as a  
 CC LDL binding reagent. The peptide can be prepared easily and at low  
 CC cost, and has excellent stability and preservability. It  
 CC specifically binds LDL, and does not cause bradykinin production,  
 CC white blood cell activation or blood agglutination.

XX SQ Sequence 5 AA;  
 Query Match 65.2%; Score 15; DB 18; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5  
 Db 4 LW 5

RESULT 65  
 AAW22920  
 ID AAW22920 standard; peptide; 5 AA.



XX AC AAW22920;  
 XX DT 02-OCT-1997 (first entry)  
 XX DE Low density lipoprotein binding peptide.  
 XX KW Low density; lipoprotein; LDL; binding; absorbent; removal;  
 XX KW body fluid; reagent.  
 XX OS Synthetic.  
 XX FH Key Location/Qualifiers  
 XX FT Modified-site 5 /note= "amidated"  
 XX PN WO9700889-A1.  
 XX PD 09-JAN-1997.  
 XX PF 21-JUN-1996; 96WO-JP01734.  
 XX PR 21-JUN-1995; 95JP-0176904.  
 XX PA (ASAH ) ASahi KASEI KOGYO KK.  
 XX PA (ASAH ) ASahi MEDICAL CO LTD.  
 XX PI Aritomi M, Hatanaka Y;  
 XX DR WPI; 1997-087320/08.  
 XX PT Peptide binding to low density lipoprotein - useful in removing LDL  
 XX PT from body fluids and as carrier peptide(s) for drugs  
 XX PS Example 11; Page 50; 61pp; Japanese.  
 XX CC The present low density lipoprotein (LDL) binding peptide can be  
 XX CC used as an absorbent to remove LDL from body fluids, or as a  
 XX CC LDL binding reagent. The peptide can be prepared easily and at low  
 XX CC cost, and has excellent stability and preservability. It  
 XX CC specifically binds LDL, and does not cause bradykinin production,  
 XX CC white blood cell activation or blood agglutination.  
 XX SQ Sequence 5 AA;  
 Query Match 65.2%; Score 15; DB 18; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 4 LW 5  
 Db 4 LW 5  
 RESULT 66  
 AAW22928  
 ID AAW22928 standard; peptide; 5 AA.  
 XX AC AAW22928;  
 XX DT 02-OCT-1997 (first entry)  
 XX DE Low density lipoprotein binding peptide.  
 XX KW Low density; lipoprotein; LDL; binding; absorbent; removal;  
 XX KW body fluid; reagent.  
 XX OS Synthetic.  
 XX FH Key Location/Qualifiers  
 XX FT Modified-site 5 /note= "amidated"  
 XX PN WO9700889-A1.  
 XX PD 09-JAN-1997.  
 XX PF 21-JUN-1996; 96WO-JP01734.  
 XX PR 21-JUN-1995; 95JP-0176904.  
 XX PA (ASAH ) ASahi KASEI KOGYO KK.  
 XX PA (ASAH ) ASahi MEDICAL CO LTD.  
 XX PI Aritomi M, Hatanaka Y;  
 XX DR WPI; 1997-087320/08.  
 XX PT Peptide binding to low density lipoprotein - useful in removing LDL  
 XX PT from body fluids and as carrier peptide(s) for drugs  
 XX PS Example 11; Page 50; 61pp; Japanese.  
 XX CC The present low density lipoprotein (LDL) binding peptide can be  
 XX CC used as an absorbent to remove LDL from body fluids, or as a  
 XX CC LDL binding reagent. The peptide can be prepared easily and at low  
 XX CC cost, and has excellent stability and preservability. It  
 XX CC specifically binds LDL, and does not cause bradykinin production,  
 XX CC white blood cell activation or blood agglutination.  
 XX SQ Sequence 5 AA;  
 Query Match 65.2%; Score 15; DB 18; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 4 LW 5  
 Db 4 LW 5  
 RESULT 66  
 AAW22928  
 ID AAW22928 standard; peptide; 5 AA.  
 XX AC AAW22928;  
 XX DT 02-OCT-1997 (first entry)  
 XX DE Low density lipoprotein binding peptide.  
 XX KW Low density; lipoprotein; LDL; binding; absorbent; removal;  
 XX KW body fluid; reagent.  
 XX OS Synthetic.  
 XX FH Key Location/Qualifiers  
 XX FT Modified-site 5 /note= "amidated"  
 XX PN WO9700889-A1.  
 XX PD 09-JAN-1997.  
 XX PF 21-JUN-1996; 96WO-JP01734.  
 XX PR 21-JUN-1995; 95JP-0176904.  
 XX PA (ASAH ) ASahi KASEI KOGYO KK.  
 XX PA (ASAH ) ASahi MEDICAL CO LTD.  
 XX PI Aritomi M, Hatanaka Y;  
 XX DR WPI; 1997-087320/08.  
 XX PT Peptide binding to low density lipoprotein - useful in removing LDL  
 XX PT from body fluids and as carrier peptide(s) for drugs  
 XX PS Example 11; Page 50; 61pp; Japanese.  
 XX CC The present low density lipoprotein (LDL) binding peptide can be  
 XX CC used as an absorbent to remove LDL from body fluids, or as a  
 XX CC LDL binding reagent. The peptide can be prepared easily and at low  
 XX CC cost, and has excellent stability and preservability. It  
 XX CC specifically binds LDL, and does not cause bradykinin production,  
 XX CC white blood cell activation or blood agglutination.  
 XX SQ Sequence 5 AA;  
 Query Match 65.2%; Score 15; DB 18; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 4 LW 5  
 Db 4 LW 5  
 RESULT 67  
 AAY20414  
 ID AAY20414 standard; Protein; 5 AA.  
 XX AC AAY20414;  
 XX DT 22-JUL-1999 (first entry)  
 XX DE Human microtubule associated protein 2 mutant fragment 110.  
 XX KW Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer;  
 KW frameshift mutation; age-related disease; neurodegenerative disorder;  
 KW Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;  
 KW Huntington's disease; multiple sclerosis; alcoholic liver disease;  
 KW diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;  
 KW ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M;  
 KW neurofilament-F; presenilin I; presenilin II; cellular tumour antigen;  
 KW glial fibrillary acidic protein; GFAP; p53; semaphorin III; HUPP-1;  
 KW bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A;  
 KW high mobility group protein-C; neuroendocrine specific protein A.  
 XX OS Synthetic.  
 XX OS Homo sapiens.  
 XX PN WO9845322-A2.  
 XX PD 15-OCT-1998.  
 XX PF 02-APR-1998; 98WO-IB00705.  
 XX PR 10-APR-1997; 97US-0043163.  
 XX PA (UYUT-) RIJKSUNIV UTRECHT.  
 XX PA (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.  
 XX PA (UYRO-) UNIV ROTTERDAM ERASMUS.

PN WO9700889-A1.  
 XX 09-JAN-1997.  
 XX 21-JUN-1996; 96WO-JP01734.  
 XX 21-JUN-1995; 95JP-0176904.  
 XX (ASAH ) ASahi KASEI KOGYO KK.  
 XX (ASAH ) ASahi MEDICAL CO LTD.  
 XX Aritomi M, Hatanaka Y;  
 XX WPI; 1997-087320/08.  
 XX Peptide binding to low density lipoprotein - useful in removing LDL  
 XX from body fluids and as carrier peptide(s) for drugs  
 XX Example 11; Page 50; 61pp; Japanese.  
 XX The present low density lipoprotein (LDL) binding peptide can be  
 XX used as an absorbent to remove LDL from body fluids, or as a  
 XX LDL binding reagent. The peptide can be prepared easily and at low  
 XX cost, and has excellent stability and preservability. It  
 XX specifically binds LDL, and does not cause bradykinin production,  
 XX white blood cell activation or blood agglutination.  
 XX Sequence 5 AA;  
 Query Match 65.2%; Score 15; DB 18; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 4 LW 5  
 Db 4 LW 5  
 RESULT 67  
 AAY20414  
 ID AAY20414 standard; Protein; 5 AA.  
 XX AC AAY20414;  
 XX 22-JUL-1999 (first entry)  
 XX Human microtubule associated protein 2 mutant fragment 110.  
 XX Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer;  
 KW frameshift mutation; age-related disease; neurodegenerative disorder;  
 KW Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;  
 KW Huntington's disease; multiple sclerosis; alcoholic liver disease;  
 KW diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;  
 KW ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M;  
 KW neurofilament-F; presenilin I; presenilin II; cellular tumour antigen;  
 KW glial fibrillary acidic protein; GFAP; p53; semaphorin III; HUPP-1;  
 KW bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A;  
 KW high mobility group protein-C; neuroendocrine specific protein A.  
 XX OS Synthetic.  
 XX OS Homo sapiens.  
 XX PN WO9845322-A2.  
 XX PD 15-OCT-1998.  
 XX PF 02-APR-1998; 98WO-IB00705.  
 XX PR 10-APR-1997; 97US-0043163.  
 XX (UYUT-) RIJKSUNIV UTRECHT.  
 XX (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.  
 XX (UYRO-) UNIV ROTTERDAM ERASMUS.

XX PI Burbach JPH, Grosveld FG, Van Leeuwen FW;  
 XX WPI; 1998-609901/51.  
 XX DR N-PSDB; AAX75757.  
 XX PT Diagnosing disease by detecting frameshift mutations in RNA or  
 PT corresponding protein mutations - used to diagnose cancer and  
 PT neurological diseases, particularly Alzheimer's disease, and also  
 PT for treatment and prevention with specific ribozymes or wild-type  
 PT RNA  
 XX PS Disclosure; Figure 6; 258pp; English.  
 XX CC This invention describes a novel method for the diagnosis of a disease  
 CC caused by, or associated with, an RNA molecule that has a frameshift  
 CC mutation. The method is used to diagnose age-related diseases, especially  
 CC cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's  
 CC disease, Down's syndrome, myotonic dystrophy, Huntington's disease,  
 CC multiple sclerosis, alcoholic liver disease, diabetes mellitus type II  
 CC and many others listed) or susceptibility to these disorders. The method  
 CC allows a definitive diagnosis of Alzheimer's disease in living patients,  
 CC at an early stage. It is based on the observation that disease may be  
 CC caused by mutations in RNA rather than DNA. The invention describes the  
 CC use of neuronal system RNA molecules, specifically proteins including  
 CC beta-amyloid precursor protein (beta-APP), the microtubule associated  
 CC proteins Tau and Big Tau, ubiquitin B, apolipoprotein E, microtubule  
 CC associated protein 2 (MAP2), neurofilament-L, neurofilament-M,  
 CC neurofilament-F, presenilin 1, presenilin 2, glial fibrillary acidic  
 CC protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma  
 CC 2 (bcl-2) proto-oncogene, semaphorin III, HUPF-1, high mobility group  
 CC protein-C (HMGP-C) and neuroendocrine specific protein A.  
 XX SQ Sequence 5 AA;  
 Query Match 65.2%; Score 15; DB 19; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 LW 5  
 ||  
 Db 1 LW 2  
 RESULT 68  
 AAW65861  
 ID AAW65861 standard; peptide; 5 AA.  
 AC AAW65861;  
 XX 19-OCT-1998 (first entry)  
 DE Endothelin receptor binding peptide part of conjugate.  
 XX endothelin receptor; antagonist; atherosclerosis; radionuclide;  
 KW tyrosine kinase blocker; chemotherapy; antibody; conjugate; cyclic.  
 XX Synthetic.  
 XX Key Location/Qualifiers  
 FH Modified-site 1 /note= "D-Glu is condensed onto D-Trp at position 5  
 FT to form a cyclic peptide"  
 FT Modified-site 3 /label= alle  
 FT /note= "D-form allo-isoleucine"  
 FT Modified-site 5  
 FT /note= "D-Trp is condensed onto D-Glu at position 1  
 FT to form a cyclic peptide"  
 XX DE19652374-A1.  
 XX 10-JUN-1998.

XX PF 04-DEC-1996; 96DE-1052374.  
 XX PR 04-DEC-1996; 96DE-1052374.  
 XX PA (SCHD ) SCHERING AG.  
 XX PI Blume F, Dinkelborg L, Hilger C, Speck U;  
 XX WPI; 1998-363559/32.  
 XX DR Therapeutic use, e.g. in treatment of atherosclerosis, of endothelin  
 PT conjugates - which comprise residue which can bind endothelin  
 PT receptor, conjugated to groups such as radionuclides or protein  
 PT tyrosine kinase blockers  
 XX PS Claim 3; Page 15; 21pp; German.  
 XX CC The invention relates to (A) the use of conjugates of the following  
 CC formula as therapeutic agents: E-Wn; where E = a residue which can bind  
 CC an endothelin receptor, and is derived from an endothelin, an endothelin  
 CC analogue, an endothelin derivative, an endothelin partial sequence or an  
 CC endothelin antagonist; W = an active group which: (i) is a radionuclide  
 CC or (ii) is derived from a chemotherapeutic agent, a complex with a  
 CC radioactive metal isotope, an antibody, an antibody fragment, a peptide,  
 CC a carbohydrate, an oligonucleotide, a protein tyrosine kinase blocker, an  
 CC anti-thrombotic agent, a coagulation cascade inhibitor, a hormone, growth  
 CC factor inhibitor, a medicament, a thrombocyte aggregation inhibitor, an  
 CC anti-inflamatory, a calcium antagonist, a lipid lowering agent or an  
 CC anti-proliferative agent; n = 1-100, especially 1-10, and (B) conjugates  
 CC of the above formula in which W is an active group which: (i) is a  
 CC radionuclide of the elements At, Ba, Br, C, F, N, O or P or (ii) is  
 CC derived from a chemotherapeutic agent, an oligonucleotide, a protein tyrosine kinase  
 CC peptide, a carbohydrate, an oligonucleotide, a protein tyrosine kinase  
 CC blocker, an anti-thrombotic agent, a growth factor inhibitor, a  
 CC medicament, a hormone, a thrombocyte aggregation inhibitor, an anti-  
 CC inflammator, a calcium antagonist, a lipid lowering agent or an anti-  
 CC proliferative agent. The conjugates may be used as therapeutic agents,  
 CC especially for treatment of cardiovascular disorders such as  
 CC atherosclerosis. They may be used in treatment of asthma, cerebral  
 CC infarction, subarachnoid haemorrhage, pre-eclampsia, renal disorders, etc.  
 CC The conjugates become enriched in cells in which endothelin receptors  
 CC are expressed. Even at low doses a therapeutically effective enrichment  
 CC of the active agent at desired sites can be achieved. Unbound conjugate  
 CC is rapidly eliminated from the body, reducing side effects. The present  
 CC sequence represents a specifically claimed endothelin receptor binding  
 CC peptide which forms part of the conjugate.  
 XX SQ Sequence 5 AA;  
 Query Match 65.2%; Score 15; DB 19; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0.  
 QY 4 LW 5  
 ||  
 Db 4 LW 5  
 RESULT 69  
 AAW50857  
 ID AAW50857 standard; peptide; 5 AA.  
 XX AC AAW50857;  
 XX 31-JUL-1998 (first entry)  
 DT Cyclic peptide which mimics surface feature of endothelin.  
 DE Endothelin; endothelina; endothelinb; ETa; ETb; receptor;  
 XX Endothelin-1; cyclic.  
 KW Synthetic.  
 XX OS

XX Key Location/Qualifiers  
 FT Modified-site 1 /note= "D-form residue, amino group of Glu is  
 condensed onto the carboxy group of Trp5 to  
 form a cyclic peptide"  
 FT Misc-difference 3 /note= "D-form residue"  
 FT Modified-site 5 /note= "D-form residue, carboxy group of Trp is  
 condensed onto the amino group of Glu1 to form  
 a cyclic peptide"  
 FT US5736509-A.  
 XX 07-APR-1998.  
 XX 10-NOV-1994; 94US-0410955.  
 XX 10-NOV-1994; 94US-0410955.  
 PR 14-DEC-1990; 90US-0628111.  
 PR 18-JUN-1992; 92US-0900623.  
 PR 05-APR-1994; 94US-0223513.  
 XX (TEXA-) TEXAS BIOTECHNOLOGY CORP.  
 XX Balaji VN, Chan MF;  
 PI WPI; 1998-239252/21.  
 XX New cyclic penta-peptides which are mimics of C-terminus of natural  
 endothelin-1 - useful for relieving symptoms of and for treating  
 endothelin mediated disorders and diseases  
 XX Example 3; Column 33; 30pp; English.  
 XX The invention relates to cyclic peptides that mimic the surface  
 features of the endothelin peptides. The peptides shown in the invention  
 are pentapeptides, hexapeptides and heptapeptides that contain an L-Trp,  
 D-Trp residue or a derivative of D- or L-Trp, such as N-Me-Trp. The  
 peptides modulate the activity of one or more members of the endothelin  
 family of peptides. They are useful for relieving symptoms of and for  
 treating endothelin mediated disorders and diseases. The present sequence  
 represents a cyclic pentapeptide.  
 XX Sequence 5 AA;  
 SQ Query Match 65.2%; Score 15; DB 19; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 LW 5  
 DB 4 LW 5  
 RESULT 70  
 ID AAW50859 standard; peptide; 5 AA.  
 AC AAW50859;  
 XX 31-JUL-1998 (first entry)  
 DT Cyclic peptide which mimics surface feature of endothelin.  
 XX Endothelin; endothelina; endothelinb; Efa; Efb; receptor;  
 KW endothelin-1; cyclic.  
 XX Synthetic.  
 OS Key Location/Qualifiers  
 FT Modified-site 1

FT /note= "D-form residue, amino group of Asp is  
 condensed onto the carboxy group of Trp5 to  
 form a cyclic peptide"  
 FT Misc-difference 3 /note= "D-form residue"  
 FT Modified-site 5 /note= "D-form residue, carboxy group of Trp is  
 condensed onto the amino group of Asp1 to form  
 a cyclic peptide"  
 FT US5736509-A.  
 XX 07-APR-1998.  
 XX 10-NOV-1994; 94US-0410955.  
 XX 10-NOV-1994; 94US-0410955.  
 PR 14-DEC-1990; 90US-0628111.  
 PR 18-JUN-1992; 92US-0900623.  
 PR 05-APR-1994; 94US-0223513.  
 XX (TEXA-) TEXAS BIOTECHNOLOGY CORP.  
 XX Balaji VN, Chan MF;  
 PI WPI; 1998-239252/21.  
 XX New cyclic penta-peptides which are mimics of C-terminus of natural  
 endothelin-1 - useful for relieving symptoms of and for treating  
 endothelin mediated disorders and diseases  
 XX Example 5; Column 33; 30pp; English.  
 XX The invention relates to cyclic peptides that mimic the surface  
 features of the endothelin peptides. The peptides shown in the invention  
 are pentapeptides, hexapeptides and heptapeptides that contain an L-Trp,  
 D-Trp residue or a derivative of D- or L-Trp, such as N-Me-Trp. The  
 peptides modulate the activity of one or more members of the endothelin  
 family of peptides. They are useful for relieving symptoms of and for  
 treating endothelin mediated disorders and diseases. The present sequence  
 represents a cyclic pentapeptide.  
 XX Sequence 5 AA;  
 SQ Query Match 65.2%; Score 15; DB 19; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 LW 5  
 DB 4 LW 5  
 RESULT 71  
 ID AAY30995 standard; peptide; 5 AA.  
 AC AAY30995;  
 XX 21-OCT-1999 (first entry)  
 DT Non-crosslinked protein particle peptide 44.  
 XX Non-crosslinked protein particle; diagnostic; therapy; monodisperse;  
 KW albumin; haemoglobin; nanometer; micrometer; clearance.  
 XX Synthetic.  
 OS US5945033-A.  
 XX 31-AUG-1999.  
 PD 12-NOV-1996; 96US-0747137.  
 PF

```

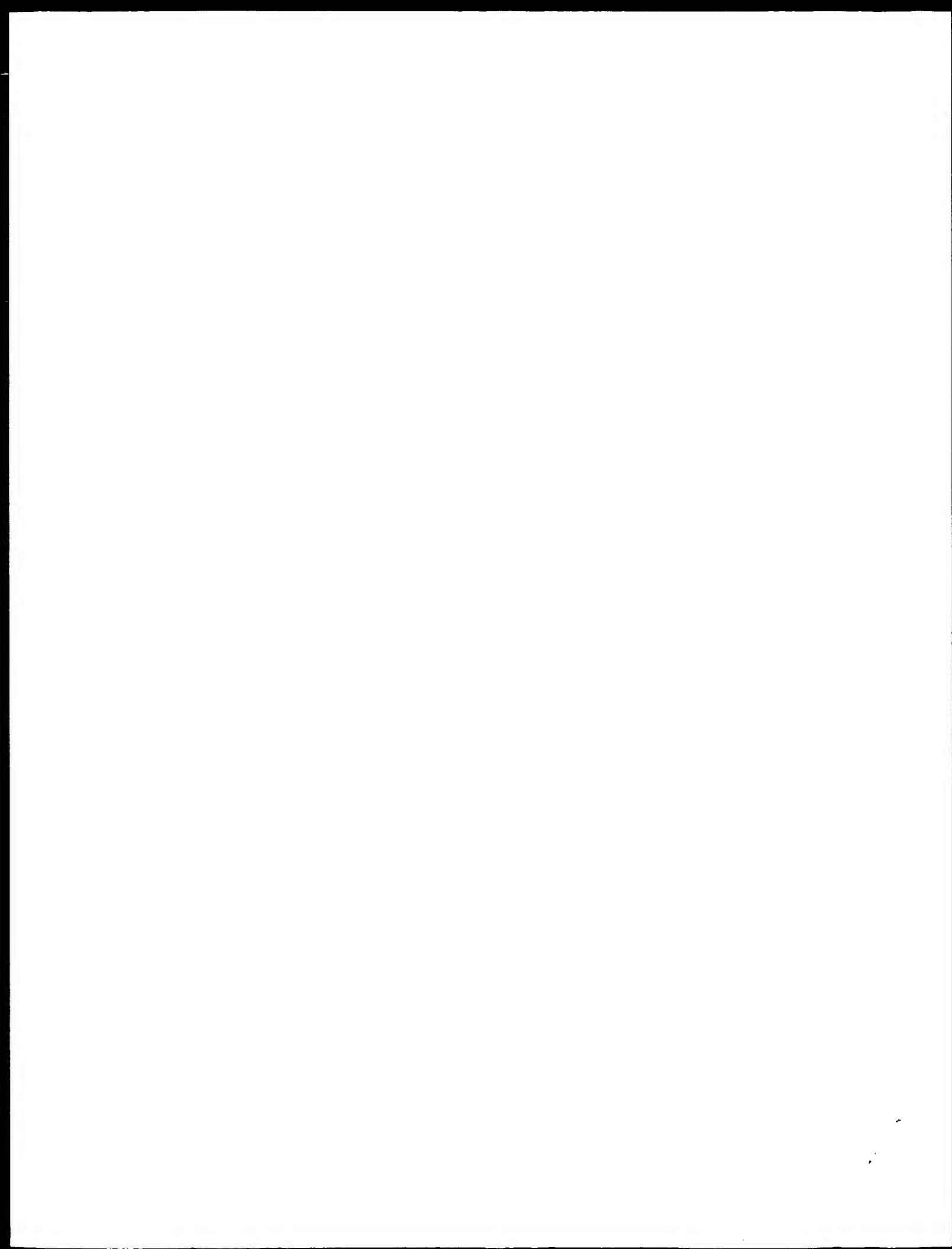
XX PR 14-MAR-1994; 94US-0212546.
XX PR 15-JAN-1991; 91US-0641720.
XX PR 13-OCT-1992; 92US-0959560.
XX PR 01-JUN-1993; 93US-0069831.
XX PR 12-NOV-1996; 96US-0747137.
XX PA (HEMO-) HEMOSPHERE INC.
XX PI Yen RCK;
XX DR WPI; 1999-508153/42.
XX PT Non-crosslinked protein particles for therapeutic and diagnostic use
XX PS Example 22; Column 65-66; 65pp; English.
XX CC This invention describes a novel aqueous suspension of monodisperse
XX CC particles on non-crosslinked, non-denatured albumin (50-5000 nm) which
XX CC is stable against dissolving upon dilution with an alcohol-free aqueous
XX CC medium. The method involves (a) forming an aqueous solution containing
XX CC albumin and hemoglobin and (b) treating the aqueous solution with an
XX CC alcohol to cause the solution to become turbid. The particles are useful
XX CC as agents for in vivo administration, either of their own administration
XX CC or as a vehicle for other therapeutic or diagnostic agents. The method
XX CC permits the formation of albumin and hemoglobin particles in the
XX CC nanometer and micrometer size range, in a form closer to their natural
XX CC form than the forms of the prior art. The particles therefore constitute
XX CC a more closely controlled agent for in vivo administration, with greater
XX CC ease of clearance from the body after their period of usefulness.
XX CC AAY30952-Y31135 represent peptides used in the method of the invention.
XX SQ Sequence 5 AA;
XX Query Match 65.2%; Score 15; DB 20; Length 5;
XX Best Local Similarity 100.0%; Pred. No. 7.8e+05;
XX Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 LW 5
Db 2 LW 3
RESULT 72
AAY31277
ID AAY31277 standard; peptide; 5 AA.
XX AC AAY31277;
XX DT 28-SEP-1999 (first entry)
XX DE Acetyl choline (muscarinic) GPCR consensus peptide motif.
XX KW Gene characterisation; recombinase; homology clamp; homology motif tag;
XX KW HMT; genetic manipulation; genetic engineering; gene transcription; GPCR;
XX KW drug target; homologous recombination; target identification; TGF-beta;
XX KW G-protein coupled receptor; transforming growth factor-beta.
XX OS Homo sapiens.
XX PN WO9937755-A2.
XX PD 29-JUL-1999.
XX PF 11-DEC-1998; 98WO-US26498.
XX PR 11-DEC-1997; 97US-0070734.
XX PA (PANG-) PANGENE CORP.
XX PI Bahman CW, Pati S, Zarling D, Zeng H;
XX DR WPI; 1999-458689/38.

XX PT New compositions and methods for targeting sequence modifications in
XX PR related family genes
XX PS Disclosure; Fig 1A; 46pp; English.
XX CC The invention provides compositions and methods for the evaluation and
XX CC characterisation of individual and sets of genes in disease states. The
XX CC composition comprises at least one recombinase and at least two single-
XX CC stranded targeting polynucleotides which are substantially complementary
XX CC to each other and each having a consensus homology clamp for a gene
XX CC family i.e. a homology motif tag (HMT). The composition is useful in kit
XX CC form which include the composition as libraries or pools of degenerate
XX CC cssDNA probes along with other reagents such as recombinase etc. The
XX CC methods and compositions are used for inactivation of a gene family gene
XX CC i.e. exogenous targeting polynucleotides can be used to inactivate,
XX CC decrease or alter the biological activity of one or more genes in a cell
XX CC (or transgenic nonhuman animal or plant). This is useful for generating
XX CC animal models of disease, or in the elucidation of gene function and
XX CC activity. Alternatively, the biological activity of the wild-type gene
XX CC may be either decreased or the wild-type activity altered to mimic
XX CC disease states. This includes genetic manipulation of non-coding gene
XX CC sequences that affect the transcription of genes, including promoter,
XX CC repressors, enhancers and transcriptional activating sequences. The
XX CC compositions are useful in identifying new members of gene families
XX CC which may be useful in functional genomic studies as well as in
XX CC identification of new drug targets. HMTs used in homologous recombination
XX CC methods can generate animals that have a wide variety of mutations in a
XX CC wide variety of related genes, potentially resulting in a wide variety of
XX CC phenotypes including those related to disease states. This may also be
XX CC done on a cellular level to identify genes involved in cellular
XX CC phenotypes i.e. target identification. Sequences AAY31248-308 represent
XX CC consensus peptide motifs of the G-protein coupled receptor (GPCR) gene
XX CC family and transforming growth factor-beta (TGF-beta) gene family.
XX SQ Sequence 5 AA;
XX Query Match 65.2%; Score 15; DB 20; Length 5;
XX Best Local Similarity 100.0%; Pred. No. 7.8e+05;
XX Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 LW 5
Db 3 LW 4
RESULT 73
AAY01560
ID AAY01560 standard; peptide; 5 AA.
XX AC AAY01560;
XX DT 18-JUN-1999 (first entry)
XX DE Antigenic peptide of streptokinase.
XX KW Antigenic peptide; streptokinase; streptokinase-specific antibody;
XX KW thrombolytic activity; thrombolytic therapy; glomerulonephritis;
XX KW rheumatic fever.
XX OS Streptococcus equisimilis.
XX PN WO9908698-A1.
XX PD 25-FEB-1999.
XX PF 18-AUG-1998; 98WO-US17114.
XX PR 18-AUG-1997; 97US-0055911.
XX PA (GEHO ) GEN HOSPITAL CORP.
XX PA (HARD ) HARVARD COLLEGE.

```

PI Parhami-Seren B, Reed GL;  
 XX WPI; 1999-190113/16.  
 XX  
 XX New polypeptides which bind streptokinase-specific antibodies -  
 PT useful in thrombolytic therapy  
 XX  
 XX Example 1; Page 24; 44pp; English.  
 XX  
 XX The present sequence represents an antigenic peptide of streptokinase.  
 CC The specification describes a polypeptide which binds to a  
 CC streptokinase-specific antibody and prevents the antibody binding to  
 CC native streptokinase. The specification also describes a synthetic  
 CC polypeptide (PI) comprising an epitope which binds to an  
 CC streptokinase-specific antibody and reduces thrombolytic activity  
 CC of streptokinase. PI is used in thrombolytic therapy, and to  
 CC prevent or treat glomerulonephritis and rheumatic fever.  
 XX  
 XX Sequence 5 AA;  
 SQ  
 Query Match 65.2%; Score 15; DB 20; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 LW 5  
 DB 3 LW 4  
 RESULT 74  
 AAW99381  
 ID AAW99381 standard; peptide; 5 AA.  
 AC AAW99381;  
 XX  
 XX 21-MAY-1999 (first entry)  
 DT  
 XX Fibrinogen peptide B(beta)123-127.  
 DE  
 XX Antibody; epitope; trypsin; human; fibrinogen; detection; enzyme;  
 KW cleavage; thrombosis; thrombus; fibrinolysis.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO9905261-A1.  
 PN  
 XX 04-FEB-1999.  
 PD  
 XX  
 XX 22-JUL-1998; 98WO-US15227.  
 PF  
 XX  
 XX 25-JUL-1997; 97US-0900895.  
 PR  
 XX (NYBL-) NEW YORK BLOOD CENT INC.  
 PA  
 XX Bini A, Kudryk B;  
 PI  
 XX WPI; 1999-142920/12.  
 DR  
 XX New monospecific antibody to fibrin(ogen) - which can selectively  
 PT bind matrix metalloproteinase-mediated cleavage fragments of fibrin  
 PT or fibrinogen  
 PS  
 XX Claim 1; Page 34; 75pp; English.  
 XX  
 XX The invention relates to a monospecific antibody that binds specifically  
 CC with an epitope defined by the amino acid sequence shown here. The  
 CC peptide corresponds to a fragment of a trypsin-digested human fibrinogen  
 CC and is designated fragment B(beta)123-127. The antibody can be used for  
 CC detecting and measuring enzyme-mediated breakdown of fibrinogen and  
 CC fibrin. The specific detection of cleavage products of fibrin and  
 CC fibrinogen permits the accurate and precise determination of thrombotic  
 CC activity in individuals. The products can be used to study thrombus  
 CC development and thrombolysis.

XX  
 SQ Sequence 5 AA;  
 Query Match 65.2%; Score 15; DB 20; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 LW 5  
 DB 2 LW 3  
 RESULT 75  
 AAB52657  
 ID AAB52657 standard; Peptide; 5 AA.  
 AC AAB52657;  
 XX  
 XX 23-FEB-2001 (first entry)  
 DT  
 XX T20/DPI178 peptide fragment #35.  
 DE  
 XX Antiinflammatory; T20/DPI178; gp41 ectodomain; HIV-1 fusion;  
 KW formyl peptide receptor family; FPR; inflammatory response up-regulation;  
 KW chemoattractant.  
 KW  
 XX Human immunodeficiency virus type 1.  
 OS  
 XX WO200066622-A1.  
 PN  
 XX 09-NOV-2000.  
 PD  
 XX 05-MAY-2000; 2000WO-US12371.  
 PF  
 XX 05-MAY-1999; 99US-0132686.  
 PR  
 XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 XX Wang JM, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;  
 PI WPI; 2000-656493/63.  
 DR  
 XX Administration of peptide agents with a sequence corresponding to a  
 PT partial-length T20/DPI178 or T21/DPI107 formyl peptide receptor  
 PT antagonist is used to modulate inflammation -  
 XX  
 XX Claim 12; Page 24; 148pp; English.  
 PS  
 XX The present sequence is a peptide fragment of T20/DPI178. T20/DPI178 is a  
 CC helical segment of the ectodomain of HIV-1 protein gp41. T20/DPI178 is  
 CC located in the carboxyl terminus of the gp41 ectodomain. gp41 plays a  
 CC critical role in the fusion of HIV-1 and host cell membranes. T20/DPI178  
 CC interacts with members of the formyl peptide receptor (FPR) family and  
 CC thereby up-regulates an inflammatory response, and acts as a potent  
 CC chemoattractant and activator of human peripheral blood phagocytes  
 CC (but not T cells). The present peptide can be used to modulate an  
 CC inflammatory response in a subject.  
 XX  
 XX Sequence 5 AA;  
 SQ  
 Query Match 65.2%; Score 15; DB 21; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 LW 5  
 DB 1 LW 2  
 Search completed: February 12, 2003, 10:51:37  
 Job time : 82 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 12, 2003, 10:52:34 ; Search time 29 Seconds  
(without alignments)  
4.405 Million cell updates/sec

Title: US-09-403-440A-1

Perfect score: 23

Sequence: 1 FXXIWW 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 140259 seqs, 25548876 residues

Total number of hits satisfying chosen parameters: 2165

Minimum DB seq length: 5

Maximum DB seq length: 5

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA.\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	82.6	5	10	US-09-214-371-2
2	19	82.6	5	10	US-09-281-717-3
3	15	65.2	5	8	US-08-424-550B-228
4	15	65.2	5	10	US-09-841-132-9
5	13	56.5	5	9	US-09-968-561A-211
6	13	56.5	5	9	US-09-968-561A-217
7	13	56.5	5	9	US-09-201-396-7
8	13	56.5	5	9	US-10-105-930-70
9	13	56.5	5	9	US-09-903-412-51
10	13	56.5	5	10	US-09-096-749A-51
11	13	56.5	5	10	US-09-192-854-120
12	13	56.5	5	10	US-09-924-703-9
13	12	52.2	5	8	US-08-239-765B-4
14	12	52.2	5	10	US-09-096-749A-94
15	12	52.2	5	10	US-09-866-135-1
16	11	47.8	5	8	US-08-484-409-35
17	11	47.8	5	8	US-08-424-550B-469
18	11	47.8	5	9	US-09-995-749A-14
19	11	47.8	5	9	US-09-764-884-2

20	11	47.8	5	9	US-09-895-593-15	Sequence 15, Appl
21	11	47.8	5	9	US-09-895-593-16	Sequence 16, Appl
22	11	47.8	5	9	US-09-423-800-62	Sequence 62, Appl
23	11	47.8	5	9	US-09-764-857-2	Sequence 2, Appl
24	11	47.8	5	9	US-09-860-670-2	Sequence 2, Appl
25	11	47.8	5	9	US-09-981-876-2	Sequence 2, Appl
26	11	47.8	5	9	US-09-984-245-2	Sequence 2, Appl
27	11	47.8	5	9	US-09-764-868-2	Sequence 2, Appl
28	11	47.8	5	9	US-10-014-485A-79	Sequence 79, Appl
29	11	47.8	5	9	US-10-104-019-42	Sequence 42, Appl
30	11	47.8	5	9	US-09-764-904-2	Sequence 2, Appl
31	11	47.8	5	9	US-09-852-797-2	Sequence 2, Appl
32	11	47.8	5	9	US-09-964-992A-11	Sequence 11, Appl
33	11	47.8	5	9	US-10-035-349-2	Sequence 2, Appl
34	11	47.8	5	9	US-10-035-349-8	Sequence 8, Appl
35	11	47.8	5	9	US-09-828-272A-6	Sequence 6, Appl
36	11	47.8	5	9	US-10-042-141-2	Sequence 2, Appl
37	11	47.8	5	9	US-10-059-749-57	Sequence 57, Appl
38	11	47.8	5	9	US-10-059-749-63	Sequence 63, Appl
39	11	47.8	5	9	US-10-059-749-69	Sequence 69, Appl
40	11	47.8	5	9	US-10-079-625-6	Sequence 6, Appl
41	11	47.8	5	9	US-10-029-301-4	Sequence 4, Appl
42	11	47.8	5	9	US-10-074-956-6	Sequence 6, Appl
43	11	47.8	5	9	US-10-078-059-5	Sequence 5, Appl
44	11	47.8	5	9	US-10-087-195-3	Sequence 3, Appl
45	11	47.8	5	9	US-09-320-713-14	Sequence 14, Appl
46	11	47.8	5	9	US-09-774-639-2	Sequence 2, Appl
47	11	47.8	5	9	US-09-798-889-2	Sequence 2, Appl
48	11	47.8	5	9	US-10-103-930-21	Sequence 21, Appl
49	11	47.8	5	9	US-10-103-930-57	Sequence 57, Appl
50	11	47.8	5	9	US-10-103-930-58	Sequence 58, Appl
51	11	47.8	5	9	US-10-103-930-59	Sequence 59, Appl
52	11	47.8	5	9	US-10-103-930-60	Sequence 60, Appl
53	11	47.8	5	9	US-10-103-930-61	Sequence 61, Appl
54	11	47.8	5	9	US-10-103-930-62	Sequence 62, Appl
55	11	47.8	5	9	US-10-103-930-63	Sequence 63, Appl
56	11	47.8	5	9	US-10-103-930-64	Sequence 64, Appl
57	11	47.8	5	9	US-10-103-930-65	Sequence 65, Appl
58	11	47.8	5	9	US-10-103-930-66	Sequence 66, Appl
59	11	47.8	5	9	US-10-103-930-67	Sequence 67, Appl
60	11	47.8	5	9	US-10-103-930-68	Sequence 68, Appl
61	11	47.8	5	9	US-10-103-930-69	Sequence 69, Appl
62	11	47.8	5	9	US-10-103-930-71	Sequence 71, Appl
63	11	47.8	5	9	US-10-103-930-72	Sequence 72, Appl
64	11	47.8	5	9	US-10-103-930-73	Sequence 73, Appl
65	11	47.8	5	9	US-10-103-930-74	Sequence 74, Appl
66	11	47.8	5	9	US-10-103-930-75	Sequence 75, Appl
67	11	47.8	5	9	US-10-103-930-76	Sequence 76, Appl
68	11	47.8	5	9	US-09-262-126C-8	Sequence 8, Appl
69	11	47.8	5	9	US-09-989-442-2	Sequence 2, Appl
70	11	47.8	5	9	US-10-116-067-3	Sequence 3, Appl
71	11	47.8	5	9	US-09-363-248-5	Sequence 5, Appl
72	11	47.8	5	9	US-09-393-696-14	Sequence 14, Appl
73	11	47.8	5	9	US-09-747-377-493	Sequence 493, App
74	11	47.8	5	9	US-09-983-802-2	Sequence 2, Appl
75	11	47.8	5	9	US-10-062-523-5	Sequence 5, Appl
76	11	47.8	5	9	US-10-125-451-22	Sequence 22, Appl
77	11	47.8	5	9	US-10-171-077-2	Sequence 2, Appl
78	11	47.8	5	9	US-10-245-803-8	Sequence 8, Appl
79	11	47.8	5	9	US-09-148-545-2	Sequence 2, Appl
80	11	47.8	5	9	US-09-376-430-5	Sequence 5, Appl
81	11	47.8	5	9	US-09-832-129-2	Sequence 2, Appl
82	11	47.8	5	9	US-09-903-412-33	Sequence 33, Appl
83	11	47.8	5	9	US-09-903-412-39	Sequence 39, Appl
84	11	47.8	5	9	US-09-903-412-42	Sequence 42, Appl
85	11	47.8	5	9	US-09-903-412-43	Sequence 43, Appl
86	11	47.8	5	9	US-09-903-412-44	Sequence 44, Appl
87	11	47.8	5	9	US-09-903-412-45	Sequence 45, Appl
88	11	47.8	5	9	US-09-903-412-49	Sequence 49, Appl
89	11	47.8	5	9	US-09-903-412-57	Sequence 57, Appl
90	11	47.8	5	9	US-09-903-412-59	Sequence 59, Appl
91	11	47.8	5	9	US-09-903-412-61	Sequence 61, Appl
92	11	47.8	5	9	US-09-903-412-67	Sequence 67, Appl

93 11 47.8 5 9 US-09-903-412-69 Sequence 69, Appl  
94 11 47.8 5 9 US-09-903-412-74 Sequence 74, Appl  
95 11 47.8 5 9 US-09-903-412-76 Sequence 76, Appl  
96 11 47.8 5 9 US-09-903-412-78 Sequence 78, Appl  
97 11 47.8 5 9 US-09-903-412-80 Sequence 80, Appl  
98 11 47.8 5 9 US-09-903-412-82 Sequence 82, Appl  
99 11 47.8 5 9 US-09-903-412-84 Sequence 84, Appl  
100 11 47.8 5 9 US-09-903-412-86 Sequence 86, Appl

## ALIGNMENTS

RESULT 1  
US-09-214-371-2  
; Sequence 2, Application US/09214371B  
; Patent No. US20010018511A1  
; GENERAL INFORMATION:  
; APPLICANT: Lane, David  
; APPLICANT: Bottger, Volker  
; APPLICANT: Bottger, Angelica  
; APPLICANT: Pickaley, Stephen  
; APPLICANT: Chene, Patrick  
; APPLICANT: Hochkeppel, Heinz-Kurt  
; APPLICANT: Garcia-Echeverria, Carlos  
; APPLICANT: Furet, Pascal  
; TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2  
; FILE REFERENCE: 4-20937/A/PCT  
; CURRENT APPLICATION NUMBER: US/09/214,371B  
; CURRENT FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: PCT/EP97/03549  
; PRIOR FILING DATE: 1997-07-04  
; NUMBER OF SEQ ID NOS: 83  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:peptide  
; OTHER INFORMATION: Where Xaa may be any amino acid  
US-09-214-371-2

Query Match 82.6%; Score 19; DB 10; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXLW 5  
| | | | |  
Db 1 FXXLW 5

RESULT 2  
US-09-281-717-3  
; Sequence 3, Application US/09281717  
; Patent No. US20020061539A1  
; GENERAL INFORMATION:  
; APPLICANT: Baxter, John D.  
; APPLICANT: Darimont, Beatrice  
; APPLICANT: Feng, Weijun  
; APPLICANT: Fletcher, Robert J.  
; APPLICANT: Kushner, Peter J.  
; APPLICANT: Wagner, Richard L.  
; APPLICANT: West, Brian  
; APPLICANT: Yamamoto, Keith R.  
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING NUCLEAR RECEPTOR  
; FILE REFERENCE: UCAL-253/02US  
; CURRENT APPLICATION NUMBER: US/09/281,717  
; CURRENT FILING DATE: 1999-03-30  
; EARLIER APPLICATION NUMBER: US 60/079,956  
; EARLIER FILING DATE: 1998-03-30  
; NUMBER OF SEQ ID NOS: 51

; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (2)-(3)  
; OTHER INFORMATION: Xaa = Any Amino Acid  
US-09-281-717-3

Query Match 82.6%; Score 19; DB 10; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXLW 5  
| | | | |  
Db 1 FXXLW 5

RESULT 3  
US-08-424-550B-228  
; Sequence 228, Application US/08424550B  
; Patent No. US20020119447A1  
; GENERAL INFORMATION:  
; APPLICANT: JOHN N. SIMONS  
; APPLICANT: TAMI J. PILOT-MATIAS  
; APPLICANT: GEORGE J. DAWSON  
; APPLICANT: GEORGE G. SCHLAUDER  
; APPLICANT: SURESH M. DESAI  
; APPLICANT: THOMAS P. LEARY  
; APPLICANT: ANTHONY SCOTT MUERHOFF  
; APPLICANT: JAMES C. ERKER  
; APPLICANT: SHERI L. BUIJK  
; APPLICANT: ISA K. MUSHAWAR  
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS  
; REAGENTS AND METHODS FOR THEIR USE  
; NUMBER OF SEQUENCES: 716  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D  
; STREET: 100 ABBOTT PARK ROAD  
; CITY: ABBOTT PARK  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60064-3500  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/424,550B  
; FILING DATE:  
; CLASSIFICATION: 435435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: POREMSKI, PRISCILLA E.  
; REGISTRATION NUMBER: 33,207  
; REFERENCE/DOCKET NUMBER: 5527.PC.01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 708-937-6365  
; TELEFAX: 708-938-2623  
; INFORMATION FOR SEQ ID NO: 228:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-424-550B-228

Query Match 65.2%; Score 15; DB 8; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



QY 4 LW 5  
||  
Db 3 LW 4

## RESULT 4

US-09-841-132-9  
; Sequence 9, Application US/09841132  
; Patent No. US20020061848A1  
; GENERAL INFORMATION:  
; APPLICANT: Bhatia, Ajay  
; APPLICANT: Probst, Peter  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND  
; FILE REFERENCE: 210121.469C8  
; CURRENT APPLICATION NUMBER: US/09/841.132  
; CURRENT FILING DATE: 2001-04-23  
; NUMBER OF SEQ ID NOS: 599  
; SOFTWARE: FastSeq for Windows Version 3.0/4.0  
; SEQ ID NO 9  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Chlamydia trachomatis  
US-09-841-132-9

Query Match 65.2%; Score 15; DB 10; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5  
||  
Db 3 LW 4

## RESULT 5

US-09-968-561A-211  
; Sequence 211, Application US/09968561A  
; Patent No. US20020164642A1  
; GENERAL INFORMATION:  
; APPLICANT: Tomlinson, Ian M  
; APPLICANT: Winter, Gregory  
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands  
; FILE REFERENCE: 8039/1073B  
; CURRENT APPLICATION NUMBER: US/09/968,561A  
; CURRENT FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: GB 9722131.1  
; PRIOR FILING DATE: 1997-10-20  
; PRIOR APPLICATION NUMBER: US 60/065,248  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: US 60/066,729  
; PRIOR FILING DATE: 1997-11-21  
; PRIOR APPLICATION NUMBER: PCT/GB98/03135  
; PRIOR FILING DATE: 1998-10-20  
; PRIOR APPLICATION NUMBER: US 09/511,939  
; PRIOR FILING DATE: 2000-02-24  
; NUMBER OF SEQ ID NOS: 350  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 211  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-968-561A-211

Query Match 56.5%; Score 13; DB 9; Length 5;  
Best Local Similarity 50.0%; Pred. No. 1.2e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5  
||  
Db 4 MW 5

## RESULT 6

US-09-968-561A-217  
; Sequence 217, Application US/09968561A  
; Patent No. US20020164642A1  
; GENERAL INFORMATION:  
; APPLICANT: Tomlinson, Ian M  
; APPLICANT: Winter, Gregory  
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands  
; FILE REFERENCE: 8039/1073B  
; CURRENT APPLICATION NUMBER: US/09/968,561A  
; CURRENT FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: GB 9722131.1  
; PRIOR FILING DATE: 1997-10-20  
; PRIOR APPLICATION NUMBER: US 60/065,248  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: US 60/066,729  
; PRIOR FILING DATE: 1997-11-21  
; PRIOR APPLICATION NUMBER: PCT/GB98/03135  
; PRIOR FILING DATE: 1998-10-20  
; PRIOR APPLICATION NUMBER: US 09/511,939  
; PRIOR FILING DATE: 2000-02-24  
; NUMBER OF SEQ ID NOS: 350  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 217  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-968-561A-217

Query Match 56.5%; Score 13; DB 9; Length 5;  
Best Local Similarity 50.0%; Pred. No. 1.2e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5  
||  
Db 4 MW 5

## RESULT 7

US-09-201-396-7  
; Sequence 7, Application US/09201396A  
; Publication No. US20030009022A1  
; GENERAL INFORMATION:  
; APPLICANT: Klein, Christine A.  
; APPLICANT: Murphy, Andrew J.  
; APPLICANT: Paul, Jeremy  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IDENTIFYING RECEPTOR  
; TITLE OF INVENTION: EFFECTORS  
; FILE REFERENCE: CPI-012CP9  
; CURRENT APPLICATION NUMBER: US/09/201,396A  
; CURRENT FILING DATE: 1998-11-30  
; EARLIER APPLICATION NUMBER: 08/582,333  
; EARLIER FILING DATE: 1996-01-17  
; EARLIER APPLICATION NUMBER: 08/322,137  
; EARLIER FILING DATE: 1994-10-13  
; EARLIER APPLICATION NUMBER: 08/309,313  
; EARLIER FILING DATE: 1994-09-20  
; EARLIER APPLICATION NUMBER: 08/190,328  
; EARLIER FILING DATE: 1994-01-31  
; EARLIER APPLICATION NUMBER: 08/041,431  
; EARLIER FILING DATE: 1993-03-31  
; NUMBER OF SEQ ID NOS: 47  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 7  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: construct  
US-09-201-396-7

Query Match 56.5%; Score 13; DB 9; Length 5;

Best Local Similarity 50.0%; Pred. No. 1.2e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5  
:|  
Db 2 MW 3

## RESULT 8

US-10-105-930-70  
; Sequence 70, Application US/10105930  
; Publication No. US20030009018A1  
; GENERAL INFORMATION:  
; APPLICANT: Maeda, Masatsugu  
; TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR12  
; FILE REFERENCE: 06501-1050S1  
; CURRENT APPLICATION NUMBER: US/10/105,930  
; CURRENT FILING DATE: 2002-03-25  
; PRIOR APPLICATION NUMBER: PCT/JP00/06654  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: JP 2000-240397  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: JP 11-273358  
; PRIOR FILING DATE: 1999-09-27  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 70  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-105-930-70

Qy 4 LW 5  
:|  
Db 3 MW 4

Query Match 56.5%; Score 13; DB 9; Length 5;  
Best Local Similarity 50.0%; Pred. No. 1.2e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

## RESULT 9

US-09-903-412-51  
; Sequence 51, Application US/09903412  
; Publication No. US20030027319A1  
; GENERAL INFORMATION:  
; APPLICANT: Koide, Shohei  
; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES  
; FILE REFERENCE: 109.050US1  
; CURRENT APPLICATION NUMBER: US/09/903,412  
; CURRENT FILING DATE: 2001-07-11  
; PRIOR APPLICATION NUMBER: US 60/217,474  
; PRIOR FILING DATE: 2000-07-11  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 51  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: The sequence of the BC loop of clone pLB24.2.  
US-09-903-412-51

Qy 4 LW 5  
:|  
Db 2 MW 3

Query Match 56.5%; Score 13; DB 9; Length 5;  
Best Local Similarity 50.0%; Pred. No. 1.2e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

## RESULT 10

US-09-096-749A-51  
; Sequence 51, Application US/09096749A  
; Patent No. US20020019517A1  
; GENERAL INFORMATION:  
; APPLICANT: Koide, Shohei  
; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES  
; NUMBER OF SEQUENCES: 118  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.  
; STREET: 121 South Eighth Street, Ste. 1600  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: USA  
; ZIP: 55402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/096,749A  
; FILING DATE: June 12, 1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ann S. Viksnins  
; REGISTRATION NUMBER: 37,748  
; REFERENCE/DOCKET NUMBER: 109.034US1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (612) 373-6900  
; TELEFAX: (612) 339-3061  
; INFORMATION FOR SEQ ID NO: 51:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHEetical: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal  
; ORIGINAL SOURCE:  
; US-09-096-749A-51

Qy 4 LW 5  
:|  
Db 2 MW 3

Query Match 56.5%; Score 13; DB 10; Length 5;  
Best Local Similarity 50.0%; Pred. No. 1.2e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

## RESULT 11

US-09-192-854-120  
; Sequence 120, Application US/09192854  
; Patent No. US20020068276A1  
; GENERAL INFORMATION:  
; APPLICANT: Tomlinson, Ian  
; TITLE OF INVENTION: Methods for Selecting Functional Peptides  
; FILE REFERENCE: 3789/72916  
; CURRENT APPLICATION NUMBER: US/09/192,854  
; CURRENT FILING DATE: 1998-11-17  
; EARLIER APPLICATION NUMBER: 60/066,729  
; EARLIER FILING DATE: 1997-11-21  
; NUMBER OF SEQ ID NOS: 212  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 120  
; LENGTH: 5  
; TYPE: PRT

; ORGANISM: Homo sapiens  
US-09-192-854-120

Query Match 56.5%; Score 13; DB 10; Length 5;  
Best Local Similarity 50.0%; Pred. No. 1.2e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5  
:|  
Db 4 MW 5

## RESULT 12

US-09-924-703-9  
; Sequence 9, Application US/09924703  
; Patent No. US20020137898A1  
; GENERAL INFORMATION:  
; APPLICANT: TRINCHIERI, GIORGIO  
; APPLICANT: PERUSSIA, BICE  
; APPLICANT: CLARK, STEVEN C.  
; APPLICANT: WONG, GORDON G.  
; APPLICANT: HEWICK, RODNEY  
; APPLICANT: KOBAYASHI, MICHIO  
; TITLE OF INVENTION: ANTIBODIES TO NATURAL KILLER STIMULATORY FACTOR  
; FILE REFERENCE: 01142.0142.0100  
; CURRENT APPLICATION NUMBER: US/09/924,703  
; CURRENT FILING DATE: 2001-08-09  
; PRIOR APPLICATION NUMBER: 09/325,958  
; PRIOR FILING DATE: 1999-06-04  
; PRIOR APPLICATION NUMBER: 08/858,000  
; PRIOR FILING DATE: 1997-05-16  
; PRIOR APPLICATION NUMBER: 08/403,013  
; PRIOR FILING DATE: 1995-03-13  
; PRIOR APPLICATION NUMBER: 07/584,941  
; PRIOR FILING DATE: 1990-09-18  
; PRIOR APPLICATION NUMBER: 07/307,817  
; PRIOR FILING DATE: 1989-02-07  
; PRIOR APPLICATION NUMBER: 07/269,945  
; PRIOR FILING DATE: 1988-11-10  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 9  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
US-09-924-703-9

Query Match 56.5%; Score 13; DB 10; Length 5;  
Best Local Similarity 50.0%; Pred. No. 1.2e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5  
:|  
Db 1 IW 2

## RESULT 13

US-08-239-765B-4  
; Sequence 4, Application US/08239765B  
; Patent No. US2002026650A1  
; GENERAL INFORMATION:  
; APPLICANT: Savakis, Charalambos  
; APPLICANT: Franz, Gerald H.  
; APPLICANT: Loukeris, Athanasios  
; TITLE OF INVENTION: Eukaryotic Transposable Element  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington

; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02173  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/239,765B  
; FILING DATE: 09-MAY-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/946,237  
; FILING DATE: 14-SEP-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brook, David E.  
; REGISTRATION NUMBER: 22,592  
; REFERENCE/DOCKET NUMBER: BT92-01Z  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 861-6240  
; TELEFAX: (617) 861-9540  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-239-765B-4

Query Match 52.2%; Score 12; DB 8; Length 5;  
Best Local Similarity 50.0%; Pred. No. 1.2e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5  
:|  
Db 2 VW 3

## RESULT 14

US-09-096-749A-94  
; Sequence 94, Application US/09096749A  
; Patent No. US20020019517A1  
; GENERAL INFORMATION:  
; APPLICANT: Koieda, Shohei  
; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES  
; NUMBER OF SEQUENCES: 118  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.  
; STREET: 121 South Eighth Street, Ste. 1600  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: USA  
; ZIP: 55402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/096,749A  
; FILING DATE: June 12, 1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ann S. Viksnins  
; REGISTRATION NUMBER: 37,748  
; REFERENCE/DOCKET NUMBER: 109.034US1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (612) 373-6900  
; TELEFAX: (612) 339-3061

```

; INFORMATION FOR SEQ ID NO: 94:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; US-09-096-749A-94

Query Match 52.2%; Score 12; DB 10; Length 5;
Best Local Similarity 50.0%; Pred. No. 1.2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5
Db 2 VW 3

RESULT 15
US-09-866-135-1
; Sequence 1, Application US/09866135
; Patent No. US20020051443A1
; GENERAL INFORMATION:
; APPLICANT: PITTSYN, Leonid R
; APPLICANT: ALTMAN, Irina B
; APPLICANT: SMIRNOV, Sergey V
; APPLICANT: ROSTOVA, Yulia G
; APPLICANT: YAMPOLSKAYA, Tatyana A
; APPLICANT: LEONOVA, Tatyana V
; APPLICANT: GUSVATINER, Mikhail M
; TITLE OF INVENTION: NEW MUTANT-ACETYLGLUTAMATE SYNTHASE AND METHOD FOR L-ARGININE PRO
; FILE REFERENCE: 209873US0
; CURRENT APPLICATION NUMBER: US/09/866,135
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: RUSSIAN FEDERATION 2000116481
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: RUSSIAN FEDERATION 2001112869
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-866-135-1

Query Match 52.2%; Score 12; DB 10; Length 5;
Best Local Similarity 50.0%; Pred. No. 1.2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5
Db 2 VW 3

RESULT 16
US-08-484-409-35
; Sequence 35, Application US/08484409
; Patent No. US20020076412A1
; GENERAL INFORMATION:
; APPLICANT: Steinman, Lawrence
; APPLICANT: Zamvil, Scott
; TITLE OF INVENTION: METHODS FOR MODULATING THE IMMUNE SYSTEM
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue

```

```

; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,409
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 690068,409C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-484-409-35

Query Match 47.8%; Score 11; DB 8; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5
Db 2 W 2

RESULT 17
US-08-424-550B-469
; Sequence 469, Application US/08424550B
; Patent No. US20020119447A1
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUERHOFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BULJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550B
; FILING DATE:
; CLASSIFICATION: 435435
; ATTORNEY/AGENT INFORMATION:
; NAME: POREBSKI, PRISCILLA E.

```

; REGISTRATION NUMBER: 33,207  
; REFERENCE/DOCKET NUMBER: 5527.PC.01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 708-937-6365  
; TELEFAX: 708-938-2623  
; INFORMATION FOR SEQ ID NO: 469:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-424-550B-469

Query Match 47.8%; Score 11; DB 8; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5  
|  
Db 5 W 5

## RESULT 18

US-09-995-749A-14  
; Sequence 14, Application US/09995749A  
; Patent No. US20020155568A1  
; GENERAL INFORMATION:  
; APPLICANT: VAN GEEL-SCHUTTEN, GERRITDINA HENDRIKA  
; APPLICANT: DIJKHUIZEN, LUBBERT  
; APPLICANT: RAHOUI, HAKIM  
; APPLICANT: LEER, ROBERT-JAN  
; TITLE OF INVENTION: NOVEL GLUCOSYLTRANSFERASES  
; FILE REFERENCE: B043388-CIP  
; CURRENT APPLICATION NUMBER: US/09/995,749A  
; CURRENT FILING DATE: 2001-11-29  
; PRIOR APPLICATION NUMBER: 09/604,957  
; PRIOR FILING DATE: 2000-06-28  
; PRIOR APPLICATION NUMBER: EPO 00201871.1  
; PRIOR FILING DATE: 2000-05-25  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Neisseria polysaccharea  
US-09-995-749A-14

Query Match 47.8%; Score 11; DB 9; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5  
|  
Db 2 W 2

## RESULT 19

US-09-764-884-2  
; Sequence 2, Application US/09764884  
; Patent No. US20020161208A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PT203  
; CURRENT APPLICATION NUMBER: US/09/764,884  
; CURRENT FILING DATE: 2001-01-17  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Homo sapiens

; FEATURE:  
; NAME/KEY: Site  
; LOCATION: (3)  
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids  
US-09-764-884-2

Query Match 47.8%; Score 11; DB 9; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5  
|  
Db 1 W 1

## RESULT 20

US-09-895-593-15  
; Sequence 15, Application US/09895593  
; Patent No. US20020160949A1  
; GENERAL INFORMATION:  
; APPLICANT: Pandey, Akhilesh  
; APPLICANT: Ozaki, Katsutoshi  
; APPLICANT: Baumann, Heinz  
; APPLICANT: Levin, Steven D.  
; APPLICANT: Farr, Andrew G.  
; APPLICANT: Ziegler, Steven F.  
; APPLICANT: Leonard, Warren J.  
; APPLICANT: Lodish, Harvey F.  
; TITLE OF INVENTION: Thymic Stromal Lymphopoietin Receptor Molecules and  
; TITLE OF INVENTION: Uses Thereof  
; FILE REFERENCE: 00-514-E  
; CURRENT APPLICATION NUMBER: US/09/895,593  
; CURRENT FILING DATE: 2001-06-28  
; PRIOR APPLICATION NUMBER: 60/215,658  
; PRIOR FILING DATE: 2000-06-28  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 15  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Type I  
; OTHER INFORMATION: cytokine receptor conserved motif  
; NAME/KEY: UNSURE  
; LOCATION: (3)  
; OTHER INFORMATION: "Xaa" can be any naturally occurring amino acid  
US-09-895-593-15

Query Match 47.8%; Score 11; DB 9; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5  
|  
Db 1 W 1

## RESULT 21

US-09-895-593-16  
; Sequence 16, Application US/09895593  
; Patent No. US20020160949A1  
; GENERAL INFORMATION:  
; APPLICANT: Pandey, Akhilesh  
; APPLICANT: Ozaki, Katsutoshi  
; APPLICANT: Baumann, Heinz  
; APPLICANT: Levin, Steven D.  
; APPLICANT: Farr, Andrew G.  
; APPLICANT: Ziegler, Steven F.  
; APPLICANT: Leonard, Warren J.  
; APPLICANT: Lodish, Harvey F.  
; TITLE OF INVENTION: Thymic Stromal Lymphopoietin Receptor Molecules and  
; TITLE OF INVENTION: Uses Thereof  
US-09-895-593-16

```
; FILE REFERENCE: 00-514-E
; CURRENT APPLICATION NUMBER: US/09/895,593
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: 60/215,658
; PRIOR FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Motif
; OTHER INFORMATION: replacing type I cytokine receptor conserved motif
; OTHER INFORMATION: in murine TSLPR polypeptide
US-09-895-593-16

Query Match          47.8%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 W 5
Db      1 W 1

RESULT 22
US-09-423-800-62
; Sequence 62, Application US/09423800
; Patent No. US20020165363A1
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: TSUNENARI, TOSHIKI
; APPLICANT: ISHII, KIMIE
; TITLE OF INVENTION: CACHEXIA REMEDY
; FILE REFERENCE: 04853-0036
; CURRENT APPLICATION NUMBER: US/09/423,800
; CURRENT FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: PCT/JP98/02116
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: JP 125505/1997
; PRIOR FILING DATE: 1997-05-15
; PRIOR APPLICATION NUMBER: JP 194445/1997
; PRIOR FILING DATE: 1997-07-18
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 62
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-423-800-62

Query Match          47.8%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 W 5
Db      3 W 3

RESULT 23
US-09-764-857-2
; Sequence 2, Application US/09764857
; Patent No. US20020164685A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ11
; CURRENT APPLICATION NUMBER: US/09/764,857
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 13

; FILE REFERENCE: 00-514-E
; CURRENT APPLICATION NUMBER: US/09/895,593
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: 60/215,658
; PRIOR FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Motif
; OTHER INFORMATION: replacing type I cytokine receptor conserved motif
; OTHER INFORMATION: in murine TSLPR polypeptide
US-09-895-593-16

Query Match          47.8%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 W 5
Db      1 W 1

RESULT 24
US-09-860-670-2
; Sequence 2, Application US/09860670
; Patent No. US20020165137A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA127P1
; CURRENT APPLICATION NUMBER: US/09/860,670
; CURRENT FILING DATE: 2001-05-21
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 289
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: Site
; LOCATION: (3)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-09-860-670-2

Query Match          47.8%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 W 5
Db      1 W 1

RESULT 25
US-09-981-876-2
; Sequence 2, Application US/09981876
; Patent No. US20020164669A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 70 Human Secreted Proteins
; FILE REFERENCE: PZ001P1
; CURRENT APPLICATION NUMBER: US/09/981,876
; CURRENT FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: 09/148,545
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,333
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/038,621
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,161
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,626
```



```

; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,576
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/047,501
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/043,670
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/056,632
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,664
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,876
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,881
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,909
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,875
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,862
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,887
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,908
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/048,964
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/057,650
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/056,884
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 280
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 5

Query Match      47.8%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 W 5
Db      1 W 1

```

## RESULT 26

```

US-09-984-245-2
; Sequence 2, Application US/09984245
; Patent No. US20020165374A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 87 Human Secreted Proteins
; FILE REFERENCE: P2004P1
; CURRENT APPLICATION NUMBER: US/09/984,245
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/154,707
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: PCT/US98/05311
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: US 60/041,277
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/042,344
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,276
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,281
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/048,094
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,350
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,188
; PRIOR FILING DATE: 1997-05-30

```

```

; PRIOR APPLICATION NUMBER: US 60/048,135
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/050,937
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,187
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,099
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,352
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,186
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,069
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,095
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,131
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,096
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,355
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,160
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,351
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,154
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/054,804
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: US 60/056,370
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: US 60/060,862
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 343
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (3)
; OTHER INFORMATION: Xaa equals any of the L-amino acids commonly found in naturally o
; OTHER INFORMATION: proteins
; US-09-984-245-2

```

## Query Match

```

Query Match      47.8%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy 5 W 5

Db 1 W 1

## RESULT 27

```

US-09-764-868-2
; Sequence 2, Application US/09764868
; Patent No. US20020168711A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PYZ32
; CURRENT APPLICATION NUMBER: US/09/764,868
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1510
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens

```



; FEATURE:  
; NAME/KEY: Site  
; LOCATION: (3)  
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids  
US-09-764-868-2

Query Match 47.8%; Score 11; DB 9; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5  
|  
Db 1 W 1

## RESULT 28

US-10-014-485A-79  
; Sequence 79, Application US/10014485A  
; Patent No. US20020168684A1  
; GENERAL INFORMATION:  
; APPLICANT: Cell Signaling Technology, Inc.  
; APPLICANT: COMB, Michael J.  
; APPLICANT: ZHANG, Hui  
; APPLICANT: TAN, Yi  
; TITLE OF INVENTION: PRODUCTION OF MOTIF-SPECIFIC AND CONTEXT-INDEPENDENT ANTIBODIES U  
; FILE OF INVENTION: PEPTIDE LIBRARIES AS ANTIGENS  
; FILE REFERENCE: CST-138 CIP2  
; CURRENT APPLICATION NUMBER: US/10/014,485A  
; PRIOR FILING DATE: 2002-03-19  
; PRIOR APPLICATION NUMBER: US 09/148,712  
; PRIOR FILING DATE: 1998-09-04  
; PRIOR APPLICATION NUMBER: US 09/535,364  
; PRIOR FILING DATE: 2000-03-24  
; NUMBER OF SEQ ID NOS: 145  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 79  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (3)..(3)  
; OTHER INFORMATION: PHOSPHORYLATION; threonine at position 3 is phosphorylated  
US-10-014-485A-79

Query Match 47.8%; Score 11; DB 9; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5  
|  
Db 2 W 2

## RESULT 29

US-10-104-019-42  
; Sequence 42, Application US/10104019  
; Patent No. US20020168379A1  
; GENERAL INFORMATION:  
; APPLICANT: PAUL, Prem  
; APPLICANT: MENG, Xiang-Jin  
; APPLICANT: MOROZOV, Igor  
; APPLICANT: HALBUR, Patrick  
; TITLE OF INVENTION: PROTEINS ENCODED BY POLYNUCLEIC ACIDS OF PORCINE  
; FILE REFERENCE: 4625-0039-55X CIP  
; CURRENT APPLICATION NUMBER: US/10/104,019  
; CURRENT FILING DATE: 2002-03-25  
; PRIOR APPLICATION NUMBER: 09/019,793  
; PRIOR FILING DATE: 1998-02-06  
; PRIOR APPLICATION NUMBER: 08/301,435  
; PRIOR FILING DATE: 1994-09-01  
; PRIOR APPLICATION NUMBER: 08/131,625

; PRIOR FILING DATE: 1993-10-05  
; PRIOR APPLICATION NUMBER: 07/969,071  
; PRIOR FILING DATE: 1992-10-30  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 42  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Peptide  
US-10-104-019-42

Query Match 47.8%; Score 11; DB 9; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5  
|  
Db 5 W 5

## RESULT 30

US-09-764-904-2  
; Sequence 2, Application US/09764904  
; Patent No. US20020173454A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PAI22  
; CURRENT APPLICATION NUMBER: US/09/764,904  
; CURRENT FILING DATE: 2001-01-17  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 137  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: Site  
; LOCATION: (3)  
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids  
US-09-764-904-2

Query Match 47.8%; Score 11; DB 9; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5  
|  
Db 1 W 1

## RESULT 31

US-09-852-797-2  
; Sequence 2, Application US/09852797  
; Patent No. US20020172994A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 28 Human Secreted Proteins  
; FILE REFERENCE: P2003P2  
; CURRENT APPLICATION NUMBER: US/09/852,797  
; CURRENT FILING DATE: 2001-05-11  
; PRIOR APPLICATION NUMBER: 60/265,583  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: 09/152,060  
; PRIOR FILING DATE: 1998-09-11  
; PRIOR APPLICATION NUMBER: PCT/US98/04858  
; PRIOR FILING DATE: 1998-03-12  
; PRIOR APPLICATION NUMBER: 60/040,762  
; PRIOR FILING DATE: 1997-03-14  
; PRIOR APPLICATION NUMBER: 60/040,710

```

; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: Site
; LOCATION: (3)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-09-852-797-2

```

```

Query Match          47.8%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred.No.1.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 5 W 5
Db 1 W 1

```

```

RESULT 32
US-09-964-992A-11
; Sequence 11, Application US/09964992A
; Patent No. US20020173633A1
; GENERAL INFORMATION:
; APPLICANT: Campos, Mikal E.
; APPLICANT: No. US20020173633A1ogaki, Hiroyuki
; APPLICANT: Suslow, Trevor
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Characterization of Phenylalanine Ammonia-Lyase (PAL)
; FILE REFERENCE: 023070-124500US
; CURRENT APPLICATION NUMBER: US/09/964,992A
; PRIOR FILING DATE: 2002-07-09
; PRIOR APPLICATION NUMBER: US 60/235,956
; PRIOR FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:PAL conserved
; OTHER INFORMATION: peptide fragment
US-09-964-992A-11

```

```

Query Match          47.8%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred.No.1.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 5 W 5
Db 5 W 5

```

```

RESULT 33
US-10-035-349-2
; Sequence 2, Application US/10035349
; Patent No. US20020172961A1
; GENERAL INFORMATION:
; APPLICANT: Schneider, Luke V.
; APPLICANT: Hall, Michael P.
; APPLICANT: Petesch, Robert
; APPLICANT: Target Discovery, Inc.
; TITLE OF INVENTION: Mass Defect Labeling for the Determination of Oligomer
; FILE REFERENCE: 020444-000710US
; CURRENT APPLICATION NUMBER: US/10/035,349
; CURRENT FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: US 60/242,165
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US 60/242,398
; PRIOR FILING DATE: 2000-10-19
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:competing 5
; OTHER INFORMATION: residue false sequence, top ranked sequence at
; OTHER INFORMATION: five residues
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Xaa = Gly labeled with 5-bromo-3-pyridylacetic
; OTHER INFORMATION: acid (5-Br-3-PAA)
US-10-035-349-2

```

```

Query Match          47.8%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred.No.1.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 5 W 5
Db 5 W 5

```

```

RESULT 34
US-10-035-349-8
; Sequence 8, Application US/10035349
; Patent No. US20020172961A1
; GENERAL INFORMATION:
; APPLICANT: Schneider, Luke V.
; APPLICANT: Hall, Michael P.
; APPLICANT: Petesch, Robert
; APPLICANT: Target Discovery, Inc.
; TITLE OF INVENTION: Mass Defect Labeling for the Determination of Oligomer
; FILE REFERENCE: 020444-000710US
; CURRENT APPLICATION NUMBER: US/10/035,349
; CURRENT FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: US 60/242,165
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US 60/242,398
; PRIOR FILING DATE: 2000-10-19
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:competing 5
; OTHER INFORMATION: residue false sequence, top ranked sequence at
; OTHER INFORMATION: five residues
US-10-035-349-8

```

Query Match 47.8%; Score 11; DB 9; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05; Indels 0; Gaps 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0;

Qy 5 W 5  
|  
Db 5 W 5

RESULT 35  
US-09-828-272A-6  
; Sequence 6, Application US/09828272A  
; Publication No. US20020183255A1  
; GENERAL INFORMATION:  
; APPLICANT: LIPTON, James M  
; APPLICANT: CATANIA, Anna P  
; TITLE OF INVENTION: USE OF KPV TRIPEPTIDE FOR DERMATOLOGICAL DISORDERS  
; FILE REFERENCE: 259/058  
; CURRENT APPLICATION NUMBER: US/09/828,272A  
; CURRENT FILING DATE: 2001-04-06  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Designed polypeptide with anti-inflammatory, anti-bacterial, anti-fungal and antipruritic properties.

US-09-828-272A-6

Query Match 47.8%; Score 11; DB 9; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05; Indels 0; Gaps 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0;

Qy 5 W 5  
|  
Db 1 W 1

RESULT 36  
US-10-042-141-2  
; Sequence 2, Application US/10042141  
; Publication No. US20020183503A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: 26 Human secreted proteins  
; FILE REFERENCE: P2040P1  
; CURRENT APPLICATION NUMBER: US/10/042,141  
; CURRENT FILING DATE: 2002-01-11  
; PRIOR APPLICATION NUMBER: 09/726,643  
; PRIOR FILING DATE: 2000-12-01  
; PRIOR APPLICATION NUMBER: PCT/US00/15187  
; PRIOR FILING DATE: 2000-06-02  
; PRIOR APPLICATION NUMBER: 60/137,725  
; PRIOR FILING DATE: 1999-06-07  
; NUMBER OF SEQ ID NOS: 190  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: Site  
; LOCATION: (3)  
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids

US-10-042-141-2

Query Match 47.8%; Score 11; DB 9; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05; Indels 0; Gaps 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0;

Qy 5 W 5  
|  
Db 1 W 1

Query Match 47.8%; Score 11; DB 9; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05; Indels 0; Gaps 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0;

Qy 5 W 5  
|  
Db 1 W 1

Query Match 47.8%; Score 11; DB 9; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05; Indels 0; Gaps 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0;

Qy 5 W 5  
|  
Db 1 W 1

Qy 5 W 5  
|  
Db 1 W 1

RESULT 37  
US-10-059-749-57  
; Sequence 57, Application US/10059749  
; Publication No. US20020183504A1  
; GENERAL INFORMATION:  
; APPLICANT: Alnemri, Emad S.  
; APPLICANT: Fernandes-Alnemri, Teresa  
; APPLICANT: Litwack, Gerald  
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids  
; Encoding Same and Methods of Use  
; NUMBER OF SEQUENCES: 87  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell & Flores LLP  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: United States  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/059,749  
; FILING DATE: 29-Jan-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/865,579  
; FILING DATE: 29-MAY-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-ID 2180  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-9849  
; INFORMATION FOR SEQ ID NO: 57:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 57:  
US-10-059-749-57

Query Match 47.8%; Score 11; DB 9; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05; Indels 0; Gaps 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0;

Qy 5 W 5  
|  
Db 1 W 1

RESULT 38  
US-10-059-749-63  
; Sequence 63, Application US/10059749  
; Publication No. US20020183504A1  
; GENERAL INFORMATION:  
; APPLICANT: Alnemri, Emad S.  
; APPLICANT: Fernandes-Alnemri, Teresa  
; APPLICANT: Litwack, Gerald  
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids  
; Encoding Same and Methods of Use  
; NUMBER OF SEQUENCES: 87  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell & Flores LLP

STREET: 4370 La Jolla Village Drive, Suite 700  
 CITY: San Diego  
 STATE: California  
 COUNTRY: United States  
 ZIP: 92122  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/10/059,749  
 FILING DATE: 29-Jan-2002  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/865,579  
 FILING DATE: 29-MAY-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Campbell, Cathryn A.  
 REGISTRATION NUMBER: 31,815  
 REFERENCE/DOCKET NUMBER: P-ID 2180  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619) 535-9001  
 TELEFAX: (619) 535-9849  
 INFORMATION FOR SEQ ID NO: 63:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 5 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 SEQUENCE DESCRIPTION: SEQ ID NO: 63:  
 US-10-059-749-63

Query Match 47.8%; Score 11; DB 9; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5  
 |  
 Db 1 W 1

## RESULT 39

US-10-059-749-69  
 ; Sequence 69, Application US/10059749  
 ; Publication No. US20020183504A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Alnemri, Emad S.  
 ; Fernandes-Alnemri, Teresa  
 ; Litwack, Gerald  
 ; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids  
 ; Encoding Same and Methods of Use  
 ; NUMBER OF SEQUENCES: 87  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESS: Campbell & Flores LLP  
 ; STREET: 4370 La Jolla Village Drive, Suite 700  
 ; CITY: San Diego  
 ; STATE: California  
 ; COUNTRY: United States  
 ; ZIP: 92122  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/10/059,749  
 ; FILING DATE: 29-Jan-2002  
 ; CLASSIFICATION: <Unknown>  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/865,579  
 ; FILING DATE: 29-MAY-1997  
 ; ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.  
 REGISTRATION NUMBER: 31,815  
 REFERENCE/DOCKET NUMBER: P-ID 2180  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619) 535-9001  
 TELEFAX: (619) 535-9849  
 INFORMATION FOR SEQ ID NO: 69:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 5 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 SEQUENCE DESCRIPTION: SEQ ID NO: 69:  
 US-10-059-749-69

Query Match 47.8%; Score 11; DB 9; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5  
 |  
 Db 1 W 1

## RESULT 40

US-10-079-625-6  
 ; Sequence 6, Application US/10079625  
 ; Publication No. US20020182676A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Tartaglia, Louis A.  
 ; APPLICANT: Tepper, Robert I.  
 ; APPLICANT: Culpepper, Janice A.  
 ; APPLICANT: White, David W.  
 ; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR  
 ; TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,  
 ; TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA  
 ; NUMBER OF SEQUENCES: 50  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Fish & Richardson, P.C.  
 ; STREET: 225 Franklin Street  
 ; CITY: Boston  
 ; STATE: MA  
 ; COUNTRY: US  
 ; ZIP: 02110-2804  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: Windows95  
 ; SOFTWARE: FastSeq for Windows Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/10/079,625  
 ; FILING DATE: 2002-FEB-19  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/864,564  
 ; FILING DATE: 28-MAY-1997  
 ; APPLICATION NUMBER: 08/708,123  
 ; FILING DATE: 03-SEP-1996  
 ; APPLICATION NUMBER: 08/638,524  
 ; FILING DATE: 26-APR-1996  
 ; APPLICATION NUMBER: 08/599,455  
 ; FILING DATE: 22-JAN-1996  
 ; APPLICATION NUMBER: 08/583,153  
 ; FILING DATE: 28-DEC-1995  
 ; APPLICATION NUMBER: 08/570,142  
 ; FILING DATE: 11-DEC-1995  
 ; APPLICATION NUMBER: 08/569,485  
 ; FILING DATE: 08-DEC-1995  
 ; APPLICATION NUMBER: 08/566,622  
 ; FILING DATE: 04-DEC-1995  
 ; APPLICATION NUMBER: 08/562,663  
 ; FILING DATE: 27-NOV-1995  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Meiklejohn, Ph.D., Anita L.

; REGISTRATION NUMBER: 35,283  
; REFERENCE/DOCKET NUMBER: 07334/019002  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-542-5070  
; TELEFAX: 617-542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-10-079-625-6

Query Match 47.8%; Score 11; DB 9; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5  
|  
Db 1 W 1

## RESULT 41

US-10-029-301-4  
; Sequence 4, Application US/10029301  
; Publication No. US20020188107A1  
; GENERAL INFORMATION:  
; APPLICANT: Mmott, Tracy Lehanne  
; APPLICANT: Engwerda, Christian  
; APPLICANT: Peek, Keith  
; TITLE OF INVENTION: Component of Stem Bromelain (as amended)  
; FILE REFERENCE: 0623.0760002  
; CURRENT APPLICATION NUMBER: US/10/029,301  
; CURRENT FILING DATE: 2001-12-28  
; PRIOR APPLICATION NUMBER: US 09/382,689  
; PRIOR FILING DATE: 1999-08-25  
; PRIOR APPLICATION NUMBER: PCT/GB98/00592  
; PRIOR FILING DATE: 1998-02-25  
; PRIOR APPLICATION NUMBER: GB 9704252.7  
; PRIOR FILING DATE: 1997-02-28  
; PRIOR APPLICATION NUMBER: GB 9703850.9  
; PRIOR FILING DATE: 1997-02-25  
; PRIOR APPLICATION NUMBER: GB 9703827.7  
; PRIOR FILING DATE: 1997-02-25  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Ananas comosus  
US-10-029-301-4

Query Match 47.8%; Score 11; DB 9; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5  
|  
Db 2 W 2

## RESULT 42

US-10-074-956-6  
; Sequence 6, Application US/10074956  
; Publication No. US2002019332A1  
; GENERAL INFORMATION:  
; APPLICANT: Hedley, Mary Lynne  
; TITLE OF INVENTION: METHODS OF TREATING BLADDER DISORDERS  
; FILE REFERENCE: 08191-022001  
; CURRENT APPLICATION NUMBER: US/10/074,956  
; CURRENT FILING DATE: 2002-06-10  
; PRIOR APPLICATION NUMBER: 60/268,175

; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-074-956-6

Query Match 47.8%; Score 11; DB 9; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5  
|  
Db 5 W 5

## RESULT 43

US-10-078-059-5  
; Sequence 5, Application US/10078059  
; Publication No. US20020193305A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Cytokine Receptor Common Gamma Chain Like  
; FILE REFERENCE: PF466P2  
; CURRENT APPLICATION NUMBER: US/10/078,059  
; CURRENT FILING DATE: 2002-02-20  
; PRIOR APPLICATION NUMBER: 60/269,876  
; PRIOR FILING DATE: 2001-02-21  
; PRIOR APPLICATION NUMBER: PCT/US00/22493  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 09/376,430  
; PRIOR FILING DATE: 1999-08-18  
; PRIOR APPLICATION NUMBER: 09/263,626  
; PRIOR FILING DATE: 1999-03-05  
; PRIOR APPLICATION NUMBER: PCT/US99/05068  
; PRIOR FILING DATE: 1999-03-05  
; PRIOR APPLICATION NUMBER: 60/086,505  
; PRIOR FILING DATE: 1998-05-22  
; PRIOR APPLICATION NUMBER: 60/078,563  
; PRIOR FILING DATE: 1998-03-19  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (3)  
; OTHER INFORMATION: Xaa equals any amino acid  
US-10-078-059-5

Query Match 47.8%; Score 11; DB 9; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5  
|  
Db 1 W 1

## RESULT 44

US-10-087-195-3  
; Sequence 3, Application US/10087195  
; Publication No. US20020193306A1  
; GENERAL INFORMATION:  
; APPLICANT: Nuttall, Patricia, Anne  
; APPLICANT: Faesen, Guido, Christiaan  
; TITLE OF INVENTION: Treatment of Allergic Rhinitis  
; FILE REFERENCE: 2488-1-004  
; CURRENT APPLICATION NUMBER: US/10/087,195

```

; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: PCT/GB00/03287
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 9920673.2
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 5
; TYPE: PRT
; ORGANISM: arthropod
US-10-087-195-3

Query Match          47.8%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5
   |
Db 4 W 4

RESULT 45
US-09-320-713-14
; Sequence 14, Application US/09320713
; Publication No. US20030003545A1
; GENERAL INFORMATION:
; APPLICANT: Reinhard Ebner
; APPLICANT: Steven M. Ruben
; TITLE OF INVENTION: INTERLEUKINS-21 AND 22
; FILE REFERENCE: PF470
; CURRENT APPLICATION NUMBER: US/09/320,713
; CURRENT FILING DATE: 1999-05-27
; EARLIER APPLICATION NUMBER: 60/087,340
; EARLIER FILING DATE: 1998-05-29
; EARLIER APPLICATION NUMBER: 60/099,805
; EARLIER FILING DATE: 1998-09-10
; EARLIER APPLICATION NUMBER: 60/131,965
; EARLIER FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (3)
; OTHER INFORMATION: x equals any amino acid
US-09-320-713-14

Query Match          47.8%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5
   |
Db 1 W 1

RESULT 46
US-09-774-639-2
; Sequence 2, Application US/09774639
; Publication No. US20030003555A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 90 Human Secreted Proteins
; FILE REFERENCE: PZ013P1
; CURRENT APPLICATION NUMBER: US/09/774,639
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/244,112
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 371

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (3)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino
US-09-798-889-2

Query Match          47.8%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5
   |
Db 1 W 1

RESULT 47
US-09-798-889-2
; Sequence 2, Application US/09798889
; Publication No. US20030004324A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 31 Human secreted proteins
; FILE REFERENCE: PZ026P1
; CURRENT APPLICATION NUMBER: US/09/798,889
; CURRENT FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/393,022
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/077,714
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/077,686
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/077,687
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/077,696
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-03-12
; NUMBER OF SEQ ID NOS: 185
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (3)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino
US-09-798-889-2

Query Match          47.8%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5
   |
Db 1 W 1

RESULT 48
US-10-105-930-21
; Sequence 21, Application US/10105930
; Publication No. US20030009018A1
; GENERAL INFORMATION:
; APPLICANT: Maeda, Masatsugu
; APPLICANT: Yasuchi, No. US20030009018A1iko
; TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR12
; FILE REFERENCE: 06501-105US1
; CURRENT APPLICATION NUMBER: US/10/105,930

```

; CURRENT FILING DATE: 2002-03-25  
; PRIOR APPLICATION NUMBER: PCT/JP00/06654  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: JP 2000-240397  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: JP 11-273358  
; PRIOR FILING DATE: 1999-09-27  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 21  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Exemplary motif  
; NAME/KEY: VARIANT  
; LOCATION: 3  
; OTHER INFORMATION: Xaa = any amino acid  
US-10-105-930-21

Query Match 47.8%; Score 11; DB 9; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5  
|  
Db 1 W 1

## RESULT 49

US-10-105-930-57  
; Sequence 57, Application US/10105930  
; Publication No. US20030009018A1  
; GENERAL INFORMATION:  
; APPLICANT: Maeda, Masatsugu  
; TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR12  
; FILE REFERENCE: 06501-105US1  
; CURRENT APPLICATION NUMBER: US/10/105,930  
; CURRENT FILING DATE: 2002-03-25  
; PRIOR APPLICATION NUMBER: PCT/JP00/06654  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: JP 2000-240397  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: JP 11-273358  
; PRIOR FILING DATE: 1999-09-27  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 57  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-105-930-57

Query Match 47.8%; Score 11; DB 9; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5  
|  
Db 1 W 1

## RESULT 50

US-10-105-930-58  
; Sequence 58, Application US/10105930  
; Publication No. US20030009018A1  
; GENERAL INFORMATION:  
; APPLICANT: Maeda, Masatsugu  
; TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR12  
; FILE REFERENCE: 06501-105US1

; CURRENT APPLICATION NUMBER: US/10/105,930  
; CURRENT FILING DATE: 2002-03-25  
; PRIOR APPLICATION NUMBER: PCT/JP00/06654  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: JP 2000-240397  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: JP 11-273358  
; PRIOR FILING DATE: 1999-09-27  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 58  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-105-930-58

Query Match 47.8%; Score 11; DB 9; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5  
|  
Db 1 W 1

## RESULT 51

US-10-105-930-59  
; Sequence 59, Application US/10105930  
; Publication No. US20030009018A1  
; GENERAL INFORMATION:  
; APPLICANT: Maeda, Masatsugu  
; TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR12  
; FILE REFERENCE: 06501-105US1  
; CURRENT APPLICATION NUMBER: US/10/105,930  
; CURRENT FILING DATE: 2002-03-25  
; PRIOR APPLICATION NUMBER: PCT/JP00/06654  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: JP 2000-240397  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: JP 11-273358  
; PRIOR FILING DATE: 1999-09-27  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 59  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-105-930-59

Query Match 47.8%; Score 11; DB 9; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5  
|  
Db 1 W 1

## RESULT 52

US-10-105-930-60  
; Sequence 60, Application US/10105930  
; Publication No. US20030009018A1  
; GENERAL INFORMATION:  
; APPLICANT: Maeda, Masatsugu  
; TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR12  
; FILE REFERENCE: 06501-105US1  
; CURRENT APPLICATION NUMBER: US/10/105,930  
; CURRENT FILING DATE: 2002-03-25  
; PRIOR APPLICATION NUMBER: PCT/JP00/06654  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: JP 2000-240397

```
/ PRIOR FILING DATE: 2000-08-03
/ PRIOR APPLICATION NUMBER: JP 11-273358
/ PRIOR FILING DATE: 1999-09-27
/ NUMBER OF SEQ ID NOS: 77
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 60
/ LENGTH: 5
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-105-930-60

Query Match      47.8%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 W 5
Db      1 W 1

RESULT 53
US-10-105-930-61
/ Sequence 61, Application US/10105930
/ Publication No. US20030009018A1
/ GENERAL INFORMATION:
/ APPLICANT: Maeda, Masatsugu
/ TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR12
/ FILE REFERENCE: 06501-105US1
/ CURRENT APPLICATION NUMBER: US/10/105,930
/ PRIOR FILING DATE: 2002-03-25
/ PRIOR APPLICATION NUMBER: JP 2000-240397
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: PCT/JP00/06654
/ PRIOR FILING DATE: 2000-08-03
/ PRIOR APPLICATION NUMBER: JP 11-273358
/ PRIOR FILING DATE: 1999-09-27
/ NUMBER OF SEQ ID NOS: 77
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 61
/ LENGTH: 5
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-105-930-61

Query Match      47.8%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 W 5
Db      1 W 1

RESULT 54
US-10-105-930-62
/ Sequence 62, Application US/10105930
/ Publication No. US20030009018A1
/ GENERAL INFORMATION:
/ APPLICANT: Maeda, Masatsugu
/ TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR12
/ FILE REFERENCE: 06501-105US1
/ CURRENT APPLICATION NUMBER: US/10/105,930
/ PRIOR FILING DATE: 2002-03-25
/ PRIOR APPLICATION NUMBER: PCT/JP00/06654
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: JP 2000-240397
/ PRIOR FILING DATE: 2000-08-03
/ PRIOR APPLICATION NUMBER: JP 11-273358
/ PRIOR FILING DATE: 1999-09-27
/ NUMBER OF SEQ ID NOS: 77
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 62
/ LENGTH: 5
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-105-930-62

Query Match      47.8%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 W 5
Db      1 W 1

RESULT 55
US-10-105-930-63
/ Sequence 63, Application US/10105930
/ Publication No. US20030009018A1
/ GENERAL INFORMATION:
/ APPLICANT: Maeda, Masatsugu
/ TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR12
/ FILE REFERENCE: 06501-105US1
/ CURRENT APPLICATION NUMBER: US/10/105,930
/ PRIOR FILING DATE: 2002-03-25
/ PRIOR APPLICATION NUMBER: PCT/JP00/06654
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: JP 2000-240397
/ PRIOR FILING DATE: 2000-08-03
/ PRIOR APPLICATION NUMBER: JP 11-273358
/ PRIOR FILING DATE: 1999-09-27
/ NUMBER OF SEQ ID NOS: 77
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 63
/ LENGTH: 5
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-105-930-63

Query Match      47.8%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 W 5
Db      1 W 1

RESULT 56
US-10-105-930-64
/ Sequence 64, Application US/10105930
/ Publication No. US20030009018A1
/ GENERAL INFORMATION:
/ APPLICANT: Maeda, Masatsugu
/ TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR12
/ FILE REFERENCE: 06501-105US1
/ CURRENT APPLICATION NUMBER: US/10/105,930
/ PRIOR FILING DATE: 2002-03-25
/ PRIOR APPLICATION NUMBER: PCT/JP00/06654
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: JP 2000-240397
/ PRIOR FILING DATE: 2000-08-03
/ PRIOR APPLICATION NUMBER: JP 11-273358
/ PRIOR FILING DATE: 1999-09-27
/ NUMBER OF SEQ ID NOS: 77
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 64
/ LENGTH: 5
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-105-930-64

Query Match      47.8%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 W 5
Db      1 W 1
```



Query Match 47.8%; Score 11; DB 9; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0;

Qy 5 W 5  
|  
Db 1 W 1

RESULT 57  
US-10-105-930-65  
; Sequence 65, Application US/10105930  
; Publication No. US20030009018A1  
; GENERAL INFORMATION:  
; APPLICANT: Maeda, Masatsugu  
; APPLICANT: Yaguchi, No. US20030009018A1iko  
; TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR12  
; FILE REFERENCE: 06501-105US1  
; CURRENT APPLICATION NUMBER: US/10/105,930  
; CURRENT FILING DATE: 2002-03-25  
; PRIOR APPLICATION NUMBER: PCT/JP00/06654  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: JP 2000-240397  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: JP 11-273358  
; PRIOR FILING DATE: 1999-09-27  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 65  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-105-930-65

Query Match 47.8%; Score 11; DB 9; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0;

Qy 5 W 5  
|  
Db 1 W 1

RESULT 58  
US-10-105-930-66  
; Sequence 66, Application US/10105930  
; Publication No. US20030009018A1  
; GENERAL INFORMATION:  
; APPLICANT: Maeda, Masatsugu  
; APPLICANT: Yaguchi, No. US20030009018A1iko  
; TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR12  
; FILE REFERENCE: 06501-105US1  
; CURRENT APPLICATION NUMBER: US/10/105,930  
; CURRENT FILING DATE: 2002-03-25  
; PRIOR APPLICATION NUMBER: PCT/JP00/06654  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: JP 2000-240397  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: JP 11-273358  
; PRIOR FILING DATE: 1999-09-27  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 66  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-105-930-66

Query Match 47.8%; Score 11; DB 9; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0;

Qy 5 W 5  
|  
Db 1 W 1

RESULT 59  
US-10-105-930-67  
; Sequence 67, Application US/10105930  
; Publication No. US20030009018A1  
; GENERAL INFORMATION:  
; APPLICANT: Maeda, Masatsugu  
; APPLICANT: Yaguchi, No. US20030009018A1iko  
; TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR12  
; FILE REFERENCE: 06501-105US1  
; CURRENT APPLICATION NUMBER: US/10/105,930  
; CURRENT FILING DATE: 2002-03-25  
; PRIOR APPLICATION NUMBER: PCT/JP00/06654  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: JP 2000-240397  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: JP 11-273358  
; PRIOR FILING DATE: 1999-09-27  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 67  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-105-930-67

Query Match 47.8%; Score 11; DB 9; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0;

Qy 5 W 5  
|  
Db 1 W 1

RESULT 60  
US-10-105-930-68  
; Sequence 68, Application US/10105930  
; Publication No. US20030009018A1  
; GENERAL INFORMATION:  
; APPLICANT: Maeda, Masatsugu  
; APPLICANT: Yaguchi, No. US20030009018A1iko  
; TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR12  
; FILE REFERENCE: 06501-105US1  
; CURRENT APPLICATION NUMBER: US/10/105,930  
; CURRENT FILING DATE: 2002-03-25  
; PRIOR APPLICATION NUMBER: PCT/JP00/06654  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: JP 2000-240397  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: JP 11-273358  
; PRIOR FILING DATE: 1999-09-27  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 68  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-105-930-68

Query Match 47.8%; Score 11; DB 9; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0;

Qy 5 W 5  
|  
Db 1 W 1

## RESULT 61

```

US-10-105-930-69
; Sequence 69, Application US/10105930
; Publication No. US20030009018A1
; GENERAL INFORMATION:
; APPLICANT: Maeda, Masatsugu
; TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR12
; FILE REFERENCE: 06501-105U51
; CURRENT APPLICATION NUMBER: US/10/105,930
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: PCT/JP00/06654
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: JP 2000-240397
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: JP 11-273358
; PRIOR FILING DATE: 1999-09-27
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 69
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-105-930-69

```

```

Query Match      47.8%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 5 W 5
Db 1 W 1

```

## RESULT 62

```

US-10-105-930-71
; Sequence 71, Application US/10105930
; Publication No. US20030009018A1
; GENERAL INFORMATION:
; APPLICANT: Maeda, Masatsugu
; TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR12
; FILE REFERENCE: 06501-105U51
; CURRENT APPLICATION NUMBER: US/10/105,930
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: PCT/JP00/06654
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: JP 2000-240397
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: JP 11-273358
; PRIOR FILING DATE: 1999-09-27
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 71
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-105-930-71

```

```

Query Match      47.8%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 5 W 5
Db 1 W 1

```

## RESULT 63

```

US-10-105-930-72
; Sequence 72, Application US/10105930
; Publication No. US20030009018A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Maeda, Masatsugu
; TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR12
; FILE REFERENCE: 06501-105U51
; CURRENT APPLICATION NUMBER: US/10/105,930
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: PCT/JP00/06654
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: JP 2000-240397
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: JP 11-273358
; PRIOR FILING DATE: 1999-09-27
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 72
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-105-930-72

```

```

Query Match      47.8%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 5 W 5
Db 1 W 1

```

## RESULT 64

```

US-10-105-930-73
; Sequence 73, Application US/10105930
; Publication No. US20030009018A1
; GENERAL INFORMATION:
; APPLICANT: Maeda, Masatsugu
; TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR12
; FILE REFERENCE: 06501-105U51
; CURRENT APPLICATION NUMBER: US/10/105,930
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: PCT/JP00/06654
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: JP 2000-240397
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: JP 11-273358
; PRIOR FILING DATE: 1999-09-27
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 73
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-105-930-73

```

```

Query Match      47.8%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 5 W 5
Db 1 W 1

```

## RESULT 65

```

US-10-105-930-74
; Sequence 74, Application US/10105930
; Publication No. US20030009018A1
; GENERAL INFORMATION:
; APPLICANT: Maeda, Masatsugu
; TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR12
; FILE REFERENCE: 06501-105U51
; CURRENT APPLICATION NUMBER: US/10/105,930

```

; CURRENT FILING DATE: 2002-03-25  
 ; PRIOR APPLICATION NUMBER: PCT/JF00/06654  
 ; PRIOR FILING DATE: 2000-09-27  
 ; PRIOR APPLICATION NUMBER: JP 2000-240397  
 ; PRIOR FILING DATE: 2000-08-03  
 ; PRIOR APPLICATION NUMBER: JP 11-273358  
 ; PRIOR FILING DATE: 1999-09-27  
 ; NUMBER OF SEQ ID NOS: 77  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 74  
 ; LENGTH: 5  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-105-930-74

Query Match 47.8%; Score 11; DB 9; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5  
 |  
 Db 4 W 4

## RESULT 66

US-10-105-930-75  
 ; Sequence 75, Application US/10105930  
 ; Publication No. US20030009018A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Maeda, Masatsugu  
 ; TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR12  
 ; FILE REFERENCE: 06501-105U1  
 ; CURRENT APPLICATION NUMBER: US/10/105,930  
 ; CURRENT FILING DATE: 2002-03-25  
 ; PRIOR APPLICATION NUMBER: PCT/JF00/06654  
 ; PRIOR FILING DATE: 2000-09-27  
 ; PRIOR APPLICATION NUMBER: JP 2000-240397  
 ; PRIOR FILING DATE: 2000-08-03  
 ; PRIOR APPLICATION NUMBER: JP 11-273358  
 ; PRIOR FILING DATE: 1999-09-27  
 ; NUMBER OF SEQ ID NOS: 77  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 75  
 ; LENGTH: 5  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-105-930-75

Query Match 47.8%; Score 11; DB 9; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5  
 |  
 Db 1 W 1

## RESULT 67

US-10-105-930-76  
 ; Sequence 76, Application US/10105930  
 ; Publication No. US20030009018A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Maeda, Masatsugu  
 ; TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR12  
 ; FILE REFERENCE: 06501-105U1  
 ; CURRENT APPLICATION NUMBER: US/10/105,930  
 ; CURRENT FILING DATE: 2002-03-25  
 ; PRIOR APPLICATION NUMBER: PCT/JF00/06654  
 ; PRIOR FILING DATE: 2000-09-27  
 ; PRIOR APPLICATION NUMBER: JP 2000-240397  
 ; PRIOR FILING DATE: 2000-08-03

; PRIOR APPLICATION NUMBER: JP 11-273358  
 ; PRIOR FILING DATE: 1999-09-27  
 ; NUMBER OF SEQ ID NOS: 77  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 76  
 ; LENGTH: 5  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-105-930-76

Query Match 47.8%; Score 11; DB 9; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5  
 |  
 Db 1 W 1

## RESULT 68

US-09-262-126C-8  
 ; Sequence 8, Application US/09262126C  
 ; Publication No. US20030013180A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Miller, Brian S.  
 ; APPLICANT: Shetty, Jayarama K.  
 ; TITLE OF INVENTION: Modified Forms of Pullulanase  
 ; FILE REFERENCE: GC396-2  
 ; CURRENT APPLICATION NUMBER: US/09/262,126C  
 ; CURRENT FILING DATE: 1999-03-03  
 ; NUMBER OF SEQ ID NOS: 9  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 8  
 ; LENGTH: 5  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Unknown  
 US-09-262-126C-8

Query Match 47.8%; Score 11; DB 9; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5  
 |  
 Db 3 W 3

## RESULT 69

US-09-989-442-2  
 ; Sequence 2, Application US/09989442  
 ; Publication No. US20030013649A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rosen et al.  
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
 ; FILE REFERENCE: PJZ08  
 ; CURRENT APPLICATION NUMBER: US/09/989,442  
 ; CURRENT FILING DATE: 2001-11-21  
 ; PRIOR APPLICATION NUMBER: 60/179,065  
 ; PRIOR FILING DATE: 2000-01-31  
 ; PRIOR APPLICATION NUMBER: 60/180,628  
 ; PRIOR FILING DATE: 2000-02-04  
 ; PRIOR APPLICATION NUMBER: 60/214,886  
 ; PRIOR FILING DATE: 2000-06-28  
 ; PRIOR APPLICATION NUMBER: 60/217,487  
 ; PRIOR FILING DATE: 2000-07-11  
 ; PRIOR APPLICATION NUMBER: 60/225,758  
 ; PRIOR FILING DATE: 2000-08-14  
 ; PRIOR APPLICATION NUMBER: 60/220,963  
 ; PRIOR FILING DATE: 2000-07-26  
 ; PRIOR APPLICATION NUMBER: 60/217,496  
 ; PRIOR FILING DATE: 2000-07-11

; PRIOR APPLICATION NUMBER: 60/225,447  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/218,290  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: 60/225,757  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/226,868  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR APPLICATION NUMBER: 60/216,647  
; PRIOR FILING DATE: 2000-07-07  
; PRIOR APPLICATION NUMBER: 60/225,267  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/216,880  
; PRIOR FILING DATE: 2000-07-07  
; PRIOR APPLICATION NUMBER: 60/225,270  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/251,869  
; PRIOR FILING DATE: 2000-12-08  
; PRIOR APPLICATION NUMBER: 60/235,834  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: 60/234,274  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: 60/234,223  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: 60/228,924  
; PRIOR FILING DATE: 2000-08-30  
; PRIOR APPLICATION NUMBER: 60/224,518  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/236,369  
; PRIOR FILING DATE: 2000-09-29  
; PRIOR APPLICATION NUMBER: 60/224,519  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/220,964  
; PRIOR FILING DATE: 2000-07-26  
; PRIOR APPLICATION NUMBER: 60/241,809  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/249,299  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/236,327  
; PRIOR FILING DATE: 2000-09-29  
; PRIOR APPLICATION NUMBER: 60/241,785  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/244,617  
; PRIOR FILING DATE: 2000-11-01  
; PRIOR APPLICATION NUMBER: 60/225,268  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/236,368  
; PRIOR FILING DATE: 2000-09-29  
; PRIOR APPLICATION NUMBER: 60/251,856  
; PRIOR FILING DATE: 2000-12-08  
; PRIOR APPLICATION NUMBER: 60/251,868  
; PRIOR FILING DATE: 2000-12-08  
; PRIOR APPLICATION NUMBER: 60/229,344  
; PRIOR FILING DATE: 2000-09-01  
; PRIOR APPLICATION NUMBER: 60/234,997  
; PRIOR FILING DATE: 2000-09-25  
; PRIOR APPLICATION NUMBER: 60/229,343  
; PRIOR FILING DATE: 2000-09-01  
; PRIOR APPLICATION NUMBER: 60/229,345  
; PRIOR FILING DATE: 2000-09-01  
; PRIOR APPLICATION NUMBER: 60/229,287  
; PRIOR FILING DATE: 2000-09-01  
; PRIOR APPLICATION NUMBER: 60/229,513  
; PRIOR FILING DATE: 2000-09-05  
; PRIOR APPLICATION NUMBER: 60/231,413  
; PRIOR FILING DATE: 2000-09-08  
; PRIOR APPLICATION NUMBER: 60/229,509  
; PRIOR FILING DATE: 2000-09-05  
; PRIOR APPLICATION NUMBER: 60/236,367  
; PRIOR FILING DATE: 2000-09-29  
; PRIOR APPLICATION NUMBER: 60/237,039  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: 60/237,038

; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: 60/236,370  
; PRIOR FILING DATE: 2000-09-29  
; PRIOR APPLICATION NUMBER: 60/236,802  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: 60/237,037  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: 60/237,040  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: 60/240,960  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/239,935  
; PRIOR FILING DATE: 2000-10-13  
; PRIOR APPLICATION NUMBER: 60/239,937  
; PRIOR FILING DATE: 2000-10-13  
; PRIOR APPLICATION NUMBER: 60/241,787  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/246,474  
; PRIOR FILING DATE: 2000-11-08  
; PRIOR APPLICATION NUMBER: 60/246,532  
; PRIOR FILING DATE: 2000-11-08  
; PRIOR APPLICATION NUMBER: 60/249,216  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,210  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/226,681  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR APPLICATION NUMBER: 60/225,759  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/225,213  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/227,182  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR APPLICATION NUMBER: 60/225,214  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/235,836  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: 60/230,438  
; PRIOR FILING DATE: 2000-09-06  
; PRIOR APPLICATION NUMBER: 60/215,135  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: 60/225,266  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/249,218  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,208  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,213  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,212  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,207  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,245  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,244  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,217  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,211  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,215  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,264  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,214  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,297  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/232,400  
; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: 60/231,242  
; PRIOR FILING DATE: 2000-09-08

;; PRIOR APPLICATION NUMBER: 60/232,081  
;; PRIOR FILING DATE: 2000-09-08  
;; PRIOR APPLICATION NUMBER: 60/232,080  
;; PRIOR FILING DATE: 2000-09-08  
;; PRIOR APPLICATION NUMBER: 60/231,414  
;; PRIOR FILING DATE: 2000-09-08  
;; PRIOR APPLICATION NUMBER: 60/231,244  
;; PRIOR FILING DATE: 2000-09-08  
;; PRIOR APPLICATION NUMBER: 60/233,064  
;; PRIOR FILING DATE: 2000-09-14  
;; PRIOR APPLICATION NUMBER: 60/233,063  
;; PRIOR FILING DATE: 2000-09-14  
;; PRIOR APPLICATION NUMBER: 60/232,397  
;; PRIOR FILING DATE: 2000-09-14  
;; PRIOR APPLICATION NUMBER: 60/232,399  
;; PRIOR FILING DATE: 2000-09-14  
;; PRIOR APPLICATION NUMBER: 60/232,401  
;; PRIOR FILING DATE: 2000-09-14  
;; PRIOR APPLICATION NUMBER: 60/241,808  
;; PRIOR FILING DATE: 2000-10-20  
;; PRIOR APPLICATION NUMBER: 60/241,826  
;; PRIOR FILING DATE: 2000-10-20  
;; PRIOR APPLICATION NUMBER: 60/241,786  
;; PRIOR FILING DATE: 2000-10-20  
;; PRIOR APPLICATION NUMBER: 60/241,221  
;; PRIOR FILING DATE: 2000-10-20  
;; PRIOR APPLICATION NUMBER: 60/246,475  
;; PRIOR FILING DATE: 2000-11-08  
;; PRIOR APPLICATION NUMBER: 60/231,243  
;; PRIOR FILING DATE: 2000-09-08  
;; PRIOR APPLICATION NUMBER: 60/233,065  
;; PRIOR FILING DATE: 2000-09-14

Query Match 47.8%; Score 11; DB 9; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5  
|  
Db 1 W 1

RESULT 70  
US-10-116-067-3  
; Sequence 3, Application US/10116067  
; Publication No. US20030012780A1  
; GENERAL INFORMATION:  
; APPLICANT: LINDBOM, Lennart  
; APPLICANT: WERR, Joachim  
; TITLE OF INVENTION: Anti-Inflammatory Medicaments  
; FILE REFERENCE: 1291-0200P  
; CURRENT APPLICATION NUMBER: US/10/116.067  
; PRIOR APPLICATION NUMBER: 2002-04-05  
; PRIOR FILING DATE: 1998-10-07  
; PRIOR APPLICATION NUMBER: SE 9803428-3  
; PRIOR FILING DATE: 1998-10-07  
; PRIOR APPLICATION NUMBER: US 60/103,558  
; PRIOR FILING DATE: 1998-10-07  
; PRIOR APPLICATION NUMBER: PCT/SE99/01801  
; PRIOR FILING DATE: 1999-10-07  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: alphasbetal integrin-binding peptide  
US-10-116-067-3

Query Match 47.8%; Score 11; DB 9; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5  
|  
Db 5 W 5

RESULT 71  
US-09-369-248-5  
; Sequence 5, Application US/09369248  
; Publication No. US20030022276A1  
; GENERAL INFORMATION:  
; APPLICANT: Young, Paul  
; APPLICANT: Ruben, Steven M.  
; TITLE OF INVENTION: Dendritic Enriched Secreted Lymphocyte Activation  
; FILE REFERENCE: PF448  
; CURRENT APPLICATION NUMBER: US/09/369,248  
; CURRENT FILING DATE: 1999-08-05  
; EARLIER APPLICATION NUMBER: 60/073,962  
; EARLIER FILING DATE: 1998-02-06  
; EARLIER APPLICATION NUMBER: 60/078,572  
; EARLIER FILING DATE: 1998-03-19  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (3)  
; OTHER INFORMATION: Xaa equals any amino acid  
US-09-369-248-5

Query Match 47.8%; Score 11; DB 9; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5  
|  
Db 1 W 1

RESULT 72  
US-09-393-696-14  
; Sequence 14, Application US/09393696  
; Publication No. US2003002277A1  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc. et al.  
; TITLE OF INVENTION: Human Neuropeptide Receptor  
; FILE REFERENCE: PF168P2  
; CURRENT APPLICATION NUMBER: US/09/393,696  
; CURRENT FILING DATE: 1999-09-10  
; EARLIER APPLICATION NUMBER: PCT/US95/05616  
; EARLIER FILING DATE: 1995-05-05  
; EARLIER APPLICATION NUMBER: US08/462,509  
; EARLIER FILING DATE: 1995-06-05  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 14  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: site  
; LOCATION: (3)  
; OTHER INFORMATION: Xaa equals any amino acid  
US-09-393-696-14

Query Match 47.8%; Score 11; DB 9; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5

Db 1 w 1

RESULT 73

US-09-747-377-493

Sequence 493, Application US/09747377

Publication No. US20030022255A1

GENERAL INFORMATION:

APPLICANT: Morris, David

TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR BREAST CANCER

FILE REFERENCE: A-6959/RMS/DCF

CURRENT APPLICATION NUMBER: US/09/747,377

CURRENT FILING DATE: 2000-12-22

NUMBER OF SEQ ID NOS: 493

SOFTWARE: PatentIn version 3.0

SEQ ID NO 493

LENGTH: 5

TYPE: PRT

ORGANISM: Unknown

FEATURE:

OTHER INFORMATION: Cytokine receptor extracellular motif found in many species.

NAME/KEY: UNSURE

LOCATION: (3), (3)

OTHER INFORMATION: "Xaa" at position 3 can be any amino acid

US-09-747-377-493

Query Match 47.8%; Score 11; DB 9; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 w 5

Db 1 w 1

RESULT 74

US-09-983-802-2

Sequence 2, Application US/09983802

Publication No. US20030022185A1

GENERAL INFORMATION:

APPLICANT: Fischer et al.

TITLE OF INVENTION: 123 Human Secreted Proteins

FILE REFERENCE: P2010P1

CURRENT APPLICATION NUMBER: US/09/983,802

CURRENT FILING DATE: 2001-10-25

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/227,357

PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-08

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US98/13684

PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-07

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,926

PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,793

PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,925

PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,929

PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,803

PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,732

PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,931

PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,932

PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,916

PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,930

PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,918

PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,920

US-09-983-802-2

Query Match 47.8%; Score 11; DB 9; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 w 5

Db 1 w 1

RESULT 75

US-10-062-523-5

Sequence 5, Application US/10062523

Publication No. US20030022327A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Dendritic Enriched Secreted Lymphocyte Activation

TITLE OF INVENTION: Molecule

FILE REFERENCE: PP448P2

CURRENT APPLICATION NUMBER: US/10/062,523

US-09-983-802-2

Query Match 47.8%; Score 11; DB 9; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 w 5

Db 1 w 1

; CURRENT FILING DATE: 2002-02-05  
; PRIOR APPLICATION NUMBER: 60/267,523  
; PRIOR FILING DATE: 2001-02-06  
; PRIOR APPLICATION NUMBER: PCT/US00/21130  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: 60/190,062  
; PRIOR FILING DATE: 2000-03-17  
; PRIOR APPLICATION NUMBER: 09/369,248  
; PRIOR FILING DATE: 1999-08-05  
; PRIOR APPLICATION NUMBER: PCT/US99/02415  
; PRIOR FILING DATE: 1999-02-04  
; PRIOR APPLICATION NUMBER: 09/244,110  
; PRIOR FILING DATE: 1999-02-04  
; PRIOR APPLICATION NUMBER: 60/078,572  
; PRIOR FILING DATE: 1998-03-19  
; PRIOR APPLICATION NUMBER: 60/073,962  
; PRIOR FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (3)  
; OTHER INFORMATION: Xaa equals any amino acid  
US-10-062-523-5

Query Match 47.8%; Score 11; DB 9; Length 5;  
Best Local Similarity 100.0%; Pred.No. 1.2e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 5 W 5  
Db 1 W 1

Search completed: February 12, 2003, 10:56:29  
Job time : 30 secs





GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 12, 2003, 10:51:44 ; Search time 131 Seconds  
(without alignments)  
24.608 Million cell updates/sec

Title: US-09-403-440A-1

Perfect score: 23

Sequence: 1 FXXLW 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters: 42829

Minimum DB seq length: 5

Maximum DB seq length: 5

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Pending Patents\_AA Main:\*

1: /cgn2\_6/ptodata/1/paa/PCTUS\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/paa/US06\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/paa/US07\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/paa/US08\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/paa/US081\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/paa/US082\_COMB.pep.\*  
7: /cgn2\_6/ptodata/1/paa/US083\_COMB.pep.\*  
8: /cgn2\_6/ptodata/1/paa/US084\_COMB.pep.\*  
9: /cgn2\_6/ptodata/1/paa/US085\_COMB.pep.\*  
10: /cgn2\_6/ptodata/1/paa/US086\_COMB.pep.\*  
11: /cgn2\_6/ptodata/1/paa/US087\_COMB.pep.\*  
12: /cgn2\_6/ptodata/1/paa/US088\_COMB.pep.\*  
13: /cgn2\_6/ptodata/1/paa/US089\_COMB.pep.\*  
14: /cgn2\_6/ptodata/1/paa/US090\_COMB.pep.\*  
15: /cgn2\_6/ptodata/1/paa/US091\_COMB.pep.\*  
16: /cgn2\_6/ptodata/1/paa/US092\_COMB.pep.\*  
17: /cgn2\_6/ptodata/1/paa/US093\_COMB.pep.\*  
18: /cgn2\_6/ptodata/1/paa/US094\_COMB.pep.\*  
19: /cgn2\_6/ptodata/1/paa/US095\_COMB.pep.\*  
20: /cgn2\_6/ptodata/1/paa/US096\_COMB.pep.\*  
21: /cgn2\_6/ptodata/1/paa/US097\_COMB.pep.\*  
22: /cgn2\_6/ptodata/1/paa/US098\_COMB.pep.\*  
23: /cgn2\_6/ptodata/1/paa/US099\_COMB.pep.\*  
24: /cgn2\_6/ptodata/1/paa/US100\_COMB.pep.\*  
25: /cgn2\_6/ptodata/1/paa/US101\_COMB.pep.\*  
26: /cgn2\_6/ptodata/1/paa/US102\_COMB.pep.\*  
27: /cgn2\_6/ptodata/1/paa/US60\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	87.0	5	1 PCT-US99-02405-11	Sequence 11, Appl
2	20	87.0	5	1 PCT-US99-26277-114	Sequence 114, App
3	20	87.0	5	20 US-09-601-558-11	Sequence 11, Appl
4	20	87.0	5	22 US-09-831-047B-114	Sequence 114, App
5	20	87.0	5	22 US-09-831-047C-114	Sequence 114, App
6	20	87.0	5	22 US-09-894-594-11	Sequence 11, Appl

5	1	PCT-US01-20969-3	19	82.6	Sequence 3, Appli
5	16	US-09-214-371-2	19	82.6	Sequence 2, Appli
5	16	US-09-281-717-3	8	82.6	Sequence 3, Appli
5	18	US-09-403-440A-1	10	82.6	Sequence 1, Appli
5	20	US-09-609-361-3	11	82.6	Sequence 3, Appli
5	23	US-09-957-806A-226	12	82.6	Sequence 226, App
5	1	PCT-US01-03988-791	13	65.2	Sequence 791, App
5	1	PCT-US02-22821-139	14	65.2	Sequence 139, App
5	1	PCT-US02-23257-8	15	65.2	Sequence 8, Appli
5	1	PCT-US02-23257-10	15	65.2	Sequence 10, Appl
5	1	PCT-US02-23257-11	15	65.2	Sequence 11, Appl
5	1	PCT-US02-23257-12	17	65.2	Sequence 12, Appl
5	1	PCT-US02-23257-13	18	65.2	Sequence 13, Appl
5	1	PCT-US98-15227-1	20	65.2	Sequence 1, Appli
5	1	PCT-US99-11219-791	21	65.2	Sequence 791, App
5	3	US-07-585-141-11	22	65.2	Sequence 11, Appl
5	3	US-07-608-569-17	23	65.2	Sequence 17, Appl
5	7	US-08-344-185B-100	24	65.2	Sequence 100, App
5	7	US-08-344-185B-454	25	65.2	Sequence 454, App
5	7	US-08-344-185C-100	26	65.2	Sequence 100, App
5	7	US-08-344-185C-454	27	65.2	Sequence 454, App
5	7	US-08-424-550A-228	28	65.2	Sequence 228, App
5	8	US-08-424-550B-228	29	65.2	Sequence 228, App
5	8	US-08-432-147-47	30	65.2	Sequence 47, Appl
5	8	US-08-467-344A-228	31	65.2	Sequence 228, App
5	8	US-08-486-749-228	32	65.2	Sequence 228, App
5	8	US-08-488-445A-228	33	65.2	Sequence 228, App
5	8	US-08-488-446-228	34	65.2	Sequence 228, App
5	9	US-08-530-325-14	35	65.2	Sequence 14, Appl
5	9	US-08-530-327-14	36	65.2	Sequence 14, Appl
5	13	US-08-981-122-15	37	65.2	Sequence 15, Appl
5	13	US-08-981-122-38	38	65.2	Sequence 38, Appl
5	13	US-08-981-122-43	39	65.2	Sequence 43, Appl
5	13	US-08-981-122-51	40	65.2	Sequence 51, Appl
5	16	US-09-209-676-30	41	65.2	Sequence 30, Appl
5	16	US-09-284-327-1	42	65.2	Sequence 1, Appli
5	17	US-09-308-823A-582	43	65.2	Sequence 582, App
5	17	US-09-350-641B-791	44	65.2	Sequence 791, App
5	17	US-09-350-641C-791	45	65.2	Sequence 791, App
5	17	US-09-350-641C-791	46	65.2	Sequence 791, App
5	18	US-09-410-568-9	47	65.2	Sequence 9, Appli
5	18	US-09-426-371-9	48	65.2	Sequence 9, Appli
5	18	US-09-454-684-9	49	65.2	Sequence 9, Appli
5	18	US-09-454-684A-9	50	65.2	Sequence 25, Appl
5	18	US-09-457-198A-25	51	65.2	Sequence 25, Appl
5	19	US-09-515-965-791	52	65.2	Sequence 791, App
5	19	US-09-515-965A-791	53	65.2	Sequence 791, App
5	19	US-09-515-965A-1657	54	65.2	Sequence 1657, Ap
5	19	US-09-536-998-1	55	65.2	Sequence 1, Appli
5	19	US-09-598-419-9	56	65.2	Sequence 9, Appli
5	20	US-09-632-426-30	57	65.2	Sequence 30, Appl
5	20	US-09-632-570-30	58	65.2	Sequence 30, Appl
5	20	US-09-636-243A-75	59	65.2	Sequence 75, Appl
5	20	US-09-642-234-75	60	65.2	Sequence 75, Appl
5	20	US-09-657-276-723	61	65.2	Sequence 723, App
5	20	US-09-657-276-724	62	65.2	Sequence 724, App
5	20	US-09-657-276-734	63	65.2	Sequence 734, App
5	20	US-09-657-276-1560	64	65.2	Sequence 1560, Ap
5	21	US-09-762-270-19	65	65.2	Sequence 19, Appl
5	21	US-09-762-270-20	66	65.2	Sequence 20, Appl
5	21	US-09-762-270-21	67	65.2	Sequence 21, Appl
5	21	US-09-762-270-22	68	65.2	Sequence 22, Appl
5	21	US-09-762-270-23	69	65.2	Sequence 23, Appl
5	22	US-09-834-784-791	70	65.2	Sequence 791, App
5	22	US-09-841-132-9	71	65.2	Sequence 9, Appli
5	22	US-09-920-306-21	72	65.2	Sequence 21, Appl
5	23	US-09-350-369C-513	73	65.2	Sequence 513, App
5	23	US-09-350-369C-1389	74	65.2	Sequence 1389, Ap
5	24	US-10-005-305-36	75	65.2	Sequence 36, Appl
5	24	US-10-005-305-95	76	65.2	Sequence 95, Appl
5	25	US-10-197-954-139	77	65.2	Sequence 139, App
5	26	US-10-200-923-8	78	65.2	Sequence 8, Appli
5	26	US-10-200-923-10	79	65.2	Sequence 10, Appl

Sequence 11, Appl  
Sequence 12, Appl  
Sequence 13, Appl  
Sequence 11, Appl  
Sequence 65, Appl  
Sequence 99, Appl  
Sequence 83, Appl  
Sequence 169, Appl  
Sequence 4, Appl  
Sequence 97, Appl  
Sequence 75, Appl  
Sequence 282, Appl  
Sequence 4, Appl  
Sequence 11, Appl  
Sequence 11, Appl  
Sequence 47, Appl  
Sequence 48, Appl  
Sequence 49, Appl  
Sequence 5, Appl  
Sequence 47, Appl

## ALIGNMENTS

RESULT 1  
US-09-02405-11  
; Sequence 11, Application PC/TUS9902405  
; GENERAL INFORMATION:  
; APPLICANT: Trustees of the University of Pennsylvania  
; TITLE OF INVENTION: Peptide Mimotopes of Carbohydrate Antigens  
; FILE REFERENCE: UPN3544  
; CURRENT APPLICATION NUMBER: PCT/US99/02405  
; CURRENT FILING DATE: 1999-02-04  
; EARLIER APPLICATION NUMBER: 60/073,690  
; EARLIER FILING DATE: 1998-02-04  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Novel Sequence  
PCT-US99-02405-11

Query Match 87.0%; Score 20; DB 1; Length 5;  
Best Local Similarity 60.0%; Pred. No. 4.2e+06;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5  
|  
Db 1 FSLW 5

RESULT 2  
PCT-US99-26277-114  
; Sequence 114, Application PC/TUS9926277  
; GENERAL INFORMATION:  
; APPLICANT: The Wistar Institute of Anatomy and Biology  
; APPLICANT: The Trustees of the University of Pennsylvania  
; APPLICANT: Blaszczyk-Thurin, Magdalena  
; APPLICANT: Kiebler-Emmons, Thomas  
; TITLE OF INVENTION: Compositions and Methods For Treatment of Cancer  
; FILE REFERENCE: WST93PCT  
; CURRENT APPLICATION NUMBER: PCT/US99/26277  
; CURRENT FILING DATE: 1999-11-05  
; EARLIER APPLICATION NUMBER: 60/107,478  
; EARLIER FILING DATE: 1998-11-06  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 114

; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: peptido-mimetic of a Lewis antigen  
PCT-US99-26277-114

Query Match 87.0%; Score 20; DB 1; Length 5;  
Best Local Similarity 60.0%; Pred. No. 4.2e+06;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5  
|  
Db 1 FSLW 5

RESULT 3  
US-09-601-558-11  
; Sequence 11, Application US/09601558  
; GENERAL INFORMATION:  
; APPLICANT: Kiebler-Emmons, Thomas

; APPLICANT: The Trustees of the University of Pennsylvania  
; TITLE OF INVENTION: Peptide Mimotopes Of Carbohydrate Antigens  
; FILE REFERENCE: UPN3567  
; CURRENT APPLICATION NUMBER: US/09/601,558  
; CURRENT FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: PCT/US99/02405  
; PRIOR FILING DATE: 1999-02-04  
; PRIOR APPLICATION NUMBER: 60/073,690  
; PRIOR FILING DATE: 1998-02-04  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 11  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Novel Sequence  
US-09-601-558-11

Query Match 87.0%; Score 20; DB 20; Length 5;  
Best Local Similarity 60.0%; Pred. No. 4.2e+06;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5  
|  
Db 1 FSLW 5

RESULT 4  
US-09-831-047B-114  
; Sequence 114, Application US/09831047B  
; GENERAL INFORMATION:  
; APPLICANT: The Wistar Institute of Anatomy and Biology  
; APPLICANT: The Trustees of the University of Pennsylvania  
; APPLICANT: Blaszczyk-Thurin, Magdalena  
; APPLICANT: Kiebler-Emmons, Thomas  
; TITLE OF INVENTION: Compositions and Methods For Treatment of Cancer  
; FILE REFERENCE: WST93AUSA  
; CURRENT APPLICATION NUMBER: US/09/831,047B  
; CURRENT FILING DATE: 2001-08-14  
; PRIOR APPLICATION NUMBER: 60/107,478  
; PRIOR FILING DATE: 1998-11-06  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 114  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: peptido-mimetic of a Lewis antigen

US-09-831-047B-114

Query Match 87.0%; Score 20; DB 22; Length 5;  
Best Local Similarity 60.0%; Pred. No. 4.2e+06;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXLW 5  
|  
Db 1 FSLWL 5

## RESULT 5

US-09-831-047C-114  
; Sequence 114, Application US/09831047C  
; GENERAL INFORMATION:  
; APPLICANT: The Wistar Institute of Anatomy and Biology  
; APPLICANT: The Trustees of the University of Pennsylvania  
; APPLICANT: Blazeczyk-Thurin, Magdalena  
; APPLICANT: Kieber-Emmons, Thomas  
; TITLE OF INVENTION: Compositions and Methods For Treatment of Cancer  
; FILE REFERENCE: WST93AUSA  
; CURRENT APPLICATION NUMBER: US/09/831,047C  
; PRIOR FILING DATE: 2001-05-03  
; PRIOR APPLICATION NUMBER: 60/107,478  
; PRIOR FILING DATE: 1998-11-06  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 114  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: peptido-mimetic of a Lewis antigen  
US-09-831-047C-114

Query Match 87.0%; Score 20; DB 22; Length 5;  
Best Local Similarity 60.0%; Pred. No. 4.2e+06;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXLW 5  
|  
Db 1 FSLWL 5

## RESULT 6

US-09-894-594-11  
; Sequence 11, Application US/09894594  
; GENERAL INFORMATION:  
; APPLICANT: Kieber-Emmons, Thomas  
; APPLICANT: Weiner, David B.  
; APPLICANT: Monzavi-Karbassi, Behjatolah  
; TITLE OF INVENTION: Peptide Mimotopes of Carbohydrate Antigens and DNA Molecules Encod  
; FILE REFERENCE: UPN-3984  
; CURRENT APPLICATION NUMBER: US/09/894,594  
; PRIOR FILING DATE: 2001-06-28  
; PRIOR FILING DATE: 2000-11-07  
; PRIOR APPLICATION NUMBER: PCT/US99/02405  
; PRIOR FILING DATE: 1999-02-04  
; PRIOR APPLICATION NUMBER: 60/073,690  
; PRIOR FILING DATE: 1998-02-04  
; PRIOR APPLICATION NUMBER: 60/214,517  
; PRIOR FILING DATE: 2000-06-28  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 11  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Novel Sequence  
US-09-894-594-11

Query Match 87.0%; Score 20; DB 22; Length 5;  
Best Local Similarity 60.0%; Pred. No. 4.2e+06;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXLW 5  
|  
Db 1 FSLWL 5

## RESULT 7

PCT-US01-20969-3  
; Sequence 3, Application PC/TUS0120969  
; GENERAL INFORMATION:  
; APPLICANT: GUY, RODNEY  
; APPLICANT: BAXTER, JOHN  
; APPLICANT: DARIMONT, BEATRICE  
; APPLICANT: FENG, WEIJUN  
; APPLICANT: ROBERT, FLETTERICK  
; APPLICANT: PETER, KUSHNER  
; APPLICANT: RICHARD, WAGNER  
; APPLICANT: BRIAN, WEST  
; APPLICANT: YAMAMOTO, KEITH  
; APPLICANT: GEISTLINGER, TIMOTHY  
; APPLICANT: ARNOLD, JAMES  
; APPLICANT: KUNTZ, IRWIN  
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING NUCLEAR RECEPTOR  
; FILE REFERENCE: 9811-016-228  
; CURRENT APPLICATION NUMBER: PCT/US01/20969  
; CURRENT FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 09/609,361  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 60/079,965  
; PRIOR FILING DATE: 1998-03-30  
; PRIOR APPLICATION NUMBER: US 60/113,146  
; PRIOR FILING DATE: 1998-12-16  
; PRIOR APPLICATION NUMBER: US09/281,717  
; PRIOR FILING DATE: 1999-03-30  
; NUMBER OF SEQ ID NOS: 83  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 3  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (2)..(3)  
; OTHER INFORMATION: Xaa is any amino acid  
PCT-US01-20969-3

Query Match 82.6%; Score 19; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 4.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXLW 5  
|  
Db 1 FXXLW 5

## RESULT 8

US-09-214-371-2  
; Sequence 2, Application US/09214371B  
; GENERAL INFORMATION:  
; APPLICANT: Lane, David  
; APPLICANT: Bottger, Volker  
; APPLICANT: Bottger, Angelica  
; APPLICANT: Pickslay, Stephen  
; APPLICANT: Chene, Patrick  
; APPLICANT: Hochkeppel, Heinz-Kurt  
; APPLICANT: Garcia-Scheverria, Carlos  
; APPLICANT: Furet, Pascal  
; TITLE OF INVENTION: Inhibitors of the Interaction of p53 and MDM2  
; FILE REFERENCE: 4-20937/A/PCT

; CURRENT APPLICATION NUMBER: US/09/214,371B  
; CURRENT FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: PCT/EP97/03549  
; PRIOR FILING DATE: 1997-07-04  
; NUMBER OF SEQ ID NOS: 83  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:peptide  
; OTHER INFORMATION: Where Xaa may be any amino acid  
US-09-214-371-2

Query Match 82.6%; Score 19; DB 16; Length 5;  
Best Local Similarity 100.0%; Pred. No. 4.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXLW 5  
|  
|  
|  
|  
Db 1 FXXLW 5

## RESULT 9

US-09-281-717-3  
; Sequence 3, Application US/09281717  
; GENERAL INFORMATION:  
; APPLICANT: Baxter, John D.  
; APPLICANT: Darimont, Beatrice  
; APPLICANT: Feng, Weijun  
; APPLICANT: Fletcher, Robert J.  
; APPLICANT: Kushner, Peter J.  
; APPLICANT: Wagner, Richard L.  
; APPLICANT: West, Brian  
; APPLICANT: Yamamoto, Keith R.  
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING NUCLEAR RECEPTOR  
; FILE REFERENCE: UCAL-253/02US  
; CURRENT APPLICATION NUMBER: US/09/281,717  
; CURRENT FILING DATE: 1999-03-30  
; EARLIER APPLICATION NUMBER: US 60/079,956  
; EARLIER FILING DATE: 1998-03-30  
; NUMBER OF SEQ ID NOS: 51  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (2)..(3)  
; OTHER INFORMATION: Xaa = Any Amino Acid  
US-09-281-717-3

Query Match 82.6%; Score 19; DB 16; Length 5;  
Best Local Similarity 100.0%; Pred. No. 4.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXLW 5  
|  
|  
|  
|  
Db 1 FXXLW 5

## RESULT 10

US-09-403-440A-1  
; Sequence 1, Application US/09403440A  
; GENERAL INFORMATION:  
; APPLICANT: Lane, David Philip  
; TITLE OF INVENTION: MATERIALS AND METHODS RELATING TO  
; FILE REFERENCE: MEWE25.001APC  
; CURRENT APPLICATION NUMBER: US/09/403,440A

; CURRENT FILING DATE: 2000-01-19  
; PRIOR APPLICATION NUMBER: PCT/GB98/01144  
; PRIOR FILING DATE: 1998-04-20  
; PRIOR APPLICATION NUMBER: GB 9708092.3  
; PRIOR FILING DATE: 1997-04-22  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: This represents a consensus sequence representing  
; OTHER INFORMATION: humans and mice.  
; NAME/KEY: UNSURE  
; LOCATION: 2, 3  
; OTHER INFORMATION: Xaa = any amino acid  
US-09-403-440A-1

Query Match 82.6%; Score 19; DB 18; Length 5;  
Best Local Similarity 100.0%; Pred. No. 4.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXLW 5  
|  
|  
|  
|  
Db 1 FXXLW 5

## RESULT 11

US-09-609-361-3  
; Sequence 3, Application US/09609361  
; GENERAL INFORMATION:  
; APPLICANT: GUY, RODNEY  
; APPLICANT: BAXTER, JOHN  
; APPLICANT: DARIMONT, BEATRICE  
; APPLICANT: FENG, WEIJUN  
; APPLICANT: ROBERT, FLETTERICK  
; APPLICANT: PETER, KUSHNER  
; APPLICANT: RICHARD, WAGNER  
; APPLICANT: BRIAN, WEST  
; APPLICANT: YAMAMOTO, KEITH  
; APPLICANT: GEISTLINGER, TIMOTHY  
; APPLICANT: ARNOLD, JAMES  
; APPLICANT: KUNTZ, IRWIN  
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING NUCLEAR RECEPTOR ACTIVITY  
; FILE REFERENCE: 9811-016-999  
; CURRENT APPLICATION NUMBER: US/09/609,361  
; CURRENT FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 60/079,965  
; PRIOR FILING DATE: 1998-03-30  
; PRIOR APPLICATION NUMBER: US 60/113,146  
; PRIOR FILING DATE: 1998-12-16  
; PRIOR APPLICATION NUMBER: US09/281,717  
; PRIOR FILING DATE: 1999-03-30  
; NUMBER OF SEQ ID NOS: 83  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 3  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (2)..(3)  
; OTHER INFORMATION: Xaa is any amino acid  
US-09-609-361-3

Query Match 82.6%; Score 19; DB 20; Length 5;  
Best Local Similarity 100.0%; Pred. No. 4.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXLW 5  
|  
|  
|  
|  
Db 1 FXXLW 5

```

; TITLE OF INVENTION: And Methods For Analyzing The Proteome And Complex
; FILE OF INVENTION: Compositions
; FILE REFERENCE: 24743-2305
; CURRENT APPLICATION NUMBER: PCT/US02/22821
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 60/306,019
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/314,123
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 60/363,433
; PRIOR FILING DATE: 2002-03-11
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 139
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo Sapien
; PCT-US02-22821-139

Query Match      65.2%; Score 15; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 LW 5
      ||
Db      2 LW 3

RESULT 15
PCT-US02-23257-8
; Sequence 8, Application PC/TUS0223257
; GENERAL INFORMATION:
; APPLICANT: The Brigham and Women's Hospital, Inc.
; TITLE OF INVENTION: ANALGESIC METHODS USING ENDOTHELIN
; FILE OF INVENTION: RECEPTOR LIGANDS
; FILE REFERENCE: 50073/010W02
; CURRENT APPLICATION NUMBER: PCT/US02/23257
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: US 60/307,228
; PRIOR FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; PCT-US02-23257-8

Query Match      65.2%; Score 15; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 LW 5
      ||
Db      4 LW 5

RESULT 16
PCT-US02-23257-10
; Sequence 10, Application PC/TUS0223257
; GENERAL INFORMATION:
; APPLICANT: The Brigham and Women's Hospital, Inc.
; TITLE OF INVENTION: ANALGESIC METHODS USING ENDOTHELIN
; FILE OF INVENTION: RECEPTOR LIGANDS
; FILE REFERENCE: 50073/010W02
; CURRENT APPLICATION NUMBER: PCT/US02/23257
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: US 60/307,228
; PRIOR FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; PCT-US02-23257-8

; Sequence 19; DB 23; Length 5;
; Score 82.6%; Pred. No. 4.2e+06;
; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Query Match      82.6%; Score 19; DB 23; Length 5;
Best Local Similarity 60.0%; Pred. No. 4.2e+06;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 FXXLW 5
      |||
Db      1 FIKLW 5

RESULT 13
PCT-US01-03988-791
; Sequence 791, Application PC/TUS0103988
; GENERAL INFORMATION:
; APPLICANT: Trimeris, Inc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE
; FILE OF INVENTION: FUSION-
; TITLE OF INVENTION: ASSOCIATED EVENTS INCLUDING RSV TRANSMISSION
; FILE REFERENCE: 7872-073-228
; CURRENT APPLICATION NUMBER: PCT/US01/03988
; CURRENT FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 09/515,965
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 1589
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 791
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
; PCT-US01-03988-791

Query Match      65.2%; Score 15; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 LW 5
      ||
Db      1 LW 2

RESULT 14
PCT-US02-22821-139
; Sequence 139, Application PC/TUS0222821
; GENERAL INFORMATION:
; APPLICANT: HK Pharmaceuticals, Inc.
; APPLICANT: Koister, Hubert
; APPLICANT: Siddiqi, Suhail
; APPLICANT: Little, Daniel
; TITLE OF INVENTION: Capture Compounds, Collections Thereof

```

SEQ ID NO 10  
 LENGTH: 5  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Synthetic  
 PCT-US02-23257-10

Query Match 65.2%; Score 15; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 4.2e+06;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0;

QY 4 LW 5  
 ||  
 Db 4 LW 5

## RESULT 17

PCT-US02-23257-11  
 Sequence 11, Application PC/TUS0223257

GENERAL INFORMATION:  
 APPLICANT: The Brigham and Women's Hospital, Inc.  
 TITLE OF INVENTION: ANALGESIC METHODS USING ENDOTHELIN  
 TITLE OF INVENTION: RECEPTOR LIGANDS  
 FILE REFERENCE: 50073/010W02  
 CURRENT APPLICATION NUMBER: PCT/US02/23257  
 CURRENT FILING DATE: 2002-07-23  
 PRIOR APPLICATION NUMBER: US 60/307,228  
 PRIOR FILING DATE: 2001-07-23  
 NUMBER OF SEQ ID NOS: 14  
 SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 11  
 LENGTH: 5  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Synthetic  
 PCT-US02-23257-11

Query Match 65.2%; Score 15; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 4.2e+06;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0;

QY 4 LW 5  
 ||  
 Db 4 LW 5

## RESULT 18

PCT-US02-23257-12  
 Sequence 12, Application PC/TUS0223257

GENERAL INFORMATION:  
 APPLICANT: The Brigham and Women's Hospital, Inc.  
 TITLE OF INVENTION: ANALGESIC METHODS USING ENDOTHELIN  
 TITLE OF INVENTION: RECEPTOR LIGANDS  
 FILE REFERENCE: 50073/010W02  
 CURRENT APPLICATION NUMBER: PCT/US02/23257  
 CURRENT FILING DATE: 2002-07-23  
 PRIOR APPLICATION NUMBER: US 60/307,228  
 PRIOR FILING DATE: 2001-07-23  
 NUMBER OF SEQ ID NOS: 14  
 SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 12  
 LENGTH: 5  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Synthetic  
 PCT-US02-23257-12

Query Match 65.2%; Score 15; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 4.2e+06;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0;

QY 4 LW 5  
 ||  
 Db 4 LW 5

## RESULT 19

PCT-US02-23257-13

Sequence 13, Application PC/TUS0223257  
 GENERAL INFORMATION:  
 APPLICANT: The Brigham and Women's Hospital, Inc.  
 TITLE OF INVENTION: ANALGESIC METHODS USING ENDOTHELIN  
 TITLE OF INVENTION: RECEPTOR LIGANDS  
 FILE REFERENCE: 50073/010W02  
 CURRENT APPLICATION NUMBER: PCT/US02/23257  
 CURRENT FILING DATE: 2002-07-23  
 PRIOR APPLICATION NUMBER: US 60/307,228  
 PRIOR FILING DATE: 2001-07-23  
 NUMBER OF SEQ ID NOS: 14  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 13  
 LENGTH: 5  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Synthetic  
 NAME/KEY: MOD\_RES  
 LOCATION: 3  
 OTHER INFORMATION: Ile at position 3 is alle  
 PCT-US02-23257-13

Query Match 65.2%; Score 15; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 4.2e+06;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0;

QY 4 LW 5  
 ||  
 Db 4 LW 5

## RESULT 20

PCT-US98-15227-1

Sequence 1, Application PC/TUS9815227  
 GENERAL INFORMATION:  
 APPLICANT: The New York Blood Center, Inc.  
 TITLE OF INVENTION: MONOSPECIFIC ANTIBODY REACTIVE WITH  
 TITLE OF INVENTION: MATRIX METALLOPROTEINASE CLEAVAGE PRODUCTS OF FIBRIN(OGEN)  
 NUMBER OF SEQUENCES: 2  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Hoffmann & Baron, LLP  
 STREET: 350 Jericho Turnpike  
 CITY: Jericho  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 11753

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage  
 COMPUTER: IBM compatible  
 OPERATING SYSTEM: MS-DOS  
 SOFTWARE: Wordperfect  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US98/15227  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/900,895  
 FILING DATE: 7/25/97  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Baron, Ronald J.  
 REGISTRATION NUMBER: 29,281  
 REFERENCE/DOCKET NUMBER: 454-16 PCT  
 TELECOMMUNICATION INFORMATION:

Query Match 65.2%; Score 15; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 4.2e+06;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0;

; TELEPHONE: (516) 822-3550  
 ; TELEFAX: (516) 822-3582  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 5 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 PCT-US98-15227-1

Query Match 65.2%; Score 15; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 4.2e+06;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5  
 DB 2 LW 3

RESULT 21  
 PCT-US99-11219-791  
 ; Sequence 791, Application PC/TUS9911219  
 ; GENERAL INFORMATION:  
 ; APPLICANT: TRIMERIS, INC.  
 ; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC  
 ; FILE OF INVENTION: PROPERTIES  
 ; CURRENT FILING DATE: 1999-05-20  
 ; NUMBER OF SEQ ID NOS: 1542  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 791  
 ; LENGTH: 5  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Core polypeptide  
 PCT-US99-11219-791

Query Match 65.2%; Score 15; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 4.2e+06;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5  
 DB 1 LW 2

RESULT 22  
 US-07-585-141-11  
 ; Sequence 11, Application US/07585141  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Schramm, Wolfgang  
 ; APPLICANT: Schramm, Hans J.  
 ; TITLE OF INVENTION: Agent For Inhibiting Symmetrical  
 ; TITLE OF INVENTION: Proteins, In Particular Enzymes  
 ; NUMBER OF SEQUENCES: 20  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Venable, Baetjer, Howard & Civiletti  
 ; STREET: 1201 New York Avenue N.W., Suite 1000  
 ; CITY: Washington  
 ; STATE: DC  
 ; COUNTRY: USA  
 ; ZIP: 20005  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/07/585.141  
 ; FILING DATE: 19901009  
 ; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: WO PCT/EP90/00219  
 ; FILING DATE: 09-FEB-1990  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: DE P 39 04 040.2  
 ; FILING DATE: 10-FEB-1989  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Innen, Jeffrey L.  
 ; REGISTRATION NUMBER: 28957  
 ; REFERENCE/DOCKET NUMBER: 18644-96040  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 202-962-4810  
 ; TELEFAX: 202-962-8300  
 ; INFORMATION FOR SEQ ID NO: 11:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 5 amino acids  
 ; TYPE: AMINO ACID  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; HYPOTHETICAL: YES  
 US-07-585-141-11

Query Match 65.2%; Score 15; DB 3; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 4.2e+06;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5  
 DB 1 LW 2

RESULT 23  
 US-07-608-569-17  
 ; Sequence 17, Application US/07608569  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Tainer, John A  
 ; APPLICANT: Kuhn, Leslie  
 ; APPLICANT: Boissinot, Maurice  
 ; APPLICANT: Fisher, Cindy  
 ; APPLICANT: Parge, Hans E  
 ; APPLICANT: Griffin, John H  
 ; APPLICANT: Mullenbach, Guy T  
 ; APPLICANT: Hallowell, Robert A  
 ; TITLE OF INVENTION: Glycosaminoglycan-Targeted Fusion  
 ; TITLE OF INVENTION: proteins, Their Design, Construction and Compositions  
 ; NUMBER OF SEQUENCES: 18  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: The Scripps Research Institute, Office of  
 ; ADDRESSEE: Patent Counsel  
 ; STREET: 10666 North Torrey Pines Road  
 ; CITY: La Jolla  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 92037  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/07/608.569  
 ; FILING DATE: 19901102  
 ; CLASSIFICATION: 424  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/608539  
 ; FILING DATE: 01-NOV-1990  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Fitting, Thomas  
 ; REGISTRATION NUMBER: 34,163  
 ; REFERENCE/DOCKET NUMBER: SCR0348P  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 619-544-2937  
 ; TELEFAX: 619-554-6312

; INFORMATION FOR SEQ ID NO: 17:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 5 amino acids  
 ; TYPE: AMINO ACID  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; FRAGMENT TYPE: internal  
 ;  
 US-07-608-569-17

Query Match 65.2%; Score 15; DB 3; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 4.2e+06;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5  
 Db 1 LW 2

RESULT 24  
 US-08-344-185B-100  
 ; Sequence 100, Application US/08344185B  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SIMONS, JOHN N.  
 ; APPLICANT: PILOT-MATIAS, T.J.  
 ; APPLICANT: DAWSON, GEORGE J.  
 ; APPLICANT: SCHLAUDER, GEORGE G.  
 ; APPLICANT: DESAI, SURESH M.  
 ; APPLICANT: LEARY, THOMAS P.  
 ; APPLICANT: MUEHROFF, ANTHONY T.  
 ; APPLICANT: BUIJK, S.L.  
 ; APPLICANT: MUSHAWAR, ISA K.  
 ; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E  
 ; TITLE OF INVENTION: HEPATITIS REAGENTS AND METHODS FOR THEIR USE  
 ; NUMBER OF SEQUENCES: 539  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: ABBOTT LABORATORIES  
 ; STREET: ONE HUNDRED ABBOTT PARK ROAD  
 ; CITY: ABBOTT PARK  
 ; STATE: IL  
 ; COUNTRY: USA  
 ; ZIP: 60064-3500  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/344,185B  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: FOREMSKI, PRISCILLA E.  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 708-937-6365  
 ; TELEFAX: 708-938-2623  
 ; INFORMATION FOR SEQ ID NO: 100:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 5 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ;  
 US-08-344-185B-100

Query Match 65.2%; Score 15; DB 7; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 4.2e+06;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5  
 Db 3 LW 4

RESULT 25

US-08-344-185B-454  
 ; Sequence 454, Application US/08344185B  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SIMONS, JOHN N.  
 ; APPLICANT: PILOT-MATIAS, T.J.  
 ; APPLICANT: DAWSON, GEORGE J.  
 ; APPLICANT: SCHLAUDER, GEORGE G.  
 ; APPLICANT: DESAI, SURESH M.  
 ; APPLICANT: LEARY, THOMAS P.  
 ; APPLICANT: MUEHROFF, ANTHONY T.  
 ; APPLICANT: BUIJK, S.L.  
 ; APPLICANT: MUSHAWAR, ISA K.  
 ; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E  
 ; TITLE OF INVENTION: HEPATITIS REAGENTS AND METHODS FOR THEIR USE  
 ; NUMBER OF SEQUENCES: 539  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: ABBOTT LABORATORIES  
 ; STREET: ONE HUNDRED ABBOTT PARK ROAD  
 ; CITY: ABBOTT PARK  
 ; STATE: IL  
 ; COUNTRY: USA  
 ; ZIP: 60064-3500  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/344,185B  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: FOREMSKI, PRISCILLA E.  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 708-937-6365  
 ; TELEFAX: 708-938-2623  
 ; INFORMATION FOR SEQ ID NO: 454:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 5 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ;  
 US-08-344-185B-454

Query Match 65.2%; Score 15; DB 7; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 4.2e+06;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5  
 Db 4 LW 5

RESULT 26  
 US-08-344-185C-100  
 ; Sequence 100, Application US/08344185C  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SIMONS, JOHN N.  
 ; APPLICANT: PILOT-MATIAS, T.J.  
 ; APPLICANT: DAWSON, GEORGE J.  
 ; APPLICANT: SCHLAUDER, GEORGE G.  
 ; APPLICANT: DESAI, SURESH M.  
 ; APPLICANT: LEARY, THOMAS P.  
 ; APPLICANT: MUEHROFF, ANTHONY T.  
 ; APPLICANT: BUIJK, S.L.  
 ; APPLICANT: MUSHAWAR, ISA K.  
 ; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E  
 ; TITLE OF INVENTION: HEPATITIS REAGENTS AND METHODS FOR THEIR USE  
 ; NUMBER OF SEQUENCES: 539  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: ABBOTT LABORATORIES  
 ; STREET: ONE HUNDRED ABBOTT PARK ROAD  
 ; CITY: ABBOTT PARK



STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/344,185C  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: FOREMSKI, PRISCILLA E.  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 708-937-6365  
TELEFAX: 708-938-2623  
INFORMATION FOR SEQ ID NO: 100:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-344-185C-100

Query Match 65.2%; Score 15; DB 7; Length 5;  
Best Local Similarity 100.0%; Pred. No. 4.2e+06;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5  
DB 3 LW 4

RESULT 27  
US-08-344-185C-454  
Sequence 454, Application US/08344185C  
GENERAL INFORMATION:  
APPLICANT: SIMONS, JOHN N.  
APPLICANT: PILOT-MATIAS, T.J.  
APPLICANT: DAWSON, GEORGE J.  
APPLICANT: SCHLAUDER, GEORGE G.  
APPLICANT: DESAI, SURESH M.  
APPLICANT: LEARY, THOMAS P.  
APPLICANT: MUEHROFF, ANTHONY T.  
APPLICANT: BUIJK, S.L.  
APPLICANT: MUSHAWAR, ISA K.  
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E  
HEPATITIS REAGENTS AND METHODS FOR THEIR USE  
NUMBER OF SEQUENCES: 539  
CORRESPONDENCE ADDRESS:  
ADDRESS: ABBOTT LABORATORIES  
STREET: ONE HUNDRED ABBOTT PARK ROAD  
CITY: ABBOTT PARK  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/344,185C  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: FOREMSKI, PRISCILLA E.  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 708-937-6365  
TELEFAX: 708-938-2623  
INFORMATION FOR SEQ ID NO: 454:  
SEQUENCE CHARACTERISTICS:

LENGTH: 5 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-344-185C-454

Query Match 65.2%; Score 15; DB 7; Length 5;  
Best Local Similarity 100.0%; Pred. No. 4.2e+06;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5  
DB 4 LW 5

RESULT 28  
US-08-424-550A-228  
Sequence 228, Application US/08424550A  
GENERAL INFORMATION:  
APPLICANT: JOHN N. SIMONS  
APPLICANT: TAMI J. PILOT-MATIAS  
APPLICANT: GEORGE J. DAWSON  
APPLICANT: GEORGE G. SCHLAUDER  
APPLICANT: SURESH M. DESAI  
APPLICANT: THOMAS P. LEARY  
APPLICANT: ANTHONY SCOTT MUEHROFF  
APPLICANT: JAMES C. ERKER  
APPLICANT: SHERI L. BUIJK  
APPLICANT: ISA K. MUSHAWAR  
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS  
NUMBER OF SEQUENCES: 716  
CORRESPONDENCE ADDRESS:  
ADDRESS: ABBOTT LABORATORIES D377/AP6D  
STREET: 100 ABBOTT PARK ROAD  
CITY: ABBOTT PARK  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/424,550A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: FOREMSKI, PRISCILLA E.  
REGISTRATION NUMBER: 33,207  
REFERENCE/DOCKET NUMBER: 5527.PC.01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 708-937-6365  
TELEFAX: 708-938-2623  
INFORMATION FOR SEQ ID NO: 228:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-424-550A-228

Query Match 65.2%; Score 15; DB 8; Length 5;  
Best Local Similarity 100.0%; Pred. No. 4.2e+06;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5  
DB 3 LW 4

RESULT 29  
US-08-424-550B-228

```

; Sequence 228, Application US/08424550B
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUERHOFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550B
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCTUS94/01321
; FILING DATE: 04-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94908724.1
; FILING DATE: 04-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lavin Jr., Lawrence M.
; REGISTRATION NUMBER: 30,768
; REFERENCE/DOCKET NUMBER: 38-21(10650)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)537-6670
; TELEFAX: (314)537-6047
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-432-147-47

Query Match 65.2%; Score 15; DB 8; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5
Db 3 LW 4

RESULT 31
US-08-467-344A-228
; Sequence 228, Application US/08467344A
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUERHOFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,344A
; FILING DATE: 07-Jun-1995
; CLASSIFICATION: <Unknown>

```

```
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/424,550
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: POREMBSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 228:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 228:
US-08-467-344A-228

Query Match      65.2%; Score 15; DB 8; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 LW 5
        ||
Db      3 LW 4

RESULT 32
US-08-486-749-228
; Sequence 228, Application US/08486749
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUERHOFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; ADDRESS: 100 ABBOTT PARK ROAD
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,749
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: POREMBSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 228:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 228:
US-08-467-344A-228

Query Match      65.2%; Score 15; DB 8; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 LW 5
        ||
Db      3 LW 4

RESULT 33
US-08-488-445A-228
; Sequence 228, Application US/08488445A
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUERHOFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; ADDRESS: 100 ABBOTT PARK ROAD
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,445A
; FILING DATE:
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: POREMBSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 228:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 228:
US-08-488-445A-228

Query Match      65.2%; Score 15; DB 8; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 LW 5
        ||
Db      3 LW 4

RESULT 34
US-08-488-446-228
```

; Sequence 228, Application US/08488446  
; GENERAL INFORMATION:  
; APPLICANT: JOHN N. SIMONS  
; APPLICANT: TAMI J. PILOT-MATIAS  
; APPLICANT: GEORGE J. DAWSON  
; APPLICANT: GEORGE G. SCHLAUDER  
; APPLICANT: SURESH M. DESAI  
; APPLICANT: THOMAS P. LEARY  
; APPLICANT: ANTHONY SCOTT MUEHROFF  
; APPLICANT: JAMES C. ERKER  
; APPLICANT: SHERI L. BUIJK  
; APPLICANT: ISA K. MUSHAWAR  
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS  
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE  
; NUMBER OF SEQUENCES: 716  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D  
; STREET: 100 ABBOTT PARK ROAD  
; CITY: ABBOTT PARK  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60064-3500  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/488,446  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/424,550  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: POREMSKI, PRISCILLA E.  
; REGISTRATION NUMBER: 33,207  
; REFERENCE/DOCKET NUMBER: 5527.PC.01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 708-937-6365  
; TELEFAX: 708-938-2623  
; INFORMATION FOR SEQ ID NO: 228:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-488-446-228

Query Match 65.2%; Score 15; DB 8; Length 5;  
Best Local Similarity 100.0%; Pred. No. 4.2e+06;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5  
||  
Db 3 LW 4

RESULT 35  
US-08-530-325-14  
; Sequence 14, Application US/08530325  
; GENERAL INFORMATION:  
; APPLICANT: HILGER, CHRISTOPH-STEPH  
; APPLICANT: DINKELBORG, LUDGER  
; APPLICANT: KRAMP, WOLFGANG  
; APPLICANT: SCHIER, HANS-MARTIN  
; TITLE OF INVENTION: CHELATING AGENTS OF THE TYPE XN1SIO1 FOR RADIOACTIVE I  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FLIESLER, DUBB, MEYER & LOVEJOY  
; STREET: Four Embarcadero Center, Suite 400  
; CITY: San Francisco  
; STATE: CA

; COUNTRY: USA  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/530,325  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/DE94/00371  
; FILING DATE: 29-MAR-1994  
; APPLICATION NUMBER: P 43 11 023.1  
; FILING DATE: 31-MAR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dubb, Hubert E  
; REGISTRATION NUMBER: 25,329  
; REFERENCE/DOCKET NUMBER: WBLT 2005 (WO) PA  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-362-3800  
; TELEFAX: 415-362-2928  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal  
; ORIGINAL SOURCE:  
; US-08-530-325-14

Query Match 65.2%; Score 15; DB 9; Length 5;  
Best Local Similarity 100.0%; Pred. No. 4.2e+06;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5  
||  
Db 4 LW 5

RESULT 36  
US-08-530-327-14  
; Sequence 14, Application US/08530327  
; GENERAL INFORMATION:  
; APPLICANT: ERBER, SEBASTIAN  
; APPLICANT: DINKELBORG, LUDGER  
; APPLICANT: ROHLFS, GERHARD  
; APPLICANT: SCHULTZE, PAUL-EBERHARD  
; APPLICANT: NOLL, BERNHARD  
; TITLE OF INVENTION: BIFUNCTIONAL CHELATORS AND THEIR USE IN RADIOPHARMACI  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FLIESLER, DUBB, MEYER & LOVEJOY  
; STREET: Four Embarcadero Center, Suite 400  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/530,327  
; FILING DATE:  
; CLASSIFICATION: 424

;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: PCT/DE94/00369  
;; FILING DATE: 29-MAR-1994  
;; APPLICATION NUMBER: P 43 11 021.5  
;; FILING DATE: 31-MAR-1993  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Dubb, Hubert E  
;; REGISTRATION NUMBER: 25,329  
;; REFERENCE/DOCKET NUMBER: WBLT 2007 (WO) PA  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 415-362-3800  
;; TELEFAX: 415-362-2928  
;; TELEX:  
;; INFORMATION FOR SEQ ID NO: 14:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 5 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; HYPOTHETICAL: NO  
;; ANTI-SENSE: NO  
;; FRAGMENT TYPE: internal  
;; ORIGINAL SOURCE:  
;; US-08-530-327-14

Query Match 65.2%; Score 15; DB 9; Length 5;  
Best Local Similarity 100.0%; Pred. No. 4.2e+06;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5  
||  
Db 4 LW 5

RESULT 37  
US-08-981-122-15  
; Sequence 15, Application US/08981122A  
; GENERAL INFORMATION:  
; APPLICANT: Hatanaka, Yoshihiro  
; APPLICANT: Aritomi, Masaharu  
; TITLE OF INVENTION: Peptide for binding thereto a low density lipoprotein  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/08/981,122A  
; CURRENT FILING DATE: 1997-12-18  
; EARLIER APPLICATION NUMBER: JP 7-176904  
; EARLIER FILING DATE: 1995-06-21  
; EARLIER APPLICATION NUMBER: PCT/JP96/01734  
; EARLIER FILING DATE: 1996-06-21  
; NUMBER OF SEQ ID NOS: 90  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 15  
; LENGTH: 5  
; TYPE: PPT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Sequence of a peptide synthesized in Example 2 from L-form  
; OTHER INFORMATION: F-moc amino acids by solid phase method using a multi-peptide  
; OTHER INFORMATION: synthesizing system (RaMPS)  
US-08-981-122-15

Query Match 65.2%; Score 15; DB 13; Length 5;  
Best Local Similarity 100.0%; Pred. No. 4.2e+06;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5  
||  
Db 1 LW 2

RESULT 38  
US-08-981-122-38  
; Sequence 38, Application US/08981122A

;; GENERAL INFORMATION:  
;; APPLICANT: Hatanaka, Yoshihiro  
;; APPLICANT: Aritomi, Masaharu  
;; TITLE OF INVENTION: Peptide for binding thereto a low density lipoprotein  
;; FILE REFERENCE:  
;; CURRENT APPLICATION NUMBER: US/08/981,122A  
;; CURRENT FILING DATE: 1997-12-18  
;; EARLIER APPLICATION NUMBER: JP 7-176904  
;; EARLIER FILING DATE: 1995-06-21  
;; EARLIER APPLICATION NUMBER: PCT/JP96/01734  
;; EARLIER FILING DATE: 1996-06-21  
;; NUMBER OF SEQ ID NOS: 90  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 38  
;; LENGTH: 5  
;; TYPE: PPT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; NAME/KEY: AMIDATION  
;; LOCATION: 5  
;; FEATURE:  
;; OTHER INFORMATION: Sequence of a peptide synthesized in Examples 11 and 12 from L-form  
;; OTHER INFORMATION: F-moc amino acids by solid phase method using an automatic peptide  
;; OTHER INFORMATION: synthesizer (9050 plus peptide synthesizer)  
US-08-981-122-38

Query Match 65.2%; Score 15; DB 13; Length 5;  
Best Local Similarity 100.0%; Pred. No. 4.2e+06;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5  
||  
Db 4 LW 5

RESULT 39  
US-08-981-122-43  
; Sequence 43, Application US/08981122A  
; GENERAL INFORMATION:  
; APPLICANT: Hatanaka, Yoshihiro  
; APPLICANT: Aritomi, Masaharu  
; TITLE OF INVENTION: Peptide for binding thereto a low density lipoprotein  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/08/981,122A  
; CURRENT FILING DATE: 1997-12-18  
; EARLIER APPLICATION NUMBER: JP 7-176904  
; EARLIER FILING DATE: 1995-06-21  
; EARLIER APPLICATION NUMBER: PCT/JP96/01734  
; EARLIER FILING DATE: 1996-06-21  
; NUMBER OF SEQ ID NOS: 90  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 43  
; LENGTH: 5  
; TYPE: PPT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: AMIDATION  
; LOCATION: 5  
; FEATURE:  
; OTHER INFORMATION: Sequence of peptides synthesized in Examples 11 and 12 from L-form  
; OTHER INFORMATION: F-moc amino acids by solid phase method using an automatic peptide  
; OTHER INFORMATION: synthesizer (9050 plus peptide synthesizer)  
US-08-981-122-43

Query Match 65.2%; Score 15; DB 13; Length 5;  
Best Local Similarity 100.0%; Pred. No. 4.2e+06;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5  
||  
Db 4 LW 5

```
RESULT 40
US-08-981-122-51
; Sequence 51, Application US/08981122A
; GENERAL INFORMATION:
; APPLICANT: Hatanaka, Yoshihiro
; APPLICANT: Aritomi, Masaharu
; TITLE OF INVENTION: Peptide for binding thereto a low density lipoprotein
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/08/981,122A
; CURRENT FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: JP 7-176904
; EARLIER FILING DATE: 1995-06-21
; EARLIER APPLICATION NUMBER: PCT/JP96/01734
; EARLIER FILING DATE: 1996-06-21
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 51
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; NAME/KEY: AMIDATION
; LOCATION: 5
; FEATURE:
; OTHER INFORMATION: Sequence of peptides synthesized in Examples 11 and 12 from L-form
; OTHER INFORMATION: F-moc amino acids by solid phase method using an automatic peptide
; OTHER INFORMATION: synthesizer (9050 plus peptide synthesizer)
US-08-981-122-51

Query Match      65.2%; Score 15; DB 13; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 LW 5
      ||
Db      4 LW 5

RESULT 41
US-09-209-676-30
; Sequence 30, Application US/09209676
; GENERAL INFORMATION:
; APPLICANT: Pangene Corporation
; TITLE OF INVENTION: The Use of Consensus Sequences for Targeted Homologous
; FILE REFERENCE: A-65678-1/RFT/NBC
; CURRENT APPLICATION NUMBER: US/09/209,676
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US 60/070,734
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: consensus
; OTHER INFORMATION: sequence
US-09-209-676-30

Query Match      65.2%; Score 15; DB 16; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 LW 5
      ||
Db      3 LW 4

RESULT 42
US-09-284-327-1
; Sequence 1, Application US/09284327
```

```
; GENERAL INFORMATION:
; APPLICANT: Genencor International, Inc.
; TITLE OF INVENTION: Novel EGIII-Like Enzymes, DNA Encoding
; TITLE OF INVENTION: Such Enzymes and Methods for Producing Such Enzymes
; FILE REFERENCE: GC516-2-PCT
; CURRENT APPLICATION NUMBER: US/09/284,327
; CURRENT FILING DATE: 1999-04-10
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-284-327-1

Query Match      65.2%; Score 15; DB 16; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 LW 5
      ||
Db      3 LW 4

RESULT 43
US-09-308-823A-582
; Sequence 582, Application US/09308823A
; GENERAL INFORMATION:
; APPLICANT: Warren, Richard
; TITLE OF INVENTION: Novel Prokaryotic Polynucleotides,
; TITLE OF INVENTION: Polypeptides and Their Uses
; FILE REFERENCE: P50596
; CURRENT APPLICATION NUMBER: US/09/308,823A
; CURRENT FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 661
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 582
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-308-823A-582

Query Match      65.2%; Score 15; DB 17; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 LW 5
      ||
Db      4 LW 5

RESULT 44
US-09-350-641-791
; Sequence 791, Application US/09350641
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC PROPERTIES
; FILE REFERENCE: 7872-067
; CURRENT APPLICATION NUMBER: US/09/350,641
; CURRENT FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1589
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 791
```

; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Core polypeptide  
US-09-350-641-791

Query Match 65.2%; Score 15; DB 17; Length 5;  
Best Local Similarity 100.0%; Pred. No. 4.2e+06;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5  
||  
Db 1 LW 2

## RESULT 45

US-09-350-641B-791

; Sequence 791, Application US/09350641B  
; GENERAL INFORMATION:  
; APPLICANT: Barney, S.  
; APPLICANT: Guthrie, K.  
; APPLICANT: Merutka, G.  
; APPLICANT: Anwer, M.  
; APPLICANT: Lambert, D.  
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC  
; FILE REFERENCE: 7872-067  
; CURRENT APPLICATION NUMBER: US/09/350,641B  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: 09/315,304  
; PRIOR FILING DATE: 1999-05-20  
; PRIOR APPLICATION NUMBER: 09/082,279  
; PRIOR FILING DATE: 1998-05-20  
; NUMBER OF SEQ ID NOS: 1757  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 791  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Core polypeptide  
US-09-350-641B-791

Query Match 65.2%; Score 15; DB 17; Length 5;  
Best Local Similarity 100.0%; Pred. No. 4.2e+06;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5  
||  
Db 1 LW 2

## RESULT 46

US-09-350-641C-791

; Sequence 791, Application US/09350641C  
; GENERAL INFORMATION:  
; APPLICANT: Barney, S.  
; APPLICANT: Guthrie, K.  
; APPLICANT: Merutka, G.  
; APPLICANT: Anwer, M.  
; APPLICANT: Lambert, D.  
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC  
; FILE REFERENCE: 7872-067  
; CURRENT APPLICATION NUMBER: US/09/350,641C  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: 09/315,304  
; PRIOR FILING DATE: 1999-05-20  
; PRIOR APPLICATION NUMBER: 09/082,279  
; PRIOR FILING DATE: 1998-05-20  
; NUMBER OF SEQ ID NOS: 1757  
; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 791  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Core polypeptide  
US-09-350-641C-791

Query Match 65.2%; Score 15; DB 17; Length 5;  
Best Local Similarity 100.0%; Pred. No. 4.2e+06;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5  
||  
Db 1 LW 2

## RESULT 47

US-09-410-568-9  
; Sequence 9, Application US/09410568  
; GENERAL INFORMATION:  
; APPLICANT: Probst, Peter  
; APPLICANT: Bhatia, Ajay  
; APPLICANT: Skeiky, Yasir  
; APPLICANT: Fang, Hang  
; APPLICANT: Jen, Shyian  
; APPLICANT: Stromberg, Erica Jean  
; APPLICANT: Enghart, Susan E.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT AND  
; FILE REFERENCE: 210121.469C2  
; CURRENT APPLICATION NUMBER: US/09/410,568  
; CURRENT FILING DATE: 1999-10-01  
; NUMBER OF SEQ ID NOS: 109  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 9  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Chlamydia trachomatis  
US-09-410-568-9

Query Match 65.2%; Score 15; DB 18; Length 5;  
Best Local Similarity 100.0%; Pred. No. 4.2e+06;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5  
||  
Db 3 LW 4

## RESULT 48

US-09-426-571-9  
; Sequence 9, Application US/09426571  
; GENERAL INFORMATION:  
; APPLICANT: Probst, Peter  
; APPLICANT: Bhatia, Ajay  
; APPLICANT: Skeiky, Yasir  
; APPLICANT: Fling, Steve  
; APPLICANT: Fang, Hang  
; APPLICANT: Jen, Shyian  
; APPLICANT: Stromberg, Erica Jean  
; APPLICANT: Enghart, Susan E.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND  
; FILE REFERENCE: 469C3  
; CURRENT APPLICATION NUMBER: US/09/426,571  
; CURRENT FILING DATE: 1999-10-22  
; NUMBER OF SEQ ID NOS: 168  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 9  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Chlamydia trachomatis

## US-09-426-571-9

Query Match 65.2%; Score 15; DB 18; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 4.2e+06;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5  
 Db 3 LW 4

## RESULT 49

US-09-454-684-9  
 ; Sequence 9, Application US/09454684  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Probst, Peter  
 ; APPLICANT: Bhatia, Ajay  
 ; APPLICANT: Skeiky, Yasir  
 ; APPLICANT: Fling, Steve  
 ; APPLICANT: Maisonneuve, Jeff  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND  
 ; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION  
 ; FILE REFERENCE: 210121.469C4  
 ; CURRENT APPLICATION NUMBER: US/09/454,684  
 ; CURRENT FILING DATE: 1999-12-03  
 ; NUMBER OF SEQ ID NOS: 303  
 ; SOFTWARE: FastSeq for Windows Version 3.0/4.0  
 ; SEQ ID NO 9  
 ; LENGTH: 5  
 ; TYPE: PRT  
 ; ORGANISM: Chlamydia trachomatis  
 ; ORGANISM: Chlamydia trachomatis

Query Match 65.2%; Score 15; DB 18; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 4.2e+06;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5  
 Db 3 LW 4

## RESULT 50

US-09-454-684A-9  
 ; Sequence 9, Application US/09454684A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Probst, Peter  
 ; APPLICANT: Bhatia, Ajay  
 ; APPLICANT: Skeiky, Yasir  
 ; APPLICANT: Fling, Steve  
 ; APPLICANT: Maisonneuve, Jeff  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND  
 ; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION  
 ; FILE REFERENCE: 210121.469C4  
 ; CURRENT APPLICATION NUMBER: US/09/454,684A  
 ; CURRENT FILING DATE: 1999-12-03  
 ; NUMBER OF SEQ ID NOS: 310  
 ; SOFTWARE: FastSeq for Windows Version 3.0/4.0  
 ; SEQ ID NO 9  
 ; LENGTH: 5  
 ; TYPE: PRT  
 ; ORGANISM: Chlamydia trachomatis  
 ; ORGANISM: Chlamydia trachomatis

Query Match 65.2%; Score 15; DB 18; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 4.2e+06;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5  
 Db 3 LW 4

## RESULT 51

US-09-457-198A-25  
 ; Sequence 25, Application US/09457198A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hartnett, James R.  
 ; APPLICANT: Christine, Andrews A.  
 ; TITLE OF INVENTION: Thermostable Enzyme for Nucleic Acid Detection  
 ; FILE REFERENCE: Thermostable/nucleic acid detection  
 ; CURRENT APPLICATION NUMBER: US/09/457,198A  
 ; CURRENT FILING DATE: 1999-12-06  
 ; PRIOR APPLICATION NUMBER: 09/358,972  
 ; PRIOR FILING DATE: 1999-07-21  
 ; NUMBER OF SEQ ID NOS: 28  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 25  
 ; LENGTH: 5  
 ; TYPE: PRT  
 ; ORGANISM: Pyrococcus furiosus  
 ; ORGANISM: Pyrococcus furiosus

Query Match 65.2%; Score 15; DB 18; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 4.2e+06;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5  
 Db 4 LW 5

## RESULT 52

US-09-515-965-791  
 ; Sequence 791, Application US/09515965  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Antczak, J.  
 ; APPLICANT: Delmedico, M.  
 ; APPLICANT: Erickson, J.  
 ; APPLICANT: Lambert, D.  
 ; APPLICANT: Sista, P.  
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-  
 ; TITLE OF INVENTION: ASSOCIATED EVENTS INCLUDING RSV TRANSMISSION  
 ; FILE REFERENCE: 7872-073  
 ; CURRENT APPLICATION NUMBER: US/09/515,965  
 ; CURRENT FILING DATE: 2000-02-29  
 ; PRIOR APPLICATION NUMBER: 09/315,304  
 ; PRIOR FILING DATE: 1999-05-20  
 ; PRIOR APPLICATION NUMBER: 09/082,279  
 ; PRIOR FILING DATE: 1998-05-20  
 ; NUMBER OF SEQ ID NOS: 1589  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 791  
 ; LENGTH: 5  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Core polypeptide  
 ; OTHER INFORMATION: Core polypeptide

Query Match 65.2%; Score 15; DB 19; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 4.2e+06;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5  
 Db 1 LW 2

## RESULT 53

US-09-515-965A-791  
 ; Sequence 791, Application US/09515965A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Antczak, J.  
 ; APPLICANT: Delmedico, M.  
 ; APPLICANT: Erickson, J.



; APPLICANT: Lambert, D.  
 ; APPLICANT: Sista, P.  
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-  
 ; TITLE OF INVENTION: ASSOCIATED EVENTS INCLUDING RSV TRANSMISSION  
 ; FILE REFERENCE: 7872-073  
 ; CURRENT APPLICATION NUMBER: US/09/515,965A  
 ; CURRENT FILING DATE: 2000-02-29  
 ; PRIOR APPLICATION NUMBER: 09/315,304  
 ; PRIOR FILING DATE: 1999-05-20  
 ; PRIOR APPLICATION NUMBER: 09/082,279  
 ; PRIOR FILING DATE: 1998-05-20  
 ; NUMBER OF SEQ ID NOS: 1994  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 791  
 ; LENGTH: 5  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Core polypeptide  
 US-09-515-965A-791

Query Match 65.2%; Score 15; DB 19; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 4.2e+06;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5  
 ||  
 Db 1 LW 2

## RESULT 54

US-09-515-965A-1657  
 ; Sequence 1657, Application US/09515965A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Antczak, J.  
 ; APPLICANT: Delmedico, M.  
 ; APPLICANT: Erickson, J.  
 ; APPLICANT: Lambert, D.  
 ; APPLICANT: Sista, P.  
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-  
 ; TITLE OF INVENTION: ASSOCIATED EVENTS INCLUDING RSV TRANSMISSION  
 ; FILE REFERENCE: 7872-073  
 ; CURRENT APPLICATION NUMBER: US/09/515,965A  
 ; CURRENT FILING DATE: 2000-02-29  
 ; PRIOR APPLICATION NUMBER: 09/315,304  
 ; PRIOR FILING DATE: 1999-05-20  
 ; PRIOR APPLICATION NUMBER: 09/082,279  
 ; PRIOR FILING DATE: 1998-05-20  
 ; NUMBER OF SEQ ID NOS: 1994  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 1657  
 ; LENGTH: 5  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Core polypeptide  
 US-09-515-965A-1657

Query Match 65.2%; Score 15; DB 19; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 4.2e+06;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5  
 ||  
 Db 1 LW 2

## RESULT 55

US-09-536-998-1  
 ; Sequence 1, Application US/09536998  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bini, Alessandra

; APPLICANT: Kudryk, Bohdan  
 ; TITLE OF INVENTION: MONOSPECIFIC ANTIBODY REACTIVE WITH MATRIXMETALLOPROTEINASE CLEAV  
 ; TITLE OF INVENTION: PRODUCTS OF FIBRIN(OGEN)  
 ; FILE REFERENCE: 454-16CIP  
 ; CURRENT APPLICATION NUMBER: US/09/536,998  
 ; CURRENT FILING DATE: 2001-04-25  
 ; PRIOR APPLICATION NUMBER: 08/900,895  
 ; PRIOR FILING DATE: 1997-07-25  
 ; NUMBER OF SEQ ID NOS: 3  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 1  
 ; LENGTH: 5  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-536-998-1

Query Match 65.2%; Score 15; DB 19; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 4.2e+06;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5  
 ||  
 Db 2 LW 3

## RESULT 56

US-09-598-419-9  
 ; Sequence 9, Application US/09598419  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Skeiky, Yasir A.W.  
 ; APPLICANT: Scholler, John  
 ; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND  
 ; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION  
 ; FILE REFERENCE: 210121.469C6  
 ; CURRENT APPLICATION NUMBER: US/09/598,419  
 ; CURRENT FILING DATE: 2000-06-20  
 ; NUMBER OF SEQ ID NOS: 357  
 ; SOFTWARE: FastSeq for Windows Version 3.0/4.0  
 ; SEQ ID NO 9  
 ; LENGTH: 5  
 ; TYPE: PRT  
 ; ORGANISM: Chlamydia trachomatis  
 US-09-598-419-9

Query Match 65.2%; Score 15; DB 19; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 4.2e+06;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5  
 ||  
 Db 3 LW 4

## RESULT 57

US-09-632-426-30  
 ; Sequence 30, Application US/09632426  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Mitchinson, Colin  
 ; APPLICANT: Ropp, Traci M.  
 ; APPLICANT: Swanson, Barbara A.  
 ; TITLE OF INVENTION: Novel Variant EGIII-Like Cellulase  
 ; TITLE OF INVENTION: Compositions  
 ; FILE REFERENCE: GCG30  
 ; CURRENT APPLICATION NUMBER: US/09/632,426  
 ; CURRENT FILING DATE: 2000-08-04  
 ; NUMBER OF SEQ ID NOS: 86  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 30  
 ; LENGTH: 5  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Box1

```

; NAME/KEY: VARIANT
; LOCATION: (1)...(5)
; OTHER INFORMATION: Xaa = Asn or Gln
US-09-632-426-30

Query Match      65.2%; Score 15; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5
   ||
Db 3 LW 4

RESULT 58
US-09-632-570-30
; Sequence 30, Application US/09632570
; GENERAL INFORMATION:
; APPLICANT: Gualfetti, Peter
; APPLICANT: Mitchinson, Colin
; APPLICANT: Phillips, Jay Ian
; TITLE OF INVENTION: Novel Variant EGIII-Like Cellulase
; FILE REFERENCE: GC631
; CURRENT APPLICATION NUMBER: US/09/632,570
; CURRENT FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(5)
; OTHER INFORMATION: Xaa = Asn or Gln
; OTHER INFORMATION: BOX1
US-09-632-570-30

Query Match      65.2%; Score 15; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5
   ||
Db 3 LW 4

RESULT 59
US-09-636-243A-75
; Sequence 75, Application US/09636243A
; GENERAL INFORMATION:
; APPLICANT: WANG, Bryan S.
; APPLICANT: PABO, Carl O.
; TITLE OF INVENTION: DIMERIZING PEPTIDES
; FILE REFERENCE: 8325-1004 / M4-US1
; CURRENT APPLICATION NUMBER: US/09/636,243A
; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/148,422
; PRIOR FILING DATE: 1999-08-11
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 75
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: sequential
; OTHER INFORMATION: block reoptimization sequence
US-09-636-243A-75

Query Match      65.2%; Score 15; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5
   ||
Db 3 LW 4

RESULT 60
US-09-642-234-75
; Sequence 75, Application US/09642234
; GENERAL INFORMATION:
; APPLICANT: WANG, Bryan S.
; APPLICANT: PABO, Carl O.
; TITLE OF INVENTION: DIMERIZING PEPTIDES
; FILE REFERENCE: 8325-1004.20 / M4-US2
; CURRENT APPLICATION NUMBER: US/09/642,234
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/148,422
; PRIOR FILING DATE: 1999-08-11
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 75
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: sequential
; OTHER INFORMATION: block reoptimization sequence
US-09-642-234-75

Query Match      65.2%; Score 15; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5
   ||
Db 3 LW 4

RESULT 61
US-09-657-276-723
; Sequence 723, Application US/09657276
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibadeau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/657,276
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 723
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-657-276-723

Query Match      65.2%; Score 15; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5
   ||
Db 3 LW 4

```

Best Local Similarity 100.0%; Pred. No. 4.2e+06; Indels 0; Gaps 0;  
Matches 2; Conservative 0; Mismatches 0;

QY 4 LW 5  
||  
Db 4 LW 5

## RESULT 62

US-09-657-276-724  
; Sequence 724, Application US/09657276  
; GENERAL INFORMATION:  
; APPLICANT: Conjuchem, Inc.  
; APPLICANT: Bridon, Dominique  
; APPLICANT: Ezrin, Alan  
; APPLICANT: Milner, Peter  
; APPLICANT: Holmes, Darren  
; APPLICANT: Thibaudeau, Karen  
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM  
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD  
; TITLE OF INVENTION: COMPONENTS  
; FILE REFERENCE: 2110  
; CURRENT APPLICATION NUMBER: US/09/657,276  
; CURRENT FILING DATE: 2000-09-07  
; PRIOR APPLICATION NUMBER: 60/134,406  
; PRIOR FILING DATE: 1999-05-17  
; PRIOR APPLICATION NUMBER: 60/153,406  
; PRIOR FILING DATE: 1999-09-10  
; PRIOR APPLICATION NUMBER: 60/159,783  
; PRIOR FILING DATE: 1999-10-18  
; NUMBER OF SEQ ID NOS: 1617  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 724  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
US-09-657-276-724

Query Match 65.2%; Score 15; DB 20; Length 5;  
Best Local Similarity 100.0%; Pred. No. 4.2e+06;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5  
||  
Db 4 LW 5

## RESULT 63

US-09-657-276-734  
; Sequence 734, Application US/09657276  
; GENERAL INFORMATION:  
; APPLICANT: Conjuchem, Inc.  
; APPLICANT: Bridon, Dominique  
; APPLICANT: Ezrin, Alan  
; APPLICANT: Milner, Peter  
; APPLICANT: Holmes, Darren  
; APPLICANT: Thibaudeau, Karen  
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM  
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD  
; TITLE OF INVENTION: COMPONENTS  
; FILE REFERENCE: 2110  
; CURRENT APPLICATION NUMBER: US/09/657,276  
; CURRENT FILING DATE: 2000-09-07  
; PRIOR APPLICATION NUMBER: 60/134,406  
; PRIOR FILING DATE: 1999-05-17  
; PRIOR APPLICATION NUMBER: 60/153,406  
; PRIOR FILING DATE: 1999-09-10  
; PRIOR APPLICATION NUMBER: 60/159,783  
; PRIOR FILING DATE: 1999-10-18  
; NUMBER OF SEQ ID NOS: 1617

; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 734  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
US-09-657-276-734

Query Match 65.2%; Score 15; DB 20; Length 5;  
Best Local Similarity 100.0%; Pred. No. 4.2e+06;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5  
||  
Db 4 LW 5

## RESULT 64

US-09-657-276-1560  
; Sequence 1560, Application US/09657276  
; GENERAL INFORMATION:  
; APPLICANT: Conjuchem, Inc.  
; APPLICANT: Bridon, Dominique  
; APPLICANT: Ezrin, Alan  
; APPLICANT: Milner, Peter  
; APPLICANT: Holmes, Darren  
; APPLICANT: Thibaudeau, Karen  
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM  
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD  
; TITLE OF INVENTION: COMPONENTS  
; FILE REFERENCE: 2110  
; CURRENT APPLICATION NUMBER: US/09/657,276  
; CURRENT FILING DATE: 2000-09-07  
; PRIOR APPLICATION NUMBER: 60/134,406  
; PRIOR FILING DATE: 1999-05-17  
; PRIOR APPLICATION NUMBER: 60/153,406  
; PRIOR FILING DATE: 1999-09-10  
; PRIOR APPLICATION NUMBER: 60/159,783  
; PRIOR FILING DATE: 1999-10-18  
; NUMBER OF SEQ ID NOS: 1617  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1560  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
US-09-657-276-1560

Query Match 65.2%; Score 15; DB 20; Length 5;  
Best Local Similarity 100.0%; Pred. No. 4.2e+06;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5  
||  
Db 2 LW 3

## RESULT 65

US-09-762-270-19  
; Sequence 19, Application US/09762270  
; GENERAL INFORMATION:  
; APPLICANT: DEPLA, ERIK  
; APPLICANT: MOEREELS, HENRI  
; APPLICANT: MAERTENS, GEERT  
; TITLE OF INVENTION: BENZODIAZEPINES AND BENZOTHAZEPINES DERIVATIVES AND  
; TITLE OF INVENTION: HBSAG PEPTIDES BINDING TO ANNEXINS, THEIR COMPOSITIONS  
; TITLE OF INVENTION: AND USE  
; FILE REFERENCE: 2551-54  
; CURRENT APPLICATION NUMBER: US/09/762,270

```

; CURRENT FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: PCT/EP99/06231
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: EP 98870186.8
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: EP 99870062.9
; PRIOR FILING DATE: 1999-03-29
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-09-762-270-19

Query Match          65.2%; Score 15; DB 21; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5
   ||
Db 3 LW 4

RESULT 66
US-09-762-270-20
; Sequence 20, Application US/09762270
; GENERAL INFORMATION:
; APPLICANT: DEPLA, ERIK
; APPLICANT: MOERRELS, HENRI
; APPLICANT: MAERTENS, GEERT
; TITLE OF INVENTION: BENZODIAZEPINES AND BENZOTHAZEPINES DERIVATIVES AND
; TITLE OF INVENTION: HBSAG PEPTIDES BINDING TO ANNEXINS, THEIR COMPOSITIONS
; TITLE OF INVENTION: AND USE
; FILE REFERENCE: 2551-54
; CURRENT APPLICATION NUMBER: US/09/762,270
; CURRENT FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: PCT/EP99/06231
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: EP 98870186.8
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: EP 99870062.9
; PRIOR FILING DATE: 1999-03-29
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-09-762-270-20

Query Match          65.2%; Score 15; DB 21; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5
   ||
Db 3 LW 4

RESULT 67
US-09-762-270-21
; Sequence 21, Application US/09762270
; GENERAL INFORMATION:
; APPLICANT: DEPLA, ERIK
; APPLICANT: MOERRELS, HENRI
; APPLICANT: MAERTENS, GEERT
; TITLE OF INVENTION: BENZODIAZEPINES AND BENZOTHAZEPINES DERIVATIVES AND
; TITLE OF INVENTION: HBSAG PEPTIDES BINDING TO ANNEXINS, THEIR COMPOSITIONS
; TITLE OF INVENTION: AND USE
; FILE REFERENCE: 2551-54
; CURRENT APPLICATION NUMBER: US/09/762,270
; CURRENT FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: PCT/EP99/06231
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: EP 98870186.8
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: EP 99870062.9
; PRIOR FILING DATE: 1999-03-29
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-09-762-270-21

Query Match          65.2%; Score 15; DB 21; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5
   ||
Db 3 LW 4

RESULT 68
US-09-762-270-22
; Sequence 22, Application US/09762270
; GENERAL INFORMATION:
; APPLICANT: DEPLA, ERIK
; APPLICANT: MOERRELS, HENRI
; APPLICANT: MAERTENS, GEERT
; TITLE OF INVENTION: BENZODIAZEPINES AND BENZOTHAZEPINES DERIVATIVES AND
; TITLE OF INVENTION: HBSAG PEPTIDES BINDING TO ANNEXINS, THEIR COMPOSITIONS
; TITLE OF INVENTION: AND USE
; FILE REFERENCE: 2551-54
; CURRENT APPLICATION NUMBER: US/09/762,270
; CURRENT FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: PCT/EP99/06231
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: EP 98870186.8
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: EP 99870062.9
; PRIOR FILING DATE: 1999-03-29
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-09-762-270-22

Query Match          65.2%; Score 15; DB 21; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5
   ||
Db 3 LW 4

RESULT 69
US-09-762-270-23
; Sequence 23, Application US/09762270
; GENERAL INFORMATION:
; APPLICANT: DEPLA, ERIK
; APPLICANT: MOERRELS, HENRI
; APPLICANT: MAERTENS, GEERT
; TITLE OF INVENTION: BENZODIAZEPINES AND BENZOTHAZEPINES DERIVATIVES AND
; TITLE OF INVENTION: HBSAG PEPTIDES BINDING TO ANNEXINS, THEIR COMPOSITIONS
; TITLE OF INVENTION: AND USE
; FILE REFERENCE: 2551-54
; CURRENT APPLICATION NUMBER: US/09/762,270
; CURRENT FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: PCT/EP99/06231

```

; PRIOR FILING DATE: 1999-08-25  
; PRIOR APPLICATION NUMBER: EP 98870186.8  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: EP 98870062.9  
; PRIOR FILING DATE: 1999-03-29  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 23  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Hepatitis B virus  
US-09-762-270-23

Query Match 65.2%; Score 15; DB 21; Length 5;  
Best Local Similarity 100.0%; Pred. No. 4.2e+06;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5  
||  
Db 3 LW 4

## RESULT 70

US-09-834-784-791  
; Sequence 791, Application US/09834784  
; GENERAL INFORMATION:  
; APPLICANT: Barney, Shawn  
; APPLICANT: Guthrie, Kelly  
; APPLICANT: Merutka, Gene  
; APPLICANT: Anwer, Mohamed  
; APPLICANT: Lambert, Dennis  
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED  
; FILE REFERENCE: 7872-043  
; CURRENT APPLICATION NUMBER: US/09/834,784  
; CURRENT FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 09/082,279  
; PRIOR FILING DATE: 1998-05-20  
; NUMBER OF SEQ ID NOS: 1515  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 791  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Core polypeptide  
US-09-834-784-791

Query Match 65.2%; Score 15; DB 22; Length 5;  
Best Local Similarity 100.0%; Pred. No. 4.2e+06;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5  
||  
Db 1 LW 2

## RESULT 71

US-09-841-132-9  
; Sequence 9, Application US/09841132  
; GENERAL INFORMATION:  
; APPLICANT: Bhatia, Ajay  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Probst, Peter  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND  
; FILE REFERENCE: 210121.469C8  
; CURRENT APPLICATION NUMBER: US/09/841,132  
; CURRENT FILING DATE: 2001-04-23  
; NUMBER OF SEQ ID NOS: 599  
; SOFTWARE: FastSeq for Windows Version 3.0/4.0  
; SEQ ID NO 9  
; LENGTH: 5

; TYPE: PRT  
; ORGANISM: Chlamydia trachomatis  
US-09-841-132-9

Query Match 65.2%; Score 15; DB 22; Length 5;  
Best Local Similarity 100.0%; Pred. No. 4.2e+06;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5  
||  
Db 3 LW 4

## RESULT 72

US-09-920-306-21  
; Sequence 21, Application US/09920306  
; GENERAL INFORMATION:  
; APPLICANT: Unilever PLC  
; APPLICANT: Unilever NV  
; TITLE OF INVENTION: Peptides Capable of Functioning as Mimotopes for  
; FILE REFERENCE: Hormonal Analyses  
; CURRENT APPLICATION NUMBER: US/09/920,306  
; CURRENT FILING DATE: 2001-08-02  
; PRIOR APPLICATION NUMBER: EP00306613.1  
; PRIOR FILING DATE: 2000-08-03  
; NUMBER OF SEQ ID NOS: 80  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 21  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
US-09-920-306-21

Query Match 65.2%; Score 15; DB 23; Length 5;  
Best Local Similarity 100.0%; Pred. No. 4.2e+06;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5  
||  
Db 2 LW 3

## RESULT 73

US-09-350-369C-513  
; Sequence 513, Application US/09350369C  
; GENERAL INFORMATION:  
; APPLICANT: Samuel E. Hopkins  
; APPLICANT: Elizabeth M. Dimassimo  
; APPLICANT: Pamela P. Ruskak  
; APPLICANT: Thomas Michael Venetta  
; TITLE OF INVENTION: Methods and Compositions for Detection of HIV GP41 Peptides  
; FILE REFERENCE: 7872-0688-999  
; CURRENT APPLICATION NUMBER: US/09/350,369C  
; CURRENT FILING DATE: 1999-07-09  
; NUMBER OF SEQ ID NOS: 2041  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 513  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Human Immunodeficiency Virus-1 (HIV-1)  
US-09-350-369C-513

Query Match 65.2%; Score 15; DB 23; Length 5;  
Best Local Similarity 100.0%; Pred. No. 4.2e+06;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5  
||

Db 1 LW 2

## RESULT 74

US-09-350-369C-1389  
; Sequence 1389, Application US/09350369C  
; GENERAL INFORMATION:  
; APPLICANT: Samuel E. Hopkins  
; APPLICANT: Elizabeth M. Dimassimo  
; APPLICANT: Pamela P. Rusnak  
; APPLICANT: Thomas Michael Venetta  
; TITLE OF INVENTION: Methods and Compositions for Detection of HIV GP41 Peptides and H  
; TITLE OF INVENTION: GP41-Like Peptides  
; FILE REFERENCE: 7872-068-999  
; CURRENT APPLICATION NUMBER: US/09/350,369C  
; CURRENT FILING DATE: 1999-07-09  
; NUMBER OF SEQ ID NOS: 2041  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 1389  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Human Immunodeficiency Virus-1 (HIV-1)  
US-09-350-369C-1389

Query Match 65.2%; Score 15; DB 23; Length 5;  
Best Local Similarity 100.0%; Pred. No. 4.2e+06;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5

Db 1 LW 2

## RESULT 75

US-10-005-305-36  
; Sequence 36, Application US/10005305  
; GENERAL INFORMATION:  
; APPLICANT: The Government of the United States of America, represented by the  
; APPLICANT: Secretary, Department of Health and Human Services  
; TITLE OF INVENTION: T20/DP178 AND T21/DP107 ARE ACTIVATORS  
; TITLE OF INVENTION: OF HUMAN PHAGOCYTE  
; TITLE OF INVENTION: FORMYL PEPTIDE RECEPTORS  
; FILE REFERENCE: NIH171.001C1  
; CURRENT APPLICATION NUMBER: US/10/005,305  
; CURRENT FILING DATE: 2001-11-02  
; PRIOR APPLICATION NUMBER: PCT/US00/12371  
; PRIOR FILING DATE: 2000-05-05  
; PRIOR APPLICATION NUMBER: 60/132,686  
; PRIOR FILING DATE: 1999-05-05  
; NUMBER OF SEQ ID NOS: 203  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 36  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Artificial Peptide  
US-10-005-305-36

Query Match 65.2%; Score 15; DB 24; Length 5;  
Best Local Similarity 100.0%; Pred. No. 4.2e+06;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5

Db 1 LW 2

Search completed: February 12, 2003, 10:55:29  
Job time: 133 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 12, 2003, 10:51:59 ; Search time 18 Seconds  
(without alignments)  
23.274 Million cell updates/sec

Title: US-09-403-440A-1

Perfect score: 23  
Sequence: 1 FXXLW 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 425801 seqs, 83787487 residues

Total number of hits satisfying chosen parameters: 1873

Minimum DB seq length: 5  
Maximum DB seq length: 5

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : Pending Patents AA New \*

1: /cgn2\_6/ptodata/1/paa/PCT\_NEW\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/paa/US06\_NEW\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/paa/US07\_NEW\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/paa/US08\_NEW\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/paa/US09\_NEW\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/paa/US10\_NEW\_COMB.pep.\*  
7: /cgn2\_6/ptodata/1/paa/US60\_NEW\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	82.6	5	5	US-09-281-717A-3
2	15	65.2	5	5	US-09-636-243B-75
3	13	56.5	5	5	US-09-968-744A-211
4	13	56.5	5	5	US-09-968-744A-217
5	13	56.5	5	5	US-10-174-717A-51
6	13	56.5	5	5	US-10-099-056-2683
7	12	52.2	5	6	US-10-174-717A-94
8	12	52.2	5	6	US-10-053-498B-320
9	11	47.8	5	1	PCT-US02-32657-65
10	11	47.8	5	1	PCT-US02-33556-34
11	11	47.8	5	1	PCT-US02-33556-36
12	11	47.8	5	1	PCT-US02-33556-40
13	11	47.8	5	1	PCT-US02-33985-2
14	11	47.8	5	1	PCT-US02-34760-21
15	11	47.8	5	1	PCT-US02-34760-46
16	11	47.8	5	1	PCT-US02-34760-47
17	11	47.8	5	1	PCT-US02-35606-2
18	11	47.8	5	1	PCT-US02-16525A-26
19	11	47.8	5	1	PCT-US02-24469-21
20	11	47.8	5	1	PCT-US02-24310-166
21	11	47.8	5	1	PCT-US02-24469A-21
22	11	47.8	5	1	PCT-US02-39109-15
23	11	47.8	5	1	PCT-US02-32307-23
24	11	47.8	5	1	PCT-US02-39643-5
25	11	47.8	5	1	PCT-US02-40891-1113
26	11	47.8	5	1	PCT-US02-40892-398
27	11	47.8	5	1	Sequence 3, Appl
28	11	47.8	5	1	Sequence 75, Appl
29	11	47.8	5	1	Sequence 211, Appl
30	11	47.8	5	1	Sequence 217, Appl
31	11	47.8	5	1	Sequence 51, Appl
32	11	47.8	5	1	Sequence 2683, Ap
33	11	47.8	5	1	Sequence 94, Appl
34	11	47.8	5	1	Sequence 320, Appl
35	11	47.8	5	1	Sequence 65, Appl
36	11	47.8	5	1	Sequence 34, Appl
37	11	47.8	5	1	Sequence 36, Appl
38	11	47.8	5	1	Sequence 40, Appl
39	11	47.8	5	1	Sequence 2, Appl
40	11	47.8	5	1	Sequence 21, Appl
41	11	47.8	5	1	Sequence 46, Appl
42	11	47.8	5	1	Sequence 47, Appl
43	11	47.8	5	1	Sequence 2, Appl
44	11	47.8	5	1	Sequence 26, Appl
45	11	47.8	5	1	Sequence 21, Appl
46	11	47.8	5	1	Sequence 166, Appl
47	11	47.8	5	1	Sequence 21, Appl
48	11	47.8	5	1	Sequence 15, Appl
49	11	47.8	5	1	Sequence 23, Appl
50	11	47.8	5	1	Sequence 5, Appl
51	11	47.8	5	1	Sequence 1113, Ap
52	11	47.8	5	1	Sequence 398, Appl
53	11	47.8	5	1	Sequence 3, Appl
54	11	47.8	5	1	Sequence 75, Appl
55	11	47.8	5	1	Sequence 211, Appl
56	11	47.8	5	1	Sequence 217, Appl
57	11	47.8	5	1	Sequence 51, Appl
58	11	47.8	5	1	Sequence 2683, Ap
59	11	47.8	5	1	Sequence 94, Appl
60	11	47.8	5	1	Sequence 320, Appl
61	11	47.8	5	1	Sequence 65, Appl
62	11	47.8	5	1	Sequence 34, Appl
63	11	47.8	5	1	Sequence 36, Appl
64	11	47.8	5	1	Sequence 40, Appl
65	11	47.8	5	1	Sequence 2, Appl
66	11	47.8	5	1	Sequence 21, Appl
67	11	47.8	5	1	Sequence 46, Appl
68	11	47.8	5	1	Sequence 47, Appl
69	11	47.8	5	1	Sequence 2, Appl
70	11	47.8	5	1	Sequence 26, Appl
71	11	47.8	5	1	Sequence 21, Appl
72	11	47.8	5	1	Sequence 166, Appl
73	11	47.8	5	1	Sequence 21, Appl
74	11	47.8	5	1	Sequence 15, Appl
75	11	47.8	5	1	Sequence 23, Appl
76	11	47.8	5	1	Sequence 5, Appl
77	11	47.8	5	1	Sequence 1113, Ap
78	11	47.8	5	1	Sequence 398, Appl
79	11	47.8	5	1	Sequence 3, Appl
80	11	47.8	5	1	Sequence 75, Appl
81	11	47.8	5	1	Sequence 211, Appl
82	11	47.8	5	1	Sequence 217, Appl
83	11	47.8	5	1	Sequence 51, Appl
84	11	47.8	5	1	Sequence 2683, Ap
85	11	47.8	5	1	Sequence 94, Appl
86	11	47.8	5	1	Sequence 320, Appl
87	11	47.8	5	1	Sequence 65, Appl
88	11	47.8	5	1	Sequence 34, Appl
89	11	47.8	5	1	Sequence 36, Appl
90	11	47.8	5	1	Sequence 40, Appl
91	11	47.8	5	1	Sequence 2, Appl
92	11	47.8	5	1	Sequence 21, Appl
93	11	47.8	5	1	Sequence 46, Appl
94	11	47.8	5	1	Sequence 47, Appl
95	11	47.8	5	1	Sequence 2, Appl
96	11	47.8	5	1	Sequence 26, Appl
97	11	47.8	5	1	Sequence 21, Appl
98	11	47.8	5	1	Sequence 166, Appl
99	11	47.8	5	1	Sequence 21, Appl
100	11	47.8	5	1	Sequence 15, Appl

Sequence 61, Appl  
Sequence 14, Appl  
Sequence 26, Appl  
Sequence 38, Appl  
Sequence 13, Appl  
Sequence 147, Appl  
Sequence 157, Appl  
Sequence 152, Appl  
Sequence 162, Appl  
Sequence 167, Appl  
Sequence 172, Appl  
Sequence 540, Appl  
Sequence 16, Appl  
Sequence 5, Appl  
Sequence 145, Appl  
Sequence 152, Appl  
Sequence 12, Appl  
Sequence 18, Appl  
Sequence 1, Appl  
Sequence 32, Appl  
Sequence 19, Appl  
Sequence 20, Appl  
Sequence 16, Appl  
Sequence 1, Appl  
Sequence 2, Appl  
Sequence 3, Appl  
Sequence 5, Appl  
Sequence 21, Appl  
Sequence 23, Appl  
Sequence 27, Appl  
Sequence 30, Appl  
Sequence 35, Appl  
Sequence 44, Appl  
Sequence 44, Appl  
Sequence 56, Appl  
Sequence 57, Appl  
Sequence 59, Appl  
Sequence 60, Appl  
Sequence 61, Appl  
Sequence 62, Appl  
Sequence 63, Appl  
Sequence 64, Appl  
Sequence 76, Appl  
Sequence 77, Appl  
Sequence 78, Appl  
Sequence 1, Appl  
Sequence 278, Appl  
Sequence 1, Appl  
Sequence 27, Appl  
Sequence 12, Appl  
Sequence 2, Appl  
Sequence 2, Appl  
Sequence 14, Appl  
Sequence 65, Appl  
Sequence 12, Appl  
Sequence 21, Appl  
Sequence 10, Appl  
Sequence 2, Appl  
Sequence 11, Appl  
Sequence 112, Appl  
Sequence 115, Appl  
Sequence 8, Appl  
Sequence 21, Appl  
Sequence 46, Appl  
Sequence 47, Appl  
Sequence 2, Appl  
Sequence 14, Appl  
Sequence 6, Appl  
Sequence 12, Appl  
Sequence 11, Appl  
Sequence 23, Appl  
Sequence 31, Appl

100 11 47.8 5 6 US-10-058-513-38

Sequence 38, Appl

## ALIGNMENTS

RESULT 1  
US-09-281-717A-3  
; Sequence 3, Application US/09281717A  
; GENERAL INFORMATION:  
; APPLICANT: Baxter, John  
; APPLICANT: Darimont, Beatrice  
; APPLICANT: Feng, Weijun  
; APPLICANT: Fletterick, Robert  
; APPLICANT: Kushner, Peter  
; APPLICANT: West, Brian  
; APPLICANT: Wagner, Richard  
; APPLICANT: Yamamoto, Keith  
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING NUCLEAR RECEPTOR  
; FILE REFERENCE: 9811-008-999  
; CURRENT APPLICATION NUMBER: US/09/281,717A  
; CURRENT FILING DATE: 1999-03-30  
; PRIOR APPLICATION NUMBER: US 60/079,956  
; PRIOR FILING DATE: 1998-03-30  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 3  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: Variant  
; LOCATION: (2)..(3)  
; OTHER INFORMATION: Xaa is any amino acid  
US-09-281-717A-3

Query Match 82.6%; Score 19; DB 5; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3.5e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXLW 5  
|||  
Db 1 FXLW 5

RESULT 2  
US-09-636-243B-75  
; Sequence 75, Application US/09636243B  
; GENERAL INFORMATION:  
; APPLICANT: WANG, Bryan S.  
; APPLICANT: PABO, Carl O.  
; TITLE OF INVENTION: DIMERIZING PEPTIDES  
; FILE REFERENCE: 8325-1004 / M4-US1  
; CURRENT APPLICATION NUMBER: US/09/636,243B  
; CURRENT FILING DATE: 2000-08-10  
; PRIOR APPLICATION NUMBER: 60/148,422  
; PRIOR FILING DATE: 1999-08-11  
; NUMBER OF SEQ ID NOS: 83  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 75  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: sequential  
; OTHER INFORMATION: block reoptimization sequence  
US-09-636-243B-75

Query Match 65.2%; Score 15; DB 5; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3.5e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5  
||  
Db 3 LW 4

RESULT 3  
US-09-968-744A-211  
; Sequence 211, Application US/09968744A  
; GENERAL INFORMATION:  
; APPLICANT: Tomlinson, Ian M  
; APPLICANT: Winter, Gregory  
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands  
; FILE REFERENCE: 8039/1073  
; CURRENT APPLICATION NUMBER: US/09/968,744A  
; CURRENT FILING DATE: 2003-01-13  
; PRIOR APPLICATION NUMBER: GB 9722131.1  
; PRIOR FILING DATE: 1997-10-20  
; PRIOR APPLICATION NUMBER: US 60/065,248  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: US 60/066,729  
; PRIOR FILING DATE: 1997-11-21  
; PRIOR APPLICATION NUMBER: PCT/GB98/03135  
; PRIOR FILING DATE: 1998-10-20  
; PRIOR APPLICATION NUMBER: US 09/511,939  
; PRIOR FILING DATE: 2000-02-24  
; NUMBER OF SEQ ID NOS: 350  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 211  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-968-744A-211

Query Match 56.5%; Score 13; DB 5; Length 5;  
Best Local Similarity 50.0%; Pred. No. 3.5e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5  
||  
Db 4 MW 5

RESULT 4  
US-09-968-744A-217  
; Sequence 217, Application US/09968744A  
; GENERAL INFORMATION:  
; APPLICANT: Tomlinson, Ian M  
; APPLICANT: Winter, Gregory  
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands  
; FILE REFERENCE: 8039/1073  
; CURRENT APPLICATION NUMBER: US/09/968,744A  
; CURRENT FILING DATE: 2003-01-13  
; PRIOR APPLICATION NUMBER: GB 9722131.1  
; PRIOR FILING DATE: 1997-10-20  
; PRIOR APPLICATION NUMBER: US 60/065,248  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: US 60/066,729  
; PRIOR FILING DATE: 1997-11-21  
; PRIOR APPLICATION NUMBER: PCT/GB98/03135  
; PRIOR FILING DATE: 1998-10-20  
; PRIOR APPLICATION NUMBER: US 09/511,939  
; PRIOR FILING DATE: 2000-02-24  
; NUMBER OF SEQ ID NOS: 350  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 217  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-968-744A-217

Query Match 56.5%; Score 13; DB 5; Length 5;  
Best Local Similarity 50.0%; Pred. No. 3.5e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;



Qy 4 LW 5  
:|  
Db 4 MW 5

## RESULT 5

US-10-174-717A-51  
; Sequence 51, Application US/10174717A  
; APPLICANT: Koide, Shohei  
; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES  
; NUMBER OF SEQUENCES: 118  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.  
; STREET: 121 South Eighth Street, St. 1600  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: USA  
; ZIP: 55402

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: WINDOWS  
SOFTWARE: FastSEQ Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/174.717A  
FILING DATE: 18-Jun-2002  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/096,749  
FILING DATE: June 12, 1998  
APPLICATION NUMBER: 60/049,410  
FILING DATE: June 12, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Ann S. Viksnins  
REGISTRATION NUMBER: 37,748  
REFERENCE/DOCKET NUMBER: 109.034US4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (612) 373-6900  
TELEFAX: (612) 339-3061

## INFORMATION FOR SEQ ID NO: 51:

SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
SEQUENCE DESCRIPTION: SEQ ID NO: 51:

US-10-174-717A-51

Query Match 56.5%; Score 13; DB 6; Length 5;  
Best Local Similarity 50.0%; Pred. No. 3.5e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5  
:|  
Db 2 MW 3

## RESULT 6

US-10-099-056-2683  
; Sequence 2683, Application US/10099056  
; GENERAL INFORMATION:  
; APPLICANT: Hybrigenics  
; APPLICANT: Pierre Legrain  
; TITLE OF INVENTION: More and more protein-protein interactions in adipocyte cells  
; FILE REFERENCE: B4838A  
; CURRENT APPLICATION NUMBER: US/10/099,056  
; CURRENT FILING DATE: 2002-03-14  
; PRIOR APPLICATION NUMBER: US 60/275,734

; PRIOR FILING DATE: 2001/03/14  
; NUMBER OF SEQ ID NOS: 2850  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2683  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; OTHER INFORMATION: Translation of SEQ ID NO:691  
US-10-099-056-2683

Query Match 56.5%; Score 13; DB 6; Length 5;  
Best Local Similarity 50.0%; Pred. No. 3.5e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5  
:|  
Db 1 IW 2

## RESULT 7

US-10-174-717A-94  
; Sequence 94, Application US/10174717A  
; APPLICANT: Koide, Shohei  
; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES  
; NUMBER OF SEQUENCES: 118  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.  
; STREET: 121 South Eighth Street, St. 1600  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: USA  
; ZIP: 55402

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: WINDOWS  
SOFTWARE: FastSEQ Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/174.717A  
FILING DATE: 18-Jun-2002  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/096,749  
FILING DATE: June 12, 1998  
APPLICATION NUMBER: 60/049,410  
FILING DATE: June 12, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Ann S. Viksnins  
REGISTRATION NUMBER: 37,748  
REFERENCE/DOCKET NUMBER: 109.034US4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (612) 373-6900  
TELEFAX: (612) 339-3061

## INFORMATION FOR SEQ ID NO: 94:

SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
SEQUENCE DESCRIPTION: SEQ ID NO: 94:

US-10-174-717A-94

Query Match 52.2%; Score 12; DB 6; Length 5;  
Best Local Similarity 50.0%; Pred. No. 3.5e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5  
:|

Db 2 VW 3

## RESULT 8

US-10-053-498B-320  
 ; Sequence 320, Application US/10053498B  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Sloan-Kettering Institute for Cancer Research  
 ; APPLICANT: Rothman, James E.  
 ; APPLICANT: Mayhew, Mark  
 ; APPLICANT: Hoe, Mee H.  
 ; APPLICANT: Houghton, Alan  
 ; APPLICANT: Hartl, Ulrich  
 ; APPLICANT: Querfelli, Quathek  
 ; APPLICANT: Morol, Yoichi  
 ; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES  
 ; FILE REFERENCE: 11746/46002  
 ; CURRENT APPLICATION NUMBER: US/10/053,498B  
 ; CURRENT FILING DATE: 2002-01-17  
 ; PRIOR APPLICATION NUMBER: 08/961,707  
 ; PRIOR FILING DATE: 1997-10-31  
 ; NUMBER OF SEQ ID NOS: 321  
 ; SOFTWARE: WordPerfect 8.0 for Windows  
 ; SEQ ID NO 320  
 ; LENGTH: 5  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Random peptide in coliphage M13  
 US-10-053-498B-320

Query Match 52.2%; Score 12; DB 6; Length 5;  
 Best Local Similarity 40.0%; Pred. No. 3.5e+05;  
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXLW 5  
 |  
 Db 1 FHWVW 5

## RESULT 9

PCT-US02-32657-65  
 ; Sequence 65, Application PC/TUS0232657  
 ; GENERAL INFORMATION:  
 ; APPLICANT: AMGEN INC.  
 ; TITLE OF INVENTION: SPECIFIC BINDING AGENTS OF HUMAN ANGIOPOIETIN-2  
 ; FILE REFERENCE: A-801B  
 ; CURRENT APPLICATION NUMBER: PCT/US02/32657  
 ; CURRENT FILING DATE: 2002-10-11  
 ; PRIOR APPLICATION NUMBER: US 60/414,155  
 ; PRIOR FILING DATE: 2002-09-27  
 ; PRIOR APPLICATION NUMBER: US 60/328,624  
 ; PRIOR FILING DATE: 2001-10-11  
 ; NUMBER OF SEQ ID NOS: 359  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 65  
 ; LENGTH: 5  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Polypeptide capable of binding to Ang-2  
 PCT-US02-32657-65

Query Match 47.8%; Score 11; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5  
 |  
 Db 1' W 1

## RESULT 10

Query Match 47.8%; Score 11; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+05;

PCT-US02-33556-34  
 ; Sequence 34, Application PC/TUS0233556  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Amgen, Inc.

; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma  
 ; TITLE OF INVENTION: Neutralizing Activity  
 ; FILE REFERENCE: A-799  
 ; CURRENT APPLICATION NUMBER: PCT/US02/33556  
 ; CURRENT FILING DATE: 2002-10-17  
 ; NUMBER OF SEQ ID NOS: 135  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 34  
 ; LENGTH: 5  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 PCT-US02-33556-34

Query Match 47.8%; Score 11; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5  
 |  
 Db 4 W 4

## RESULT 11

PCT-US02-33556-36  
 ; Sequence 36, Application PC/TUS0233556  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Amgen, Inc.  
 ; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma  
 ; TITLE OF INVENTION: Neutralizing Activity  
 ; FILE REFERENCE: A-799  
 ; CURRENT APPLICATION NUMBER: PCT/US02/33556  
 ; CURRENT FILING DATE: 2002-10-17  
 ; NUMBER OF SEQ ID NOS: 135  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 36  
 ; LENGTH: 5  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 PCT-US02-33556-36

Query Match 47.8%; Score 11; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5  
 |  
 Db 4 W 4

## RESULT 12

PCT-US02-33556-40  
 ; Sequence 40, Application PC/TUS0233556  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Amgen, Inc.  
 ; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma  
 ; TITLE OF INVENTION: Neutralizing Activity  
 ; FILE REFERENCE: A-799  
 ; CURRENT APPLICATION NUMBER: PCT/US02/33556  
 ; CURRENT FILING DATE: 2002-10-17  
 ; NUMBER OF SEQ ID NOS: 135  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 40  
 ; LENGTH: 5  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 PCT-US02-33556-40

Query Match 47.8%; Score 11; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5  
Db 4 W 4

## RESULT 13

PCT-US02-33985-2  
; Sequence 2, Application PC/TUS0233985  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; TITLE OF INVENTION: 16 Human Secreted Proteins  
; FILE REFERENCE: PS739PCT  
; CURRENT APPLICATION NUMBER: PCT/US02/33985  
; CURRENT FILING DATE: 2002-10-24  
; PRIOR APPLICATION NUMBER: 60/330,629  
; PRIOR FILING DATE: 2001-10-26  
; NUMBER OF SEQ ID NOS: 62  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: Site  
; LOCATION: (3)  
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids  
PCT-US02-33985-2

Query Match 47.8%; Score 11; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3.5e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5  
Db 1 W 1

## RESULT 14

PCT-US02-34760-21  
; Sequence 21, Application PC/TUS0234760  
; GENERAL INFORMATION:  
; APPLICANT: Abbott Laboratories  
; APPLICANT: Haviv, Fortuna  
; APPLICANT: Bradley, Michael F.  
; TITLE OF INVENTION: TETRA-, PENTA-, HEXA- AND HEPTAPEPTIDES  
; FILE REFERENCE: 6854.WO.01  
; CURRENT APPLICATION NUMBER: PCT/US02/34760  
; CURRENT FILING DATE: 2002-10-30  
; PRIOR APPLICATION NUMBER: 10/263,811  
; PRIOR FILING DATE: 2002-10-04  
; PRIOR APPLICATION NUMBER: 10/000,540  
; PRIOR FILING DATE: 2001-10-31  
; PRIOR APPLICATION NUMBER: 10/000,007  
; PRIOR FILING DATE: 2001-10-31  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 21  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antiangiogenic Peptide  
; NAME/KEY: VARIANT  
; LOCATION: (2)...(2)  
; OTHER INFORMATION: Xaa = Nva at position 2  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (5)...(5)  
; OTHER INFORMATION: Xaa = prolylethylamide at position 5

PCT-US02-34760-21

Query Match 47.8%; Score 11; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3.5e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5  
Db 1 W 1

## RESULT 15

PCT-US02-34760-46  
; Sequence 46, Application PC/TUS0234760  
; GENERAL INFORMATION:  
; APPLICANT: Abbott Laboratories  
; APPLICANT: Haviv, Fortuna  
; APPLICANT: Bradley, Michael F.  
; TITLE OF INVENTION: TETRA-, PENTA-, HEXA- AND HEPTAPEPTIDES  
; FILE REFERENCE: 6854.WO.01  
; CURRENT APPLICATION NUMBER: PCT/US02/34760  
; CURRENT FILING DATE: 2002-10-30  
; PRIOR APPLICATION NUMBER: 10/263,811  
; PRIOR FILING DATE: 2002-10-04  
; PRIOR APPLICATION NUMBER: 10/000,540  
; PRIOR FILING DATE: 2001-10-31  
; PRIOR APPLICATION NUMBER: 10/000,007  
; PRIOR FILING DATE: 2001-10-31  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 46  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antiangiogenic Peptide  
; NAME/KEY: VARIANT  
; LOCATION: (5)...(5)  
; OTHER INFORMATION: Xaa = proethylamide at position 5  
PCT-US02-34760-46

Query Match 47.8%; Score 11; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3.5e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5  
Db 2 W 2

## RESULT 16

PCT-US02-34760-47  
; Sequence 47, Application PC/TUS0234760  
; GENERAL INFORMATION:  
; APPLICANT: Abbott Laboratories  
; APPLICANT: Haviv, Fortuna  
; APPLICANT: Bradley, Michael F.  
; TITLE OF INVENTION: TETRA-, PENTA-, HEXA- AND HEPTAPEPTIDES  
; FILE REFERENCE: 6854.WO.01  
; CURRENT APPLICATION NUMBER: PCT/US02/34760  
; CURRENT FILING DATE: 2002-10-30  
; PRIOR APPLICATION NUMBER: 10/263,811  
; PRIOR FILING DATE: 2002-10-04  
; PRIOR APPLICATION NUMBER: 10/000,540  
; PRIOR FILING DATE: 2001-10-31  
; PRIOR APPLICATION NUMBER: 10/000,007  
; PRIOR FILING DATE: 2001-10-31  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 47

```
/ LENGTH: 5
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Antiangiogenic Peptide
/ FEATURE:
/ NAME/KEY: VARIANT
/ LOCATION: (5)...(5)
/ OTHER INFORMATION: Xaa = proethylamide at position 5
PCT-US02-34760-47

Query Match          47.8%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 W 5
      1 W 1
Db

RESULT 17
PCT-US02-35606-2
; Sequence 2, Application PC/TUS0235606
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: 41 Human Secreted Proteins
; FILE REFERENCE: PS740PCT
; CURRENT APPLICATION NUMBER: PCT/US02/35606
; CURRENT FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/331,046
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: Site
; LOCATION: (3)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
PCT-US02-35606-2

Query Match          47.8%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 W 5
      1 W 1
Db

RESULT 18
PCT-US02-16525A-26
; Sequence 26, Application PC/TUS0216525A
; GENERAL INFORMATION:
; APPLICANT: Bell et al.
; TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
; FILE REFERENCE: PF556PCT
; CURRENT APPLICATION NUMBER: PCT/US02/16525A
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 60/293,212
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (3)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
```

```
PCT-US02-16525A-26

Query Match          47.8%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 W 5
      1 W 1
Db

RESULT 19
PCT-US02-24469-21
; Sequence 21, Application PC/TUS0224469
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; TITLE OF INVENTION: Biological Assay Detection Method
; FILE REFERENCE: PCT 20900Y
; CURRENT APPLICATION NUMBER: PCT/US02/24469
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: 60/310,599
; PRIOR FILING DATE: 2001-08-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Xaa is a variable which may be
; OTHER INFORMATION: A,R,N,D,C,Q,E,G,H,I,L,K,M,F,P,S,T,W,Y,V
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(5)
; OTHER INFORMATION: Xaa = Any Amino Acid
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(5)
; OTHER INFORMATION: Xaa = Any Amino Acid
PCT-US02-24469-21

Query Match          47.8%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 W 5
      3 W 3
Db

RESULT 20
PCT-US02-24310-166
; Sequence 166, Application PC/TUS0224310
; GENERAL INFORMATION:
; APPLICANT: CUBIST PHARMACEUTICALS, INC.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATING TO THE DAPTOMYCIN
; FILE REFERENCE: CUB-12 PCT CIP
; CURRENT APPLICATION NUMBER: PCT/US02/24310
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: PCT/US01/32354
; PRIOR FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: 60/310,385
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: 60/379,866
; PRIOR FILING DATE: 2002-05-10
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 166
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
```

; OTHER INFORMATION: Description of Artificial Sequence: Illustrative  
; OTHER INFORMATION: thioesterase motif  
PCT-US02-24310-1166

Query Match 47.8%; Score 11; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3.5e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5  
|  
Db 2 W 2

## RESULT 21

PCT-US02-24469A-21  
; Sequence 21, Application PC/TUS0224469A  
; GENERAL INFORMATION:  
; APPLICANT: Merck & Co., Inc.  
; TITLE OF INVENTION: Biological Assay Detection Method  
; FILE REFERENCE: PCT 20900Y  
; CURRENT APPLICATION NUMBER: PCT/US02/24469A  
; CURRENT FILING DATE: 2002-08-02  
; PRIOR APPLICATION NUMBER: 60/310,599  
; PRIOR FILING DATE: 2001-08-07  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 21  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Xaa is a variable which may be  
; OTHER INFORMATION: A,R,N,D,C,Q,E,G,H,I,L,K,M,F,P,S,T,W,Y,V  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (1)...(5)  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (1)...(5)  
; OTHER INFORMATION: Xaa = Any Amino Acid  
PCT-US02-24469A-21

Query Match 47.8%; Score 11; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3.5e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5  
|  
Db 3 W 3

## RESULT 22

PCT-US02-39109-15  
; Sequence 15, Application PC/TUS0239109  
; GENERAL INFORMATION:  
; APPLICANT: The Government of the United States of America, as represented by the  
; APPLICANT: Secretary, Department of Health and Human Services  
; APPLICANT: Ruscetti, Francis W.  
; APPLICANT: Ruff, Michael R.  
; TITLE OF INVENTION: PEPTIDE T STIMULATES CTL RESPONSES  
; FILE REFERENCE: 14014.0404P1  
; CURRENT APPLICATION NUMBER: PCT/US02/39109  
; CURRENT FILING DATE: 2002-12-06  
; PRIOR APPLICATION NUMBER: 60/338,971  
; PRIOR FILING DATE: 2001-12-07  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 15  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:/note =  
; OTHER INFORMATION: Synthetic Construct  
PCT-US02-39109-15

Query Match 47.8%; Score 11; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3.5e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5  
|  
Db 3 W 3

## RESULT 23

PCT-US02-32307-23  
; Sequence 23, Application PC/TUS0232307  
; GENERAL INFORMATION:  
; APPLICANT: IMMUNOMEDICS, INC.  
; TITLE OF INVENTION: COMBINATION THERAPY WITH CLASS III ANTI-CEA MONOCLONAL ANTIBODIES  
; FILE REFERENCE: 018733-1148  
; CURRENT APPLICATION NUMBER: PCT/US02/32307  
; CURRENT FILING DATE: 2002-10-11  
; PRIOR APPLICATION NUMBER: US 60/416,531  
; PRIOR FILING DATE: 2002-10-08  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 23  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Murinae gen. sp.  
PCT-US02-32307-23

Query Match 47.8%; Score 11; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3.5e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5  
|  
Db 3 W 3

## RESULT 24

PCT-US02-39643-5  
; Sequence 5, Application PC/TUS0239643  
; GENERAL INFORMATION:  
; APPLICANT: Smith, Thomas M  
; APPLICANT: Kitley, Terence L  
; TITLE OF INVENTION: APYRASE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME  
; FILE REFERENCE: 0091830/0502531  
; CURRENT APPLICATION NUMBER: PCT/US02/39643  
; CURRENT FILING DATE: 2002-12-12  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
PCT-US02-39643-5

Query Match 47.8%; Score 11; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3.5e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5  
|  
Db 2 W 2

## RESULT 25

PCT-US02-40891-1113  
; Sequence 1113, Application PC/TUS0240891  
; GENERAL INFORMATION:



;  
; PRIOR FILING DATE: 2002-08-19  
; PRIOR APPLICATION NUMBER: US 60/431684  
; PRIOR FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 53  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
PCT-US03-00440-14

Query Match 47.8%; Score 11; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3.5e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0;

QY 5 W 5  
|  
Db 3 W 3

RESULT 29  
PCT-US03-00440-26  
; Sequence 26, Application PC/TUS0300440  
; GENERAL INFORMATION:  
; APPLICANT: Medarex, Inc. et al.  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST CD30  
; FILE REFERENCE: MXI-180PC  
; CURRENT APPLICATION NUMBER: PCT/US03/00440  
; CURRENT FILING DATE: 2003-01-07  
; PRIOR APPLICATION NUMBER: US 60/347649  
; PRIOR FILING DATE: 2002-01-09  
; PRIOR APPLICATION NUMBER: US 60/404427  
; PRIOR FILING DATE: 2002-08-19  
; PRIOR APPLICATION NUMBER: US 60/431684  
; PRIOR FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 53  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 26  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
PCT-US03-00440-26

Query Match 47.8%; Score 11; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3.5e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0;

QY 5 W 5  
|  
Db 4 W 4

RESULT 30  
PCT-US03-00440-38  
; Sequence 38, Application PC/TUS0300440  
; GENERAL INFORMATION:  
; APPLICANT: Medarex, Inc. et al.  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST CD30  
; FILE REFERENCE: MXI-180PC  
; CURRENT APPLICATION NUMBER: PCT/US03/00440  
; CURRENT FILING DATE: 2003-01-07  
; PRIOR APPLICATION NUMBER: US 60/347649  
; PRIOR FILING DATE: 2002-01-09  
; PRIOR APPLICATION NUMBER: US 60/404427  
; PRIOR FILING DATE: 2002-08-19  
; PRIOR APPLICATION NUMBER: US 60/431684  
; PRIOR FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 53  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 38  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Homo sapiens

PCT-US03-00440-38

Query Match 47.8%; Score 11; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3.5e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0;

QY 5 W 5  
|  
Db 4 W 4

RESULT 31  
US-08-832-443C-13  
; Sequence 13, Application US/08832443C  
; GENERAL INFORMATION:  
; APPLICANT: TSYRLOVA, IRENA  
; TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND  
; USES THEREOF  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHVE P.C.  
; STREET: 1100 NORTH GLEBE ROAD  
; CITY: ARLINGTON  
; STATE: VIRGINIA  
; COUNTRY: U.S.A.  
; ZIP: 22201-4714  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: MS Word  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/832,443C  
; FILING DATE: 03-Apr-1997  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/627,173  
; FILING DATE: 03-APR-1996  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:  
US-08-832-443C-13

Query Match 47.8%; Score 11; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3.5e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0;

QY 5 W 5  
|  
Db 3 W 3

RESULT 32  
US-08-908-416B-147  
; Sequence 147, Application US/08908416B  
; GENERAL INFORMATION:  
; APPLICANT: JONCZYK, ALFRED  
; APPLICANT: GOODMAN, SIMON  
; APPLICANT: DIEFENBACH, BEATE  
; APPLICANT: KESSLER, HORST  
; APPLICANT: FINSINGER, DIRK  
; TITLE OF INVENTION: BIOTIN DERIVATIVES  
; FILE REFERENCE: MERCK-1851  
; CURRENT APPLICATION NUMBER: US/08/908,416B  
; CURRENT FILING DATE: 1997-08-07  
; PRIOR APPLICATION NUMBER: 08/710,251  
; PRIOR FILING DATE: 1996-09-13

; NUMBER OF SEQ ID NOS: 175  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 147  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
US-08-908-416B-147

Query Match 47.8%; Score 11; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3.5e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5  
|  
Db 1 W 1

## RESULT 33

US-08-908-416B-152  
; Sequence 152, Application US/08908416B  
; GENERAL INFORMATION:  
; APPLICANT: JONCZYK, ALFRED  
; APPLICANT: GOODMAN, SIMON  
; APPLICANT: DIERFENBACH, BEATE  
; APPLICANT: KESSLER, HORST  
; APPLICANT: FINSINGER, DIRK  
; TITLE OF INVENTION: BIOTIN DERIVATIVES  
; FILE REFERENCE: MERCK-1851  
; CURRENT APPLICATION NUMBER: US/08/908,416B  
; CURRENT FILING DATE: 1997-08-07  
; PRIOR FILING DATE: 1996-09-13  
; NUMBER OF SEQ ID NOS: 175  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 152  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
US-08-908-416B-152

Query Match 47.8%; Score 11; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3.5e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5  
|  
Db 1 W 1

## RESULT 34

US-08-908-416B-157  
; Sequence 157, Application US/08908416B  
; GENERAL INFORMATION:  
; APPLICANT: JONCZYK, ALFRED  
; APPLICANT: GOODMAN, SIMON  
; APPLICANT: DIERFENBACH, BEATE  
; APPLICANT: KESSLER, HORST  
; APPLICANT: FINSINGER, DIRK  
; TITLE OF INVENTION: BIOTIN DERIVATIVES  
; FILE REFERENCE: MERCK-1851  
; CURRENT APPLICATION NUMBER: US/08/908,416B  
; CURRENT FILING DATE: 1997-08-07  
; PRIOR FILING DATE: 1996-09-13  
; NUMBER OF SEQ ID NOS: 175  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 157

; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
US-08-908-416B-157

Query Match 47.8%; Score 11; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3.5e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5  
|  
Db 1 W 1

## RESULT 35

US-08-908-416B-162  
; Sequence 162, Application US/08908416B  
; GENERAL INFORMATION:  
; APPLICANT: JONCZYK, ALFRED  
; APPLICANT: GOODMAN, SIMON  
; APPLICANT: DIERFENBACH, BEATE  
; APPLICANT: KESSLER, HORST  
; APPLICANT: FINSINGER, DIRK  
; TITLE OF INVENTION: BIOTIN DERIVATIVES  
; FILE REFERENCE: MERCK-1851  
; CURRENT APPLICATION NUMBER: US/08/908,416B  
; CURRENT FILING DATE: 1997-08-07  
; PRIOR FILING DATE: 1996-09-13  
; NUMBER OF SEQ ID NOS: 175  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 162  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
US-08-908-416B-162

Query Match 47.8%; Score 11; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3.5e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5  
|  
Db 1 W 1

## RESULT 36

US-08-908-416B-167  
; Sequence 167, Application US/08908416B  
; GENERAL INFORMATION:  
; APPLICANT: JONCZYK, ALFRED  
; APPLICANT: GOODMAN, SIMON  
; APPLICANT: DIERFENBACH, BEATE  
; APPLICANT: KESSLER, HORST  
; APPLICANT: FINSINGER, DIRK  
; TITLE OF INVENTION: BIOTIN DERIVATIVES  
; FILE REFERENCE: MERCK-1851  
; CURRENT APPLICATION NUMBER: US/08/908,416B  
; CURRENT FILING DATE: 1997-08-07  
; PRIOR FILING DATE: 1996-09-13  
; NUMBER OF SEQ ID NOS: 175  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 167  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence



FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: peptide  
US-08-908-416B-167

Query Match 47.8%; Score 11; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3.5e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5  
|  
Db 1 W 1

## RESULT 37

US-08-908-416B-172  
Sequence 172, Application US/08908416B  
GENERAL INFORMATION:  
APPLICANT: JONCZYK, ALFRED  
APPLICANT: GOODMAN, SIMON  
APPLICANT: DIEFENBACH, BEATE  
APPLICANT: KESSLER, HORST  
APPLICANT: FINSINGER, DIRK  
TITLE OF INVENTION: BIOTIN DERIVATIVES  
FILE REFERENCE: MERCK-1851  
CURRENT APPLICATION NUMBER: US/08/908.416B  
CURRENT FILING DATE: 1997-08-07  
PRIOR APPLICATION NUMBER: 08/710,251  
PRIOR FILING DATE: 1996-09-13  
NUMBER OF SEQ ID NOS: 175  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 172  
LENGTH: 5  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: peptide  
US-08-908-416B-172

Query Match 47.8%; Score 11; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3.5e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5  
|  
Db 1 W 1

## RESULT 38

US-09-721-456-540  
Sequence 540, Application US/09721456  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
Lingner, Joachim  
Nakamura, Toru  
Chapman, Karen B.  
Morin, Gregg B.  
Harley, Calvin B.  
Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
NUMBER OF SEQUENCES: 727  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/721,456  
FILING DATE: 22-Nov-2000  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/974,549A  
FILING DATE: 19-NOV-1997  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
APPLICATION NUMBER: US 08/911,312  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/912,951  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/915,503  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: WO PCT/US97/17618  
FILING DATE: 01-OCT-1997  
APPLICATION NUMBER: WO PCT/US97/17885  
FILING DATE: 01-OCT-1997

ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph Ted  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002610US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 540:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 540:  
US-09-721-456-540

Query Match 47.8%; Score 11; DB 5; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3.5e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5  
|  
Db 1 W 1

## RESULT 39

US-09-533-800-16  
Sequence 16, Application US/09533800  
GENERAL INFORMATION:  
APPLICANT: Firestone, Raymond A.  
APPLICANT: Rettig, Wolfgang J.  
APPLICANT: Lenter, Martin U.  
APPLICANT: Peters, Stefan  
APPLICANT: Garin-Chesa, Pilar  
APPLICANT: Mack, Juergen  
APPLICANT: Leipert, Dietmar  
APPLICANT: Park, John E.  
APPLICANT: Telan, Leila A.  
TITLE OF INVENTION: FAP-Activated Anti-Tumour Compounds  
FILE REFERENCE: 1/1087 US  
CURRENT APPLICATION NUMBER: US/09/533,800  
CURRENT FILING DATE: 2000-03-24  
PRIOR APPLICATION NUMBER: US 60/134,136  
PRIOR FILING DATE: 1999-05-14

; NUMBER OF SEQ ID NOS: 28  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 16  
 ; LENGTH: 5  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Precursor  
 ;  
 US-09-533-800-16

Query Match 47.8%; Score 11; DB 5; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5  
 |  
 Db 4 W 4

## RESULT 40

US-09-813-484-1  
 ; Sequence 1, Application US/09813484  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Unger, Evan C.  
 ; TITLE OF INVENTION: Novel Methods Of Ultrasound Treatment Using Gas Or Gaseous Precursor  
 ; FILE REFERENCE: Filled Compositions  
 ; FILE REFERENCE: UNGR1600  
 ; CURRENT APPLICATION NUMBER: US/09/813,484  
 ; CURRENT FILING DATE: 2001-03-21  
 ; PRIOR APPLICATION NUMBER: 08/929,847  
 ; PRIOR FILING DATE: 1997-09-15  
 ; NUMBER OF SEQ ID NOS: 39  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 1  
 ; LENGTH: 5  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Completely synthetic sequence  
 ; NAME/KEY: misc feature  
 ; LOCATION: (4)-(4)  
 ; OTHER INFORMATION: Xaa is azetidine  
 ;  
 US-09-813-484-1

Query Match 47.8%; Score 11; DB 5; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5  
 |  
 Db 1 W 1

## RESULT 41

US-09-726-348B-5  
 ; Sequence 5, Application US/09726348B  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wei, Ying-Fei  
 ; APPLICANT: et al,  
 ; TITLE OF INVENTION: Transforming Growth Factor Alpha HIII  
 ; FILE REFERENCE: PF220P1  
 ; CURRENT APPLICATION NUMBER: US/09/726,348B  
 ; CURRENT FILING DATE: 2000-12-01  
 ; PRIOR APPLICATION NUMBER: 08/778,545  
 ; PRIOR FILING DATE: 1997-01-03  
 ; PRIOR APPLICATION NUMBER: 60/011,136  
 ; PRIOR FILING DATE: 1996-01-04  
 ; PRIOR APPLICATION NUMBER: 60/168,387  
 ; PRIOR FILING DATE: 1999-12-02  
 ; NUMBER OF SEQ ID NOS: 21  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 5 ;

; LENGTH: 5  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: WSXWS motif  
 ; FEATURE:  
 ; NAME/KEY: SITE  
 ; LOCATION: (3)..(3)  
 ; OTHER INFORMATION: Xaa equals any amino acid  
 ;  
 US-09-726-348B-5

Query Match 47.8%; Score 11; DB 5; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5  
 |  
 Db 1 W 1

## RESULT 42

US-09-653-812B-145  
 ; Sequence 145, Application US/09653812B  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KAZAZIAN, HAIG H.  
 ; APPLICANT: BOEKE, JEF D.  
 ; APPLICANT: MORAN, JOHN V.  
 ; APPLICANT: BETH, DOMBROSKI A.  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS OF USE OF MAMMALIAN RETROTRANSPOSONS  
 ; FILE REFERENCE: 9596-23U3 (053893-5006-02)  
 ; CURRENT APPLICATION NUMBER: US/09/653,812B  
 ; CURRENT FILING DATE: 2000-09-01  
 ; PRIOR APPLICATION NUMBER: US 08/847,844  
 ; PRIOR FILING DATE: 1997-04-28  
 ; PRIOR APPLICATION NUMBER: US 08/749,805  
 ; PRIOR FILING DATE: 1996-11-15  
 ; PRIOR APPLICATION NUMBER: US 60/006,831  
 ; PRIOR FILING DATE: 1995-11-16  
 ; NUMBER OF SEQ ID NOS: 152  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 145  
 ; LENGTH: 5  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Wild type L1.2mneoI construct  
 ;  
 US-09-653-812B-145

Query Match 47.8%; Score 11; DB 5; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5  
 |  
 Db 2 W 2

## RESULT 43

US-09-653-812B-152  
 ; Sequence 152, Application US/09653812B  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KAZAZIAN, HAIG H.  
 ; APPLICANT: BOEKE, JEF D.  
 ; APPLICANT: MORAN, JOHN V.  
 ; APPLICANT: BETH, DOMBROSKI A.  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS OF USE OF MAMMALIAN RETROTRANSPOSONS  
 ; FILE REFERENCE: 9596-23U3 (053893-5006-02)  
 ; CURRENT APPLICATION NUMBER: US/09/653,812B  
 ; CURRENT FILING DATE: 2000-09-01  
 ; PRIOR APPLICATION NUMBER: US 08/847,844  
 ; PRIOR FILING DATE: 1997-04-28  
 ; PRIOR APPLICATION NUMBER: US 08/749,805  
 ; PRIOR FILING DATE: 1996-11-15

; PRIOR APPLICATION NUMBER: US 60/006,831  
; PRIOR FILING DATE: 1995-11-16  
; NUMBER OF SEQ ID NOS: 152  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 152  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Mutant L1.2mneoI construct  
US-09-653-812B-152

Query Match 47.8%; Score 11; DB 5; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3.5e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5  
|  
Db 2 W 2

## RESULT 44

US-09-556-972-12  
; Sequence 12, Application US/09556972  
; GENERAL INFORMATION:  
; APPLICANT: TORIGOE, Kakuji  
; OKURA, Takamori  
; KURIMOTO, Musashi  
; TITLE OF INVENTION: POLYPEPTIDES  
; NUMBER OF SEQUENCES: 37  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/556,972  
FILING DATE: 24-Apr-2000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/996,338  
FILING DATE: 22-DEC-1997  
APPLICATION NUMBER: JP 74,697/1997  
FILING DATE: 12-MAR-1997  
APPLICATION NUMBER: JP 215,488/1997  
FILING DATE: 28-JUL-1997  
APPLICATION NUMBER: JP 291,837/1997  
FILING DATE: 09-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: TORIGOE=3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal fragment  
SEQUENCE DESCRIPTION: SEQ ID NO: 12:  
US-09-556-972-12

Query Match 47.8%; Score 11; DB 5; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3.5e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 5 W 5  
|  
Db 1 W 1

## RESULT 45

US-09-610-650B-18  
; Sequence 18, Application US/09610650B  
; GENERAL INFORMATION:  
; APPLICANT: Olsen et al.  
; TITLE OF INVENTION: Human Frezzled-Like Protein  
; FILE REFERENCE: PF389CI  
; CURRENT APPLICATION NUMBER: US/09/610,650B  
; CURRENT FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: 09/132,315  
; PRIOR FILING DATE: 1998-08-11  
; PRIOR APPLICATION NUMBER: 60/055,715  
; PRIOR FILING DATE: 1997-08-12  
; PRIOR APPLICATION NUMBER: 60/081,438  
; PRIOR FILING DATE: 1998-04-10  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 18  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MISC\_FEATURE  
; LOCATION: (3)..(3)  
; OTHER INFORMATION: Xaa is any amino acid  
US-09-610-650B-18

Query Match 47.8%; Score 11; DB 5; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3.5e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5  
|  
Db 1 W 1

## RESULT 46

US-09-943-120-1  
; Sequence 1, Application US/09943120  
; GENERAL INFORMATION:  
; APPLICANT: Rothschild, Kenneth J.  
; Sonar, Sanjay M.  
; Olejnik, Jerzy  
; TITLE OF INVENTION: Methods for the Detection and Isolation  
; OF Proteins  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MEDLEN & CARROLL, LLP  
; STREET: 220 Montgomery Street, Suite 2200  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/943,120  
; FILING DATE: 30-Aug-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/307,579  
; FILING DATE: 07-May-1999  
; APPLICATION NUMBER: 08/884,325

; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Carroll, Peter G.  
; REGISTRATION NUMBER: 32,837  
; REFERENCE/DOCKET NUMBER: AMBER-03242  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-705-8410  
; TELEFAX: 415-397-8338  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: not relevant  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-943-120-1

Query Match 47.8%; Score 11; DB 5; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3.5e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5  
|  
Db 5 W 5

RESULT 47  
US-09-936-759-32  
; Sequence 32, Application US/09936759  
; GENERAL INFORMATION:  
; APPLICANT: JEFFERSON, RICHARD  
; APPLICANT: MAYER, JORGE E.  
; TITLE OF INVENTION: MICROBIAL BETA-GLUCURONIDASE GENES, GENE PRODUCTS AND  
; FILE REFERENCE: 076518-0150  
; CURRENT APPLICATION NUMBER: US/09/936,759  
; PRIOR FILING DATE: 2002-04-22  
; PRIOR APPLICATION NUMBER: PCT/US00/07107  
; PRIOR FILING DATE: 2000-03-16  
; PRIOR APPLICATION NUMBER: 09/270,957  
; PRIOR FILING DATE: 1999-03-17  
; PRIOR APPLICATION NUMBER: 09/149,927  
; PRIOR FILING DATE: 1998-09-08  
; PRIOR APPLICATION NUMBER: 60/058,263  
; PRIOR FILING DATE: 1997-09-09  
; NUMBER OF SEQ ID NOS: 120  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 32  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Escherichia coli  
US-09-936-759-32

Query Match 47.8%; Score 11; DB 5; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3.5e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5  
|  
Db 1 W 1

RESULT 48  
US-09-969-748C-19  
; Sequence 19, Application US/09969748C  
; GENERAL INFORMATION:  
; APPLICANT: ARIZEKE PHARMACEUTICALS, INC.  
; APPLICANT: HOUSTON, Lou, L.  
; APPLICANT: SHERIDAN, Philip, J.  
; APPLICANT: HAWLEY, Stephen  
; APPLICANT: GLYNN, Jacqueline, M.  
; APPLICANT: CHAPIN, Steven

; APPLICANT: BASU, Amareesh  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TRANSPORT OF BIOLOGICALLY ACTIVE  
; FILE REFERENCE: 057220-0303  
; CURRENT APPLICATION NUMBER: US/09/969,748C  
; CURRENT FILING DATE: 2002-12-10  
; PRIOR APPLICATION NUMBER: US 60/267,601  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: US 60/248,819  
; PRIOR FILING DATE: 2000-11-14  
; PRIOR APPLICATION NUMBER: US 60/248,478  
; PRIOR FILING DATE: 2000-11-13  
; PRIOR APPLICATION NUMBER: US 60/237,929  
; PRIOR FILING DATE: 2000-10-02  
; NUMBER OF SEQ ID NOS: 115  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 19  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: amino acid sequence conserved in pIgr protein  
US-09-969-748C-19

Query Match 47.8%; Score 11; DB 5; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3.5e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5  
|  
Db 2 W 2

RESULT 49  
US-09-969-748C-20  
; Sequence 20, Application US/09969748C  
; GENERAL INFORMATION:  
; APPLICANT: ARIZEKE PHARMACEUTICALS, INC.  
; APPLICANT: HOUSTON, Lou, L.  
; APPLICANT: SHERIDAN, Philip, J.  
; APPLICANT: HAWLEY, Stephen  
; APPLICANT: GLYNN, Jacqueline, M.  
; APPLICANT: CHAPIN, Steven  
; APPLICANT: BASU, Amareesh  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TRANSPORT OF BIOLOGICALLY ACTIVE  
; FILE REFERENCE: 057220-0303  
; CURRENT APPLICATION NUMBER: US/09/969,748C  
; CURRENT FILING DATE: 2002-12-10  
; PRIOR APPLICATION NUMBER: US 60/267,601  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: US 60/248,819  
; PRIOR FILING DATE: 2000-11-14  
; PRIOR APPLICATION NUMBER: US 60/248,478  
; PRIOR FILING DATE: 2000-11-13  
; PRIOR APPLICATION NUMBER: US 60/237,929  
; NUMBER OF SEQ ID NOS: 115  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 20  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: amino acid sequence conserved in pIgr protein  
US-09-969-748C-20

Query Match 47.8%; Score 11; DB 5; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3.5e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5  
|

Db 2" W 2

RESULT 50

US-09-553-800D-16

; Sequence 16, Application US/09553800D

; GENERAL INFORMATION:

; APPLICANT: Firestone, Raymond A.

; APPLICANT: Rettig, Wolfgang J.

; APPLICANT: Lenter, Martin U.

; APPLICANT: Peters, Stefan

; APPLICANT: Garin-Chesa, Pilar

; APPLICANT: Mack, Juergen

; APPLICANT: Leipert, Dietmar

; APPLICANT: Park, John E.

; APPLICANT: Telan, Leila A.

; TITLE OF INVENTION: FAP-Activated Anti-Tumour Compounds

; FILE REFERENCE: 1/1087 US

; CURRENT APPLICATION NUMBER: US/09/553,800D

; CURRENT FILING DATE: 2000-04-21

; PRIOR APPLICATION NUMBER: US 60/134,136

; PRIOR FILING DATE: 1999-05-14

; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 16

; LENGTH: 5

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Precursor

US-09-553-800D-16

Query Match 47.8%; Score 11; DB 5; Length 5;

Best Local Similarity 100.0%; Pred. No. 3.5e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5

Db 4 W 4

RESULT 51

US-09-720-278A-1

; Sequence 1, Application US/09720278A

; GENERAL INFORMATION:

; APPLICANT: Swart, Pieter Jacob

; APPLICANT: Kuipers, Maria Elizabeth

; APPLICANT: Meijer, Dirk Klaas Fokke

; APPLICANT: Hageman, Robert Johan Joseph

; APPLICANT: Van Den Berg, Jeroen Johannes Maria

; TITLE OF INVENTION: Pharmaceutical preparations for use in combatting or

; FILE REFERENCE: 702-002214

; CURRENT APPLICATION NUMBER: US/09/720,278A

; CURRENT FILING DATE: 2001-05-24

; PRIOR APPLICATION NUMBER: PCT/EP99/04067

; PRIOR FILING DATE: 1999-06-28

; PRIOR APPLICATION NUMBER: EP 98203765.7

; PRIOR FILING DATE: 1998-11-06

; PRIOR APPLICATION NUMBER: NL 1010284

; PRIOR FILING DATE: 1998-10-09

; PRIOR APPLICATION NUMBER: NL 1009505

; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: Microsoft Word 97 SR-2

; SEQ ID NO 1

; LENGTH: 5

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: polypeptide

US-09-720-278A-1

Query Match 47.8%; Score 11; DB 5; Length 5;

Best Local Similarity 100.0%; Pred. No. 3.5e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5

Db 4 W 4

RESULT 52

US-09-720-278A-2

; Sequence 2, Application US/09720278A

; GENERAL INFORMATION:

; APPLICANT: Swart, Pieter Jacob

; APPLICANT: Kuipers, Maria Elizabeth

; APPLICANT: Meijer, Dirk Klaas Fokke

; APPLICANT: Hageman, Robert Johan Joseph

; APPLICANT: Van Den Berg, Jeroen Johannes Maria

; TITLE OF INVENTION: Pharmaceutical preparations for use in combatting or

; FILE REFERENCE: 702-002214

; CURRENT APPLICATION NUMBER: US/09/720,278A

; CURRENT FILING DATE: 2001-05-24

; PRIOR APPLICATION NUMBER: PCT/EP99/04067

; PRIOR FILING DATE: 1999-06-28

; PRIOR APPLICATION NUMBER: EP 98203765.7

; PRIOR FILING DATE: 1998-11-06

; PRIOR APPLICATION NUMBER: NL 1010284

; PRIOR FILING DATE: 1998-10-09

; PRIOR APPLICATION NUMBER: NL 1009505

; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: Microsoft Word 97 SR-2

; SEQ ID NO 2

; LENGTH: 5

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: polypeptide

US-09-720-278A-2

Query Match 47.8%; Score 11; DB 5; Length 5;

Best Local Similarity 100.0%; Pred. No. 3.5e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5

Db 4 W 4

RESULT 53

US-09-720-278A-3

; Sequence 3, Application US/09720278A

; GENERAL INFORMATION:

; APPLICANT: Swart, Pieter Jacob

; APPLICANT: Kuipers, Maria Elizabeth

; APPLICANT: Meijer, Dirk Klaas Fokke

; APPLICANT: Hageman, Robert Johan Joseph

; APPLICANT: Van Den Berg, Jeroen Johannes Maria

; TITLE OF INVENTION: Pharmaceutical preparations for use in combatting or

; FILE REFERENCE: 702-002214

; CURRENT APPLICATION NUMBER: US/09/720,278A

; CURRENT FILING DATE: 2001-05-24

; PRIOR APPLICATION NUMBER: PCT/EP99/04067

; PRIOR FILING DATE: 1999-06-28

; PRIOR APPLICATION NUMBER: EP 98203765.7

; PRIOR FILING DATE: 1998-11-06

; PRIOR APPLICATION NUMBER: NL 1010284

; PRIOR FILING DATE: 1998-10-09

; PRIOR APPLICATION NUMBER: NL 1009505

; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: Microsoft Word 97 SR-2

; SEQ ID NO 1

; LENGTH: 5

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: polypeptide

US-09-720-278A-3

Query Match 47.8%; Score 11; DB 5; Length 5;

Best Local Similarity 100.0%; Pred. No. 3.5e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5

Db 4 W 4

```

; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 3
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: polypeptide
US-09-720-278A-3

Query Match          47.8%; Score 11; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 W 5
      |
Db      4 W 4

RESULT 54
US-09-720-278A-5
; Sequence 5, Application US/09720278A
; GENERAL INFORMATION:
; APPLICANT: Swart, Pieter Jacob
; APPLICANT: Kuipers, Maria Elizabeth
; APPLICANT: Meijer, Dirk Klaas Fokke
; APPLICANT: Hageman, Robert Johan Joseph
; APPLICANT: Van Den Berg, Jeroen Johannes Maria
; TITLE OF INVENTION: Pharmaceutical preparations for use in combatting or
; FILE REFERENCE: 702-002214
; CURRENT APPLICATION NUMBER: US/09/720,278A
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: PCT/EP99/04067
; PRIOR FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: EP 98203765.7
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: NL 1010284
; PRIOR FILING DATE: 1998-10-09
; PRIOR APPLICATION NUMBER: NL 1009505
; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 5
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: polypeptide
US-09-720-278A-5

Query Match          47.8%; Score 11; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 W 5
      |
Db      2 W 2

RESULT 55
US-09-720-278A-21
; Sequence 21, Application US/09720278A
; GENERAL INFORMATION:
; APPLICANT: Swart, Pieter Jacob
; APPLICANT: Kuipers, Maria Elizabeth
; APPLICANT: Meijer, Dirk Klaas Fokke
; APPLICANT: Hageman, Robert Johan Joseph
; APPLICANT: Van Den Berg, Jeroen Johannes Maria
; TITLE OF INVENTION: Pharmaceutical preparations for use in combatting or
; FILE REFERENCE: 702-002214
; CURRENT APPLICATION NUMBER: US/09/720,278A
; CURRENT FILING DATE: 2001-05-24

```

```

; PRIOR APPLICATION NUMBER: PCT/EP99/04067
; PRIOR FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: EP 98203765.7
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: NL 1010284
; PRIOR FILING DATE: 1998-10-09
; PRIOR APPLICATION NUMBER: NL 1009505
; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 21
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: polypeptide
US-09-720-278A-21

Query Match          47.8%; Score 11; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 W 5
      |
Db      3 W 3

RESULT 56
US-09-720-278A-23
; Sequence 23, Application US/09720278A
; GENERAL INFORMATION:
; APPLICANT: Swart, Pieter Jacob
; APPLICANT: Kuipers, Maria Elizabeth
; APPLICANT: Meijer, Dirk Klaas Fokke
; APPLICANT: Hageman, Robert Johan Joseph
; APPLICANT: Van Den Berg, Jeroen Johannes Maria
; TITLE OF INVENTION: Pharmaceutical preparations for use in combatting or
; FILE REFERENCE: 702-002214
; CURRENT APPLICATION NUMBER: US/09/720,278A
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: PCT/EP99/04067
; PRIOR FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: EP 98203765.7
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: NL 1010284
; PRIOR FILING DATE: 1998-10-09
; PRIOR APPLICATION NUMBER: NL 1009505
; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 23
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: polypeptide
US-09-720-278A-23

Query Match          47.8%; Score 11; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 W 5
      |
Db      3 W 3

RESULT 57
US-09-720-278A-27
; Sequence 27, Application US/09720278A
; GENERAL INFORMATION:
; APPLICANT: Swart, Pieter Jacob

```

; APPLICANT: Kuipers, Maria Elizabeth  
 ; APPLICANT: Meijer, Dirk Klaas Fokke  
 ; APPLICANT: Hageman, Robert Johan Joseph  
 ; APPLICANT: Van Den Berg, Jeroen Johannes Maria  
 ; TITLE OF INVENTION: Pharmaceutical preparations for use in combatting or  
 ; TITLE OF INVENTION: Preventing surface infections caused by microorganisms  
 ; FILE REFERENCE: 702-002214  
 ; CURRENT APPLICATION NUMBER: US/09/720,278A  
 ; CURRENT FILING DATE: 2001-05-24  
 ; PRIOR APPLICATION NUMBER: PCT/EP99/04067  
 ; PRIOR FILING DATE: 1999-06-28  
 ; PRIOR APPLICATION NUMBER: EP 98203765.7  
 ; PRIOR FILING DATE: 1998-11-06  
 ; PRIOR APPLICATION NUMBER: NL 1010284  
 ; PRIOR FILING DATE: 1998-10-09  
 ; PRIOR APPLICATION NUMBER: NL 1009505  
 ; PRIOR FILING DATE: 1998-06-26  
 ; NUMBER OF SEQ ID NOS: 28  
 ; SOFTWARE: Microsoft Word 97 SR-2  
 ; SEQ ID NO 27  
 ; LENGTH: 5  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: polypeptide  
 US-09-720-278A-27

Query Match 47.8%; Score 11; DB 5; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5  
 Db 3 W 3

RESULT 58  
 US-09-636-243B-30  
 ; Sequence 30, Application US/09636243B  
 ; GENERAL INFORMATION:  
 ; APPLICANT: WANG, Bryan S.  
 ; APPLICANT: PABO, Carl O.  
 ; TITLE OF INVENTION: DIMERIZING PEPTIDES  
 ; FILE REFERENCE: 8325-1004 / M4-US1  
 ; CURRENT APPLICATION NUMBER: US/09/636,243B  
 ; CURRENT FILING DATE: 2000-08-10  
 ; PRIOR APPLICATION NUMBER: 60/148,422  
 ; PRIOR FILING DATE: 1999-08-11  
 ; NUMBER OF SEQ ID NOS: 83  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 30  
 ; LENGTH: 5  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: sequential  
 ; OTHER INFORMATION: block reoptimization sequence  
 US-09-636-243B-30

Query Match 47.8%; Score 11; DB 5; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5  
 Db 5 W 5

RESULT 59  
 US-09-636-243B-35  
 ; Sequence 35, Application US/09636243B  
 ; GENERAL INFORMATION:  
 ; APPLICANT: WANG, Bryan S.

; APPLICANT: PABO, Carl O.  
 ; TITLE OF INVENTION: DIMERIZING PEPTIDES  
 ; FILE REFERENCE: 8325-1004 / M4-US1  
 ; CURRENT APPLICATION NUMBER: US/09/636,243B  
 ; CURRENT FILING DATE: 2000-08-10  
 ; PRIOR APPLICATION NUMBER: 60/148,422  
 ; PRIOR FILING DATE: 1999-08-11  
 ; NUMBER OF SEQ ID NOS: 83  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 35  
 ; LENGTH: 5  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: sequential  
 ; OTHER INFORMATION: block reoptimization sequence  
 US-09-636-243B-35

Query Match 47.8%; Score 11; DB 5; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5  
 Db 4 W 4

RESULT 60  
 US-09-636-243B-44  
 ; Sequence 44, Application US/09636243B  
 ; GENERAL INFORMATION:  
 ; APPLICANT: WANG, Bryan S.  
 ; APPLICANT: PABO, Carl O.  
 ; TITLE OF INVENTION: DIMERIZING PEPTIDES  
 ; FILE REFERENCE: 8325-1004 / M4-US1  
 ; CURRENT APPLICATION NUMBER: US/09/636,243B  
 ; CURRENT FILING DATE: 2000-08-10  
 ; PRIOR APPLICATION NUMBER: 60/148,422  
 ; PRIOR FILING DATE: 1999-08-11  
 ; NUMBER OF SEQ ID NOS: 83  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 44  
 ; LENGTH: 5  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: sequential  
 ; OTHER INFORMATION: block reoptimization sequence  
 US-09-636-243B-44

Query Match 47.8%; Score 11; DB 5; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5  
 Db 1 W 1

RESULT 61  
 US-09-636-243B-56  
 ; Sequence 56, Application US/09636243B  
 ; GENERAL INFORMATION:  
 ; APPLICANT: WANG, Bryan S.  
 ; APPLICANT: PABO, Carl O.  
 ; TITLE OF INVENTION: DIMERIZING PEPTIDES  
 ; FILE REFERENCE: 8325-1004 / M4-US1  
 ; CURRENT APPLICATION NUMBER: US/09/636,243B  
 ; CURRENT FILING DATE: 2000-08-10  
 ; PRIOR APPLICATION NUMBER: 60/148,422  
 ; PRIOR FILING DATE: 1999-08-11  
 ; NUMBER OF SEQ ID NOS: 83  
 ; SOFTWARE: PatentIn Ver. 2.0

```
; SEQ ID NO 56
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: sequential
; OTHER INFORMATION: block reoptimization sequence
US-09-636-243B-56

Query Match          47.8%; Score 11; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5
Db 3 W 3

RESULT 62
US-09-636-243B-57
; Sequence 57, Application US/09636243B
; GENERAL INFORMATION:
; APPLICANT: WANG, Bryan S.
; TITLE OF INVENTION: DIMERIZING PEPTIDES
; FILE REFERENCE: 8325-1004 / M4-US1
; CURRENT APPLICATION NUMBER: US/09/636,243B
; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/148,422
; PRIOR FILING DATE: 1999-08-11
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 57
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: sequential
; OTHER INFORMATION: block reoptimization sequence
US-09-636-243B-57

Query Match          47.8%; Score 11; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5
Db 3 W 3

RESULT 63
US-09-636-243B-58
; Sequence 58, Application US/09636243B
; GENERAL INFORMATION:
; APPLICANT: WANG, Bryan S.
; TITLE OF INVENTION: DIMERIZING PEPTIDES
; FILE REFERENCE: 8325-1004 / M4-US1
; CURRENT APPLICATION NUMBER: US/09/636,243B
; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/148,422
; PRIOR FILING DATE: 1999-08-11
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 58
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: sequential
; OTHER INFORMATION: block reoptimization sequence
US-09-636-243B-58

Query Match          47.8%; Score 11; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5
Db 3 W 3

RESULT 64
US-09-636-243B-59
; Sequence 59, Application US/09636243B
; GENERAL INFORMATION:
; APPLICANT: WANG, Bryan S.
; TITLE OF INVENTION: DIMERIZING PEPTIDES
; FILE REFERENCE: 8325-1004 / M4-US1
; CURRENT APPLICATION NUMBER: US/09/636,243B
; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/148,422
; PRIOR FILING DATE: 1999-08-11
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 59
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: sequential
; OTHER INFORMATION: block reoptimization sequence
US-09-636-243B-59

Query Match          47.8%; Score 11; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5
Db 3 W 3

RESULT 65
US-09-636-243B-60
; Sequence 60, Application US/09636243B
; GENERAL INFORMATION:
; APPLICANT: WANG, Bryan S.
; TITLE OF INVENTION: DIMERIZING PEPTIDES
; FILE REFERENCE: 8325-1004 / M4-US1
; CURRENT APPLICATION NUMBER: US/09/636,243B
; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/148,422
; PRIOR FILING DATE: 1999-08-11
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: sequential
; OTHER INFORMATION: block reoptimization sequence
US-09-636-243B-60

Query Match          47.8%; Score 11; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5
Db 3 W 3
```



## RESULT 66

US-09-636-243B-61  
; Sequence 61, Application US/09636243B  
; GENERAL INFORMATION:  
; APPLICANT: WANG, Bryan S.  
; APPLICANT: PABO, Carl O.  
; TITLE OF INVENTION: DIMERIZING PEPTIDES  
; FILE REFERENCE: 8325-1004 / M4-US1  
; CURRENT APPLICATION NUMBER: US/09/636,243B  
; CURRENT FILING DATE: 2000-08-10  
; PRIOR APPLICATION NUMBER: 60/148,422  
; PRIOR FILING DATE: 1999-08-11  
; NUMBER OF SEQ ID NOS: 83  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 61  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: sequential  
; OTHER INFORMATION: block reoptimization sequence  
US-09-636-243B-61

Query Match 47.8%; Score 11; DB 5; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3.5e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5

DB 3 W 3

## RESULT 67

US-09-636-243B-62  
; Sequence 62, Application US/09636243B  
; GENERAL INFORMATION:  
; APPLICANT: WANG, Bryan S.  
; APPLICANT: PABO, Carl O.  
; TITLE OF INVENTION: DIMERIZING PEPTIDES  
; FILE REFERENCE: 8325-1004 / M4-US1  
; CURRENT APPLICATION NUMBER: US/09/636,243B  
; CURRENT FILING DATE: 2000-08-10  
; PRIOR APPLICATION NUMBER: 60/148,422  
; PRIOR FILING DATE: 1999-08-11  
; NUMBER OF SEQ ID NOS: 83  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 62  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: sequential  
; OTHER INFORMATION: block reoptimization sequence  
US-09-636-243B-62

Query Match 47.8%; Score 11; DB 5; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3.5e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5

DB 3 W 3

## RESULT 68

US-09-636-243B-63  
; Sequence 63, Application US/09636243B  
; GENERAL INFORMATION:  
; APPLICANT: WANG, Bryan S.  
; APPLICANT: PABO, Carl O.  
; TITLE OF INVENTION: DIMERIZING PEPTIDES  
; FILE REFERENCE: 8325-1004 / M4-US1  
; CURRENT APPLICATION NUMBER: US/09/636,243B

; CURRENT FILING DATE: 2000-08-10  
; PRIOR APPLICATION NUMBER: 60/148,422  
; PRIOR FILING DATE: 1999-08-11  
; NUMBER OF SEQ ID NOS: 83  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 63  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: sequential  
; OTHER INFORMATION: block reoptimization sequence  
US-09-636-243B-63

Query Match 47.8%; Score 11; DB 5; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3.5e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5

DB 1 W 1

## RESULT 69

US-09-636-243B-64  
; Sequence 64, Application US/09636243B  
; GENERAL INFORMATION:  
; APPLICANT: WANG, Bryan S.  
; APPLICANT: PABO, Carl O.  
; TITLE OF INVENTION: DIMERIZING PEPTIDES  
; FILE REFERENCE: 8325-1004 / M4-US1  
; CURRENT APPLICATION NUMBER: US/09/636,243B  
; CURRENT FILING DATE: 2000-08-10  
; PRIOR APPLICATION NUMBER: 60/148,422  
; PRIOR FILING DATE: 1999-08-11  
; NUMBER OF SEQ ID NOS: 83  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 64  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: sequential  
; OTHER INFORMATION: block reoptimization sequence  
US-09-636-243B-64

Query Match 47.8%; Score 11; DB 5; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3.5e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5

DB 3 W 3

## RESULT 70

US-09-636-243B-76  
; Sequence 76, Application US/09636243B  
; GENERAL INFORMATION:  
; APPLICANT: WANG, Bryan S.  
; APPLICANT: PABO, Carl O.  
; TITLE OF INVENTION: DIMERIZING PEPTIDES  
; FILE REFERENCE: 8325-1004 / M4-US1  
; CURRENT APPLICATION NUMBER: US/09/636,243B  
; CURRENT FILING DATE: 2000-08-10  
; PRIOR APPLICATION NUMBER: 60/148,422  
; PRIOR FILING DATE: 1999-08-11  
; NUMBER OF SEQ ID NOS: 83  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 76  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence

; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: sequential  
; OTHER INFORMATION: block reoptimization sequence  
US-09-636-243B-76

Query Match 47.8%; Score 11; DB 5; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3.5e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5  
|  
Db 4 W 4

RESULT 71  
US-09-636-243B-77  
; Sequence 77, Application US/09636243B  
; GENERAL INFORMATION:  
; APPLICANT: WANG, Bryan S.  
; TITLE OF INVENTION: DIMERIZING PEPTIDES  
; FILE REFERENCE: 8325-1004 / M4-US1  
; CURRENT APPLICATION NUMBER: US/09/636,243B  
; PRIOR FILING DATE: 2000-08-10  
; PRIOR APPLICATION NUMBER: 60/148,422  
; PRIOR FILING DATE: 1999-08-11  
; NUMBER OF SEQ ID NOS: 83  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 77  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: sequential  
; OTHER INFORMATION: block reoptimization sequence  
US-09-636-243B-77

Query Match 47.8%; Score 11; DB 5; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3.5e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5  
|  
Db 4 W 4

RESULT 72  
US-09-636-243B-78  
; Sequence 78, Application US/09636243B  
; GENERAL INFORMATION:  
; APPLICANT: WANG, Bryan S.  
; TITLE OF INVENTION: DIMERIZING PEPTIDES  
; FILE REFERENCE: 8325-1004 / M4-US1  
; CURRENT APPLICATION NUMBER: US/09/636,243B  
; PRIOR FILING DATE: 2000-08-10  
; PRIOR APPLICATION NUMBER: 60/148,422  
; PRIOR FILING DATE: 1999-08-11  
; NUMBER OF SEQ ID NOS: 83  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 78  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: sequential  
; OTHER INFORMATION: block reoptimization sequence  
US-09-636-243B-78

Query Match 47.8%; Score 11; DB 5; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3.5e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5  
|  
Db 4 W 4

RESULT 73  
US-09-254-180C-1  
; Sequence 1, Application US/09254180C  
; GENERAL INFORMATION:  
; APPLICANT: OKUMURA, Ko  
; APPLICANT: EDA, Yasuyuki  
; APPLICANT: MAEDA, Hiroaki  
; APPLICANT: USHIO, Yoshitaka  
; APPLICANT: HIGUCHI, Hirofumi  
; APPLICANT: NAKATA, Motomi  
; TITLE OF INVENTION: Humanized Immunoglobulins Specifically Reactive to Fas Ligand or  
; TITLE OF INVENTION: Fragments Thereof, and Apoptosis-Induced Site From Fas Ligand  
; FILE REFERENCE: 050006-0055  
; CURRENT APPLICATION NUMBER: US/09/254,180C  
; CURRENT FILING DATE: 1999-04-15  
; PRIOR APPLICATION NUMBER: PCT/JP97/02983  
; PRIOR FILING DATE: 1997-08-27  
; PRIOR APPLICATION NUMBER: 271546/1996  
; PRIOR FILING DATE: 1996-09-20  
; PRIOR APPLICATION NUMBER: 231472/1996  
; PRIOR FILING DATE: 1996-09-02  
; NUMBER OF SEQ ID NOS: 183  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-254-180C-1

Query Match 47.8%; Score 11; DB 5; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3.5e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5  
|  
Db 3 W 3

RESULT 74  
US-09-676-475A-278  
; Sequence 278, Application US/09676475A  
; GENERAL INFORMATION:  
; APPLICANT: Ruoslahti, Erkki  
; APPLICANT: Pasqualini, Renata  
; APPLICANT: Rajotte, Daniel  
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using  
; TITLE OF INVENTION: Membrane Dipeptidase  
; FILE REFERENCE: P-LA 4377  
; CURRENT APPLICATION NUMBER: US/09/676,475A  
; CURRENT FILING DATE: 1998-03-13  
; PRIOR APPLICATION NUMBER: 09/042,107  
; PRIOR FILING DATE: 1998-03-13  
; NUMBER OF SEQ ID NOS: 452  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 278  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-676-475A-278

Query Match 47.8%; Score 11; DB 5; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3.5e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5  
|

Db 1 W 1

## RESULT 75

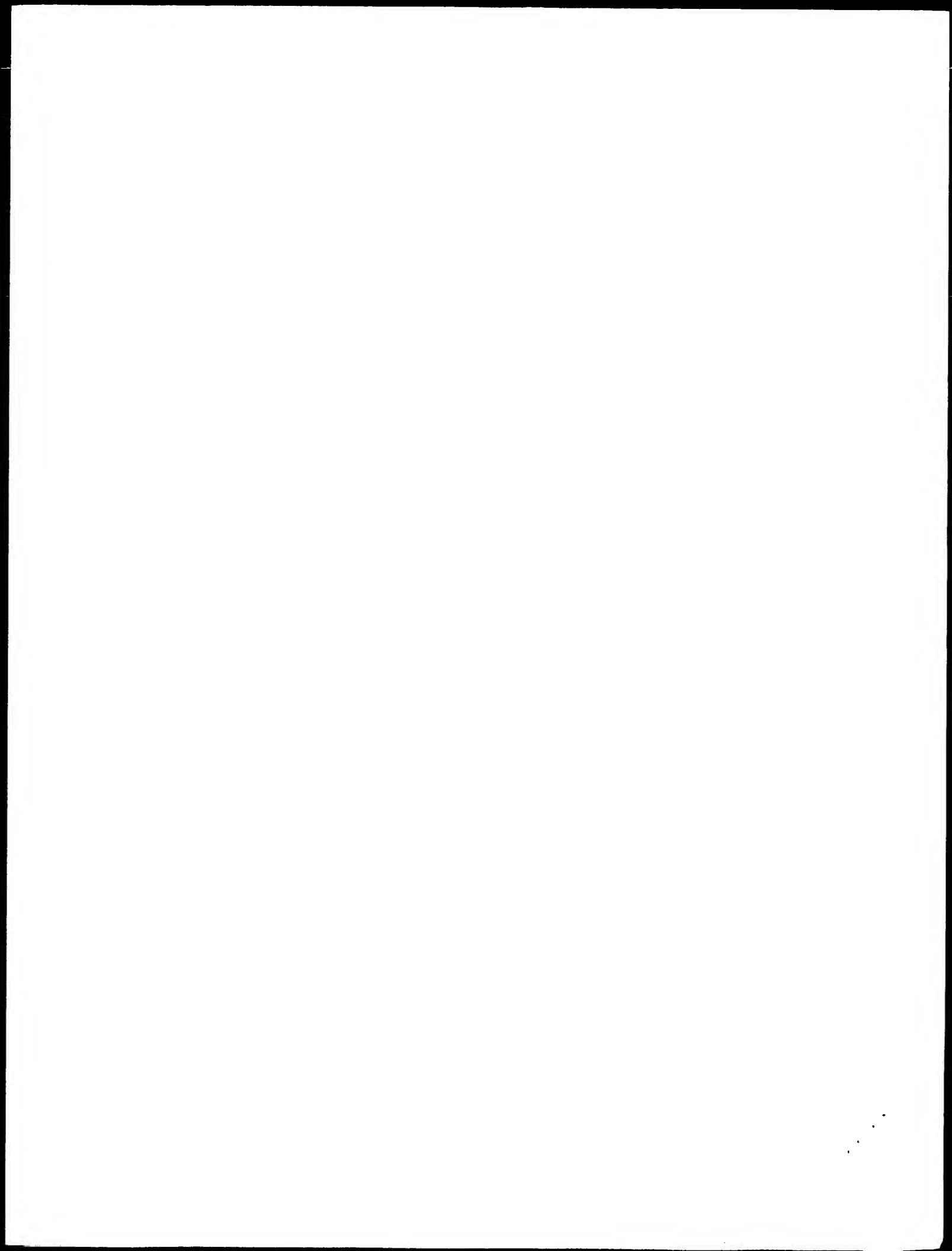
US-09-920-262A-1  
; Sequence 1, Application US/09920262A  
; GENERAL INFORMATION:  
; APPLICANT: Shealy, David  
; APPLICANT: Knight, David  
; APPLICANT: Scallon, Bernie  
; APPLICANT: Giles-Komar, Jill  
; APPLICANT: Peritt, David  
; TITLE OF INVENTION: ANTI-IL-12 ANTIBODIES, COMPOSITIONS, METHODS AND USES  
; FILE REFERENCE: CEN0248  
; CURRENT APPLICATION NUMBER: US/09/920,262A  
; CURRENT FILING DATE: 2002-05-06  
; PRIOR APPLICATION NUMBER: 60/223,358  
; PRIOR FILING DATE: 2000-08-07  
; PRIOR APPLICATION NUMBER: 60/236,827  
; PRIOR FILING DATE: 2000-09-29  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver 3.1  
; SEQ ID NO 1  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-920-262A-1

Query Match 47.8%; Score 11; DB 5; Length 5;  
Best Local Similarity 100.0%; Pred. NO. 3.5e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 5 W 5

Db 3 W 3

Search completed: February 12, 2003, 10:55:52  
Job time : 18 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 12, 2003, 10:50:14 ; Search time 13 Seconds

(without alignments)  
11.317 Million cell updates/sec

Title: US-09-403-440A-1

Perfect score: 23

Sequence: 1 FXXLW 5

Scoring table: BLOSUM62

scoring table. **DESCRIPTORS**  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 10533

Minimum DB seq length: 5

Maximum	DB	seq	length:	5
Maximum	DB	seq	length:	5

Post-processing: Minimum Match 0%

POST-PROCESSING: Minimum Match 0%  
Maximum Match 100%

Maximum Match 100%  
Listing first 100 summaries

Database : Issued Patents AA: \*

```
Database :
Issued Dates: Fri,
1: /cqn2 6/ptodata/1/iaa/5A COMB.ppe: *
```

2: /cqn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*

3: /cqn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*

4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*

5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pe

6: /cgn2\_6/ptodata/1/iaa/backfiles1.pe

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB	ID	SUMMARIES	
						Description	
1	19	82.6	5	1	US-08-424-957-4	Sequence 4, Appli	
2	19	82.6	5	1	US-08-424-957-5	Sequence 5, Appli	
3	19	82.6	5	4	US-09-035-686-4	Sequence 4, Appli	
4	19	82.6	5	4	US-09-035-686-5	Sequence 5, Appli	
5	16	69.6	5	4	US-09-099-053-3	Sequence 3, Appli	
6	15	65.2	5	1	US-07-893-930-37	Sequence 37, Appli	
7	15	65.2	5	1	US-08-073-028-44	Sequence 44, Appli	
8	15	65.2	5	1	US-08-133-011-148	Sequence 148, Appli	
9	15	65.2	5	1	US-08-584-579-11	Sequence 11, Appli	
10	15	65.2	5	1	US-08-704-170-103	Sequence 103, Appli	
11	15	65.2	5	2	US-08-747-137-44	Sequence 44, Appli	
12	15	65.2	5	2	US-08-830-326-14	Sequence 14, Appli	
13	15	65.2	5	2	US-08-850-187A-2	Sequence 2, Appli	
14	15	65.2	5	3	US-08-900-895-1	Sequence 1, Appli	
15	15	65.2	5	3	US-08-862-625A-3	Sequence 3, Appli	
16	15	65.2	5	3	US-08-981-122-15	Sequence 15, Appli	
17	15	65.2	5	3	US-08-981-122-38	Sequence 38, Appli	
18	15	65.2	5	3	US-08-981-132-43	Sequence 43, Appli	
19	15	65.2	5	3	US-08-981-122-51	Sequence 51, Appli	
20	15	65.2	5	4	US-08-554-616-44	Sequence 44, Appli	
21	15	65.2	5	4	US-08-530-342A-14	Sequence 14, Appli	
22	15	65.2	5	4	US-09-208-277-9	Sequence 9, Appli	
23	15	65.2	5	4	US-08-907-739-148	Sequence 148, Appli	
24	15	65.2	5	4	US-09-082-279B-791	Sequence 791, Appli	
25	15	65.2	5	4	US-09-315-304B-791	Sequence 791, Appli	
26	15	65.2	5	4	US-09-556-877-9	Sequence 9, Appli	
27	15	65.2	5	4	US-09-288-594A-9	Sequence 9, Appli	

## ALIGNMENTS

```

RESULT 1
US-08-424-957-4
; Sequence 4, Application US/08424957
; Patent No. 5770377
; GENERAL INFORMATION:
; APPLICANT: Pickseley, Steven M.
; ADDRESS: Lane, David P.
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,957
; FILING DATE: 19-APR-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/277,660
; FILING DATE: 20-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-61228/WHd
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; US-08-424-957-4

Query Match      82.6%; Score 19; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXLW 5
Db 1 FXXLW 5

RESULT 2
US-08-424-957-5
; Sequence 5, Application US/08424957
; Patent No. 5770377
; GENERAL INFORMATION:
; APPLICANT: Pickseley, Steven M.
; ADDRESS: Lane, David P.
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/035,686
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/424,957
; FILING DATE: 19-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.

```

```

; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,957
; FILING DATE: 19-APR-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/277,660
; FILING DATE: 20-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-61228/WHd
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; US-08-424-957-5

Query Match      82.6%; Score 19; DB 1; Length 5;
Best Local Similarity 80.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FXXLW 5
Db 1 FXELW 5

RESULT 3
US-09-035-686-4
; Sequence 4, Application US/09035686
; Patent No. 6153391
; GENERAL INFORMATION:
; APPLICANT: Pickseley, Steven M.
; ADDRESS: Lane, David P.
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/035,686
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/424,957
; FILING DATE: 19-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.

```

REGISTRATION NUMBER: 24,190  
 REFERENCE/DOCKET NUMBER: A-61228/WHD  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 781-1989  
 TELEFAX: (415) 398-3249  
 TELEX: 910 277299  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 5 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: unknown  
 US-09-035-686-4

Query Match 82.6%; Score 19; DB 4; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXLW 5  
 |||||  
 Db 1 FXXLW 5

## RESULT 4

US-09-035-686-5  
 ; Sequence 5, Application US/09035686  
 ; Patent No. 6153391  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Pickle, Steven M.  
 ; APPLICANT: Lane, David P.  
 ; TITLE OF INVENTION: Interruption of Binding of MDM2 and p53  
 ; TITLE OF INVENTION: Protein and Therapeutic Application Thereof  
 ; NUMBER OF SEQUENCES: 50  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert  
 ; STREET: Four Embarcadero Center, Suite 3400  
 ; CITY: San Francisco  
 ; STATE: California  
 ; COUNTRY: United States  
 ; ZIP: 94111-4187  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/035,686  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/424,957  
 ; FILING DATE: 19-APR-1995  
 ; APPLICATION NUMBER: US 08/277,660  
 ; FILING DATE: 20-JUL-1994  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Dreger, Walter H.  
 ; REGISTRATION NUMBER: 24,190  
 ; REFERENCE/DOCKET NUMBER: A-61228/WHD  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (415) 781-1989  
 ; TELEFAX: (415) 398-3249  
 ; TELEX: 910 277299  
 ; INFORMATION FOR SEQ ID NO: 5:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 5 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS:  
 ; TOPOLOGY: unknown  
 ; US-09-035-686-5

Query Match 82.6%; Score 19; DB 4; Length 5;  
 Best Local Similarity 80.0%; Pred. No. 2e+05;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FXXLW 5  
 |||||  
 Db 1 FXXLW 5

## RESULT 5

US-09-099-053-3  
 ; Sequence 3, Application US/09099053  
 ; Patent No. 6388063  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Greg Plowman  
 ; APPLICANT: Susan Onrust  
 ; APPLICANT: David Markby  
 ; APPLICANT: Sara Courtneidge  
 ; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF  
 ; TITLE OF INVENTION: SAD RELATED DISORDERS  
 ; NUMBER OF SEQUENCES: 28  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Lyon & Lyon  
 ; STREET: 633 West Fifth Street  
 ; STREET: Suite 4700  
 ; CITY: Los Angeles  
 ; STATE: California  
 ; COUNTRY: U.S.A.  
 ; ZIP: 90071-2066  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 ; MEDIUM TYPE: Storage  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0  
 ; SOFTWARE: FastSeq for Windows 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/099,053  
 ; FILING DATE: Herewith  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 60/049,914  
 ; FILING DATE: June 18, 1997  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Warburg, Richard J.  
 ; REGISTRATION NUMBER: 32,327  
 ; REFERENCE/DOCKET NUMBER: 235/121  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (213) 489-1600  
 ; TELEFAX: (213) 955-0440  
 ; TELEX: 67-3510  
 ; INFORMATION FOR SEQ ID NO: 3:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 5 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; FEATURE:  
 ; OTHER INFORMATION: "Xaa" in position 3 stands for  
 ; OTHER INFORMATION: either Glu or Asp.  
 ; US-09-099-053-3

Query Match 69.6%; Score 16; DB 4; Length 5;  
 Best Local Similarity 60.0%; Pred. No. 2e+05;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FXXLW 5  
 |||||  
 Db 1 FGXW 5

## RESULT 6

US-07-893-930-37  
 ; Sequence 37, Application US/07893930  
 ; Patent No. 5317014  
 ; GENERAL INFORMATION:

```

; APPLICANT: Fauchere, Jean-luc
; APPLICANT: Kucharczyk, Nathalie
; APPLICANT: Morris, Angela D.
; APPLICANT: Paladino, Joseph
; APPLICANT: Bonnet, Jacqueline
; APPLICANT: Thureau, Christophe
; TITLE OF INVENTION: NEW PEPTIDES AND PSEUDO-
; TITLE OF INVENTION: PEPTIDES
; TITLE OF INVENTION: COMPOUNDS DERIVED FROM TACHYKININ
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gordon W. Hueschen
; STREET: 715 The "H" Bldg., 310 East Michigan
; CITY: Kalamazoo
; STATE: MI
; COUNTRY: USA
; ZIP: 49007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version
; SOFTWARE: #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/893,930
; FILING DATE: 19920603
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91.06721
; FILING DATE: 04-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hueschen, Gordon W.
; REGISTRATION NUMBER: 16,157
; REFERENCE/DOCKET NUMBER: ADIR128/dlk
; TELEPHONE: 616-382-0030
; TELEFAX: 616-382-2030
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: mRNA
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "Benzhydryl
; OTHER INFORMATION: carbonyl"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 2
; OTHER INFORMATION: /note= "abo"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 5
; OTHER INFORMATION: /note= "NH2"
; US-07-893-930-37
;
; Query Match 65.2%; Score 15; DB 1; Length 5;
; Best Local Similarity 100.0%; Pred. No. 2e+05;
; Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 4 LW 5
; |
; Db 3 LW 4
;
; RESULT 7
; US-08-073-028-44
; Sequence 44, Application US/08073028
; Patent No. 5464933
; GENERAL INFORMATION:

```

```

; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/073,028
; FILING DATE: 07-JUN-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-073-028-44
;
; Query Match 65.2%; Score 15; DB 1; Length 5;
; Best Local Similarity 100.0%; Pred. No. 2e+05;
; Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 4 LW 5
; |
; Db 1 LW 2
;
; RESULT 8
; US-08-133-011-148
; Sequence 148, Application US/08133011
; Patent No. 5658727
; GENERAL INFORMATION:
; APPLICANT: Kang, Angray
; APPLICANT: Barbas, Carlos
; APPLICANT: Lerner, Richard A.
; TITLE OF INVENTION: HETERODIMERIC RECEPTOR LIBRARIES USING
; TITLE OF INVENTION: PHAGEMIDS
; NUMBER OF SEQUENCES: 161
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5658727th Torrey Pines Road, TPC-8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/133,011

```



; FILING DATE: 08-JUN-1994  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/683,602  
 ; FILING DATE: 10-APR-1991  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/826,623  
 ; FILING DATE: 27-JAN-1992  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US 92/03091  
 ; FILING DATE: 10-APR-1992  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Fitting, Thomas  
 ; REGISTRATION NUMBER: 34,163  
 ; REFERENCE/DOCKET NUMBER: SCRF 238.2  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 619-554-2937  
 ; TELEFAX: 619-554-6312  
 ; INFORMATION FOR SEQ ID NO: 148:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 5 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; FRAGMENT TYPE: internal  
 ; US-08-133-011-148

Query Match 65.2%; Score 15; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5

DB 4 LW 5

## RESULT 9

; US-08-584-579-11  
 ; Sequence 11, Application US/08584579  
 ; Patent No. 5674979  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Schramm, Wolfgang  
 ; APPLICANT: Schramm, Hans J.  
 ; TITLE OF INVENTION: Agent For Inhibiting Symmetrical  
 ; TITLE OF INVENTION: Proteins, In Particular Enzymes  
 ; NUMBER OF SEQUENCES: 20  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Venable, Baetjer, Howard & Civiletti  
 ; STREET: 1201 New York Avenue N.W., Suite 1000  
 ; CITY: Washington  
 ; STATE: DC  
 ; COUNTRY: USA  
 ; ZIP: 20005  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/584,579  
 ; FILING DATE:  
 ; CLASSIFICATION: 530  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/332,447  
 ; FILING DATE: 31-OCT-1994  
 ; APPLICATION NUMBER: US 08/112,215  
 ; FILING DATE: 26-AUG-1993  
 ; APPLICATION NUMBER: US 07/976,003  
 ; FILING DATE: 13-NOV-1992  
 ; APPLICATION NUMBER: US 07/585,141  
 ; FILING DATE: 07-DEC-1990  
 ; APPLICATION NUMBER: WO PCT/EP90/00219  
 ; FILING DATE: 09-FEB-1990

; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: DE P 39 04 040.2  
 ; FILING DATE: 10-FEB-1989  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Innen, Jeffrey L.  
 ; REGISTRATION NUMBER: 28957  
 ; REFERENCE/DOCKET NUMBER: 18644-96040  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 202-962-4810  
 ; TELEFAX: 202-962-8300  
 ; INFORMATION FOR SEQ ID NO: 11:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 5 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; HYPOTHETICAL: YES  
 ; US-08-584-579-11

Query Match 65.2%; Score 15; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5

DB 1 LW 2

## RESULT 10

; US-08-704-170-103  
 ; Sequence 103, Application US/08704170  
 ; Patent No. 5707626  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Douvas, Angeline  
 ; APPLICANT: Takehana, Yoshi  
 ; APPLICANT: Ehresmann, Glenn  
 ; TITLE OF INVENTION: THERAPEUTIC STRATEGIES FOR  
 ; TITLE OF INVENTION: IMMUNOINFECTION CLUSTER VIRUS INFECTIONS  
 ; NUMBER OF SEQUENCES: 121  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Robbins, Berliner & Carson  
 ; STREET: 201 No. 5707626th Figueroa Street, Suite 500  
 ; CITY: Los Angeles  
 ; STATE: California  
 ; COUNTRY: U.S.A.  
 ; ZIP: 90012  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/704,170  
 ; FILING DATE:  
 ; CLASSIFICATION: 424  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/029,850  
 ; FILING DATE: 11-MAR-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Spitals, John P.  
 ; REGISTRATION NUMBER: 29,215  
 ; REFERENCE/DOCKET NUMBER: 1920-331  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (213) 977-1001  
 ; TELEFAX: (213) 977-1003  
 ; INFORMATION FOR SEQ ID NO: 103:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 5 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; US-08-704-170-103

Query Match 65.2%; Score 15; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2e+05; Indels 0;  
 Matches 2; Conservative 0; Mismatches 0; Gaps 0;

QY 4 LW 5  
 ||  
 Db 4 LW 5

RESULT 11  
 US-08-747-137-44  
 ; Sequence 44, Application US/08747137  
 ; Patent No. 5945033  
 ; GENERAL INFORMATION:  
 ; APPLICANT: YEN, Richard C.K.  
 ; TITLE OF INVENTION: NON-CROSSLINKED PROTEIN PARTICLES FOR  
 ; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC USE  
 ; NUMBER OF SEQUENCES: 184  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Townsend and Townsend and Crew LLP  
 ; STREET: Two Embarcadero Center, 8th Floor  
 ; CITY: San Francisco  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 94111  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/747,137  
 ; FILING DATE: 12-NOV-1996  
 ; CLASSIFICATION: 424  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/212,546  
 ; FILING DATE: 14-MAR-1994  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/069,831  
 ; FILING DATE: 01-JUN-1993  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/959,560  
 ; FILING DATE: 13-OCT-1992  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/641,720  
 ; FILING DATE: 15-JAN-1991  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Apple, Randolph T.  
 ; REGISTRATION NUMBER: 36,429  
 ; REFERENCE/DOCKET NUMBER: 016197-000840US  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 415-576-0200  
 ; INFORMATION FOR SEQ ID NO: 44:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 5 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: not relevant  
 ; TOPOLOGY: not relevant  
 ; US-08-747-137-44

QY 4 LW 5  
 ||  
 Db 2 LW 3

RESULT 12  
 US-08-530-326-14  
 ; Sequence 14, Application US/08530326  
 ; Patent No. 5961954

; GENERAL INFORMATION:  
 ; APPLICANT: HILGER, CHRISTOPH-STEPH  
 ; APPLICANT: DINKELBORG, LUDGER  
 ; APPLICANT: KRAMP, WOLFGANG  
 ; APPLICANT: SCHIER, HANS-MARTIN  
 ; TITLE OF INVENTION: CHELATORS OF TYPE XN1S101 FOR RADIOACTIVE ISOTOPES, 7TH  
 ; NUMBER OF SEQUENCES: 15  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: FLIESLER, DUBB, MEYER & LOVEJOY  
 ; STREET: Four Embarcadero Center, Suite 400  
 ; CITY: San Francisco  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 94111  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FastSeq Version 1.5  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/530,326  
 ; FILING DATE:  
 ; CLASSIFICATION: 424  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/DE94/00372  
 ; FILING DATE: 29-MAR-1994  
 ; APPLICATION NUMBER: P 43 10 999.3  
 ; FILING DATE: 31-MAR-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Dubb, Hubert E  
 ; REGISTRATION NUMBER: 25,329  
 ; REFERENCE/DOCKET NUMBER: WBLT 2006 (WO) PA  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 415-362-3800  
 ; TELEFAX: 415-362-2928  
 ; TELEX:  
 ; INFORMATION FOR SEQ ID NO: 14:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 5 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; HYPOTHETICAL: NO  
 ; ANTI-SENSE: NO  
 ; FRAGMENT TYPE: internal  
 ; ORIGINAL SOURCE:  
 ; US-08-530-326-14

Query Match 65.2%; Score 15; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2e+05; Indels 0;  
 Matches 2; Conservative 0; Mismatches 0; Gaps 0;

QY 4 LW 5  
 ||  
 Db 4 LW 5

RESULT 13  
 US-08-854-187A-2  
 ; Sequence 2, Application US/08854187A  
 ; Patent No. 5962642  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Tsugita, Akira  
 ; TITLE OF INVENTION: Method for Sequencing of  
 ; TITLE OF INVENTION: Protein or Peptide  
 ; NUMBER OF SEQUENCES: 2  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Adams & Wilks  
 ; STREET: 50 Broadway, 31st Floor  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: United States of America

;/ ZIP: 10004  
;/ COMPUTER READABLE FORM:  
;/ MEDIUM TYPE: Diskette, 3.50 inch,  
;/ MEDIUM TYPE: 1.44 Mb storage  
;/ COMPUTER: NEC PowerMate VP75  
;/ OPERATING SYSTEM: Windows 98  
;/ SOFTWARE: Wordperfect 5.1  
;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/08/854,187A  
;/ FILING DATE: 09-MAY-1997  
;/ CLASSIFICATION:  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER: JP 08-115087  
;/ FILING DATE: 09-MAY-1996  
;/ APPLICATION NUMBER: JP 08-154580  
;/ FILING DATE: 14-JUN-1996  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Adams, Bruce L.  
;/ REGISTRATION NUMBER: 25,386  
;/ REFERENCE/DOCKET NUMBER: S004-3185  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: (212) 809-3700  
;/ TELEFAX: (212) 809-3704  
;/ INFORMATION FOR SEQ ID NO: 2:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 5  
;/ TYPE: amino acid  
;/ STRANDEDNESS: not applicable  
;/ TOPOLOGY: linear  
;/ MOLECULE TYPE: peptide  
;/ US-08-854-187A-2

Query Match 65.2%; Score 15; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5  
DB 1 LW 2

RESULT 14  
US-08-900-895-1  
;/ Sequence 1, Application US/08900895  
;/ Patent No. 6043087  
;/ GENERAL INFORMATION:  
;/ APPLICANT: Alessandra Bini and Bohdan J. Kudryk  
;/ TITLE OF INVENTION: MONOSPECIFIC ANTIBODY REACTIVE WITH  
;/ NUMBER OF SEQUENCES: 2  
;/ CORRESPONDENCE ADDRESS:  
;/ ADDRESSEE: Hoffmann & Baron, LLP  
;/ STREET: 350 Jericho Turnpike  
;/ CITY: Jericho  
;/ STATE: New York  
;/ COUNTRY: USA  
;/ ZIP: 11753  
;/ COMPUTER READABLE FORM:  
;/ MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage  
;/ COMPUTER: IBM compatible  
;/ OPERATING SYSTEM: MS-DOS  
;/ SOFTWARE: Wordperfect  
;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/08/900,895  
;/ FILING DATE: 7/25/97  
;/ CLASSIFICATION: 435  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: O'Dea, Sean W.  
;/ REGISTRATION NUMBER: 37690  
;/ REFERENCE/DOCKET NUMBER: 454-16  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: (516) 822-3550  
;/ TELEFAX: (516) 822-3582

;/ INFORMATION FOR SEQ ID NO: 1:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 5 amino acids  
;/ TYPE: amino acid  
;/ TOPOLOGY: linear  
;/ MOLECULE TYPE: peptide  
;/ US-08-900-895-1  
;/ Query Match 65.2%; Score 15; DB 3; Length 5;  
;/ Best Local Similarity 100.0%; Pred. No. 2e+05;  
;/ Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 LW 5  
DB 2 LW 3  
RESULT 15  
US-08-862-625A-3  
;/ Sequence 3, Application US/08862625A  
;/ Patent No. 6046053  
;/ GENERAL INFORMATION:  
;/ APPLICANT: Tsugita, Akira  
;/ TITLE OF INVENTION: A Method for Amino Acid  
;/ TITLE OF INVENTION: Sequencing of Protein or  
;/ TITLE OF INVENTION: Peptide from Carboxy Terminus  
;/ NUMBER OF SEQUENCES: 3  
;/ CORRESPONDENCE ADDRESS:  
;/ ADDRESSEE: Adams & Wilks  
;/ STREET: 50 Broadway, 31st Floor  
;/ CITY: New York  
;/ STATE: New York  
;/ COUNTRY: United States of America  
;/ ZIP: 10004  
;/ COMPUTER READABLE FORM:  
;/ MEDIUM TYPE: Diskette, 3.50 inch,  
;/ MEDIUM TYPE: 1.44 Mb storage  
;/ COMPUTER: IBM PS/2  
;/ OPERATING SYSTEM: DOS 3.3  
;/ SOFTWARE: Wordperfect 5.1  
;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/08/862,625A  
;/ FILING DATE: 24-MAY-1997  
;/ CLASSIFICATION: 436  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER: JP 08-130381  
;/ FILING DATE: 24-MAY-1996  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER: JP 09-035312  
;/ FILING DATE: 19-FEBRUARY-1997  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER: JP 09-036610  
;/ FILING DATE: 20-FEBRUARY-1997  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER: JP 09-091215  
;/ FILING DATE: 09-APRIL-1997  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Adams, Bruce L.  
;/ REGISTRATION NUMBER: 25,386  
;/ REFERENCE/DOCKET NUMBER: S004-3197  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: (212) 809-3700  
;/ TELEFAX: (212) 809-3704  
;/ INFORMATION FOR SEQ ID NO: 3:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 5  
;/ TYPE: amino acid  
;/ STRANDEDNESS: not applicable  
;/ TOPOLOGY: linear  
;/ MOLECULE TYPE: peptide  
;/ US-08-862-625A-3

```
Query Match      65.2%; Score 15; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 LW 5
      ||
Db      1 LW 2

RESULT 16
US-08-981-122-15
; Sequence 15, Application US/08981122B
; Patent No. 6127339
; GENERAL INFORMATION:
; APPLICANT: Hatanaka, Yoshihiro
; APPLICANT: Aritomi, Masaharu
; TITLE OF INVENTION: Peptide for binding thereto a low density lipoprotein
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/08/981,122B
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: JP 7-176904
; PRIOR FILING DATE: 1995-06-21
; PRIOR APPLICATION NUMBER: PCT/JP96/01734
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence of a peptide synthesized in Example 2 from L-form
; Patent No. 6127339
; OTHER INFORMATION: F-moc amino acids by solid phase method using a multi-peptide
; OTHER INFORMATION: synthesizing system (RAMPS)
; US-08-981-122-15

Query Match      65.2%; Score 15; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 LW 5
      ||
Db      1 LW 2

RESULT 17
US-08-981-122-38
; Sequence 38, Application US/08981122B
; Patent No. 6127339
; GENERAL INFORMATION:
; APPLICANT: Hatanaka, Yoshihiro
; APPLICANT: Aritomi, Masaharu
; TITLE OF INVENTION: Peptide for binding thereto a low density lipoprotein
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/08/981,122B
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: JP 7-176904
; PRIOR FILING DATE: 1995-06-21
; PRIOR APPLICATION NUMBER: PCT/JP96/01734
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence of a peptide synthesized in Examples 11 and 12 from L-form
; Patent No. 6127339
; OTHER INFORMATION: F-moc amino acids by solid phase method using an automatic peptide
```

```
; OTHER INFORMATION: synthesizer (9050 plus peptide synthesizer)
US-08-981-122-38

Query Match      65.2%; Score 15; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 LW 5
      ||
Db      4 LW 5

RESULT 18
US-08-981-122-43
; Sequence 43, Application US/08981122B
; Patent No. 6127339
; GENERAL INFORMATION:
; APPLICANT: Hatanaka, Yoshihiro
; APPLICANT: Aritomi, Masaharu
; TITLE OF INVENTION: Peptide for binding thereto a low density lipoprotein
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/08/981,122B
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: JP 7-176904
; PRIOR FILING DATE: 1995-06-21
; PRIOR APPLICATION NUMBER: PCT/JP96/01734
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: AMIDATION
; LOCATION: 5
; OTHER INFORMATION: Sequence of peptides synthesized in Examples 11 and 12 from L-form
; Patent No. 6127339
; OTHER INFORMATION: F-moc amino acids by solid phase method using an automatic peptide
; OTHER INFORMATION: synthesizer (9050 plus peptide synthesizer)
US-08-981-122-43

Query Match      65.2%; Score 15; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 LW 5
      ||
Db      4 LW 5

RESULT 19
US-08-981-122-51
; Sequence 51, Application US/08981122B
; Patent No. 6127339
; GENERAL INFORMATION:
; APPLICANT: Hatanaka, Yoshihiro
; APPLICANT: Aritomi, Masaharu
; TITLE OF INVENTION: Peptide for binding thereto a low density lipoprotein
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/08/981,122B
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: JP 7-176904
; PRIOR FILING DATE: 1995-06-21
; PRIOR APPLICATION NUMBER: PCT/JP96/01734
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 51
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
```

NAME/KEY: AMIDATION  
 LOCATION: 5  
 OTHER INFORMATION: Sequence of peptides synthesized in Examples 11 and 12 from L-fo  
 Patent No. 6127339  
 OTHER INFORMATION: F-moc amino acids by solid phase method using an automatic peptid  
 OTHER INFORMATION: synthesizer (9050 plus peptide synthesizer)  
 US-08-981-122-51

Query Match 65.2%; Score 15; DB 3; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5  
 DB 4 LW 5

RESULT 20  
 US-08-554-616-44  
 Sequence 44, Application US/08554616  
 Patent No. 6133418  
 GENERAL INFORMATION:  
 APPLICANT: Bolognesi, Dani P.  
 APPLICANT: Matthews, Thomas J.  
 APPLICANT: Wild, Carl T.  
 TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV  
 TITLE OF INVENTION: TRANSMISSION  
 NUMBER OF SEQUENCES: 74  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Pennie & Edmonds  
 STREET: 1155 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 10036

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/554,616  
 FILING DATE: 06-NOV-1995  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/073,028  
 FILING DATE: 07-JUN-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Coruzzi, Laura A.  
 REGISTRATION NUMBER: 30,742  
 REFERENCE/DOCKET NUMBER: 7872-004-999  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 869-8864/9741  
 TELEFAX: (212) 869-8864/9741  
 TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 44:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 5 amino acids  
 TYPE: amino acid  
 TOPOLOGY: unknown  
 MOLECULE TYPE: peptide  
 US-08-554-616-44

Query Match 65.2%; Score 15; DB 4; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5  
 DB 1 LW 2

RESULT 21

US-08-530-342A-14  
 Sequence 14, Application US/08530342A  
 Patent No. 6143275  
 GENERAL INFORMATION:  
 APPLICANT: HILGER, CHRISTOPH-STEPH  
 APPLICANT: DINKELBORG, LUDGER  
 APPLICANT: KRAMP, WOLFGANG  
 APPLICANT: SCHIER, HANS-MARTIN  
 TITLE OF INVENTION: TYPE 33N2 CHELATORS FOR RADIO  
 TITLE OF INVENTION: ACTIVE ISOTOPES, THEIR METAL COMPLEXES AND  
 TITLE OF INVENTION: THEIR DIAGNOSTIC AND THERAPEUTICAL USE  
 NUMBER OF SEQUENCES: 15  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: WOOD, PHILLIPS, VAN SANTEN, CLARK &  
 ADDRESSEE: MORTIMER  
 STREET: 500 West Madison Street, Suite 3800  
 CITY: Chicago  
 STATE: IL  
 COUNTRY: USA  
 ZIP: 60661-2511

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: COMPAQ Prolinea 4/25s  
 OPERATING SYSTEM: DOS  
 SOFTWARE: WordPerfect for Windows 6.0a  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/530,342A  
 FILING DATE: 08-MAR-1996  
 CLASSIFICATION: 424  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/DE94/00370  
 FILING DATE: 29-MAR-1994  
 APPLICATION NUMBER: P 43 11 022.3  
 FILING DATE: 31-MAR-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Mortimer, John S.  
 REGISTRATION NUMBER: 30,407  
 REFERENCE/DOCKET NUMBER: 1214.00008  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 312/876-1800  
 TELEFAX: 312/876-2020  
 TELEX:

INFORMATION FOR SEQ ID NO: 14:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 5 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 FRAGMENT TYPE: internal  
 ORIGINAL SOURCE:  
 US-08-530-342A-14

Query Match 65.2%; Score 15; DB 4; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5  
 DB 4 LW 5

RESULT 22

US-09-208-277-9  
 Sequence 9, Application US/09208277  
 Patent No. 6166177  
 GENERAL INFORMATION:  
 APPLICANT: Probst, Peter  
 APPLICANT: Bhatia, Ajay  
 APPLICANT: Skeiky, Yasir A.W.  
 TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE TREATMENT AND DIAGNOSIS

; TITLE OF INVENTION: OF CHLAMYDIAL INFECTION  
; FILE REFERENCE: 210121.469  
; CURRENT APPLICATION NUMBER: US/09/208,277  
; CURRENT FILING DATE: 1998-12-08  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 9  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Chlamydia trachomatis  
US-09-208-277-9

Query Match 65.2%; Score 15; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0;

QY 4 LW 5  
DB 3 LW 4

RESULT 23  
US-08-907-739-148  
; Sequence 148, Application US/08907739  
; Patent No. 6235469  
; GENERAL INFORMATION:  
; APPLICANT: Kang, Angray  
; APPLICANT: Barbas, Carlos  
; APPLICANT: Lerner, Richard A.  
; TITLE OF INVENTION: HETERODIMERIC RECEPTOR LIBRARIES USING  
; TITLE OF INVENTION: PHAGEMIDS  
; NUMBER OF SEQUENCES: 161  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Patent Counsel  
; STREET: 10666 No. 6235469th Torrey Pines Road, TPC-8  
; CITY: La Jolla  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/907,739  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/133,011  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/826,623  
; FILING DATE: 27-JAN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US 92/03091  
; FILING DATE: 10-APR-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fitting, Thomas  
; REGISTRATION NUMBER: 34,163  
; REFERENCE/DOCKET NUMBER: SCRF 238.2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-554-2937  
; TELEFAX: 619-554-6312  
; INFORMATION FOR SEQ ID NO: 148:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: internal  
US-08-907-739-148

Query Match 65.2%; Score 15; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0;

QY 4 LW 5  
DB 4 LW 5

RESULT 24  
US-09-082-279B-791  
; Sequence 791, Application US/09082279B  
; Patent No. 6258782  
; GENERAL INFORMATION:  
; APPLICANT: Barney, Shawn  
; APPLICANT: Guthrie, Kelly  
; APPLICANT: Merutka, Gene  
; APPLICANT: Anwer, Mohmed  
; APPLICANT: Lambert, Dennis  
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED  
; TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES  
; FILE REFERENCE: 7872-043  
; CURRENT APPLICATION NUMBER: US/09/082,279B  
; CURRENT FILING DATE: 1998-05-20  
; NUMBER OF SEQ ID NOS: 1515  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 791  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Core polypeptide  
US-09-082-279B-791

Query Match 65.2%; Score 15; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0;

QY 4 LW 5  
DB 1 LW 2

RESULT 25  
US-09-315-304B-791  
; Sequence 791, Application US/09315304B  
; Patent No. 6348568  
; GENERAL INFORMATION:  
; APPLICANT: Barney, S.  
; APPLICANT: Guthrie, K.  
; APPLICANT: Merutka, G.  
; APPLICANT: Anwer, M.  
; APPLICANT: Lambert, D.  
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC  
; TITLE OF INVENTION: PROPERTIES  
; FILE REFERENCE: 7872-052  
; CURRENT APPLICATION NUMBER: US/09/315,304B  
; CURRENT FILING DATE: 1999-05-20  
; PRIOR APPLICATION NUMBER: 09/082,279  
; PRIOR FILING DATE: 1998-05-20  
; NUMBER OF SEQ ID NOS: 1667  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 791  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Core polypeptide  
US-09-315-304B-791

Query Match 65.2%; Score 15; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5  
||  
Db 1 LW 2

## RESULT 26

US-09-556-877-9  
; Sequence 9, Application US/09556877  
; Patent No. 6432916  
; GENERAL INFORMATION:  
; APPLICANT: Probst, Peter  
; APPLICANT: Bhatia, Ajay  
; APPLICANT: Skeiky, Yasir  
; APPLICANT: Fling, Steve  
; APPLICANT: Maisonneuve, Jeff  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND  
; FILE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION  
; FILE REFERENCE: 210121.469C5  
; CURRENT APPLICATION NUMBER: US/09/556.877  
; CURRENT FILING DATE: 2000-04-19  
; NUMBER OF SEQ ID NOS: 305  
; SOFTWARE: FastSEQ for Windows Version 3.0/4.0  
; SEQ ID NO 9  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Chlamydia trachomatis  
US-09-556-877-9

Query Match 65.2%; Score 15; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5  
||  
Db 3 LW 4

## RESULT 27

US-09-288-594A-9  
; Sequence 9, Application US/09288594A  
; Patent No. 6447779  
; GENERAL INFORMATION:  
; APPLICANT: Probst, Peter  
; APPLICANT: Bhatia, Ajay  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Fling, Steven P.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE TREATMENT  
; FILE OF INVENTION: AND DIAGNOSIS OF CHLAMYDIAL INFECTION  
; FILE REFERENCE: 210121.469C1  
; CURRENT APPLICATION NUMBER: US/09/288.594A  
; CURRENT FILING DATE: 1999-04-08  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 9  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Chlamydia trachomatis  
US-09-288-594A-9

Query Match 65.2%; Score 15; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5  
||  
Db 3 LW 4

## RESULT 28

US-09-620-412C-9  
; Sequence 9, Application US/09620412C

Patent No. 6448234  
; GENERAL INFORMATION:  
; APPLICANT: Steven P. Fling  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND  
; FILE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION  
; FILE REFERENCE: 210121.469C7  
; CURRENT APPLICATION NUMBER: US/09/620.412C  
; CURRENT FILING DATE: 2000-07-20  
; NUMBER OF SEQ ID NOS: 363  
; SOFTWARE: FastSEQ for Windows Version 3.0/4.0  
; SEQ ID NO 9  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Chlamydia trachomatis  
US-09-620-412C-9

Query Match 65.2%; Score 15; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5  
||  
Db 3 LW 4

## RESULT 29

US-08-469-260A-228  
; Sequence 228, Application US/08469260A  
; Patent No. 6451578  
; GENERAL INFORMATION:  
; APPLICANT: JOHN N. SIMONS  
; APPLICANT: TAMI J. PILOT-MATTIAS  
; APPLICANT: GEORGE J. DAWSON  
; APPLICANT: GEORGE G. SCHLAUDER  
; APPLICANT: SURESH M. DESAI  
; APPLICANT: THOMAS P. LEARY  
; APPLICANT: ANTHONY SCOTT MUERHOFF  
; APPLICANT: JAMES C. ERKER  
; APPLICANT: SHERI L. BUIJK  
; APPLICANT: ISA K. MUSHAWAR  
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS  
; FILE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE  
; NUMBER OF SEQUENCES: 716  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D  
; STREET: 100 ABBOTT PARK ROAD  
; CITY: ABBOTT PARK  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60064-3500  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/469.260A  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/424.550  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: FOREMSKI, PRISCILLA E.  
; REGISTRATION NUMBER: 33,207  
; REFERENCE/DOCKET NUMBER: 5527.PC.01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 708-937-6365  
; TELEFAX: 708-938-2623  
; INFORMATION FOR SEQ ID NO: 228:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid

; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-469-260A-228

Query Match 65.2%; Score 15; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0;

Qy 4 LW 5  
Db 3 LW 4

## RESULT 30

US-09-729-597-148  
; Sequence 148, Application US/09729597  
; Patent No. 6468738  
; GENERAL INFORMATION:  
; APPLICANT: Kang, Angray  
; Barbas, Carlos  
; Lerner, Richard A.  
; TITLE OF INVENTION: HETERODIMERIC RECEPTOR LIBRARIES USING  
; PHAGEMIDS  
; NUMBER OF SEQUENCES: 161  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: The Scripps Research Institute, Office of  
; Patent Counsel  
; STREET: 10666 No. 6468738th Torrey Pines Road, TPC-8  
; CITY: La Jolla  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92037

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/729,597  
FILING DATE: 04-Dec-2000  
CLASSIFICATION: 435

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/133,011  
FILING DATE: 1994-09-29  
APPLICATION NUMBER: US 07/826,623  
FILING DATE: 27-JAN-1992  
APPLICATION NUMBER: PCT/US 92/03091  
FILING DATE: 10-APR-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: SCRF 238.2  
TELEPHONE: 619-554-2937  
TELEFAX: 619-554-6312

INFORMATION FOR SEQ ID NO: 148:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid

## TOPOLOGY: linear

MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
SEQUENCE DESCRIPTION: SEQ ID NO: 148:  
US-09-729-597-148

Query Match 65.2%; Score 15; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0;

Qy 4 LW 5  
Db 4 LW 5

RESULT 31  
PCT-US94-01321-47  
; Sequence 47, Application PC/TUS9401321  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: Altered Linolenic and Linoleic Acid Content  
; in Plants  
; NUMBER OF SEQUENCES: 72  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/01321  
; FILING DATE: 04-FEB-1994  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/156551  
; FILING DATE: 22-NOV-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/014431  
; FILING DATE: 05-FEB-1993  
; INFORMATION FOR SEQ ID NO: 47:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
PCT-US94-01321-47

Query Match 65.2%; Score 15; DB 5; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0;

Qy 4 LW 5  
Db 3 LW 4

## RESULT 32

PCT-US94-02631-103  
; Sequence 103, Application PC/TUS9402631  
; GENERAL INFORMATION:  
; APPLICANT: Douvas, Angeline  
; APPLICANT: Takehana, Yoshi  
; APPLICANT: Ehresmann, Glenn  
; TITLE OF INVENTION: THERAPEUTIC STRATEGIES FOR  
; IMMUNOINFECTIVE CLUSTER VIRUS INFECTIONS  
; NUMBER OF SEQUENCES: 121  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Robbins, Berliner & Carson  
; STREET: 201 North Figueroa Street, Suite 500  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90012  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/02631  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/029,850  
; FILING DATE: 11-MAR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Spitals, John P.  
; REGISTRATION NUMBER: 29,215



; REFERENCE/DOCKET NUMBER: 1920-331  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 977-1001  
; TELEFAX: (213) 977-1003  
; INFORMATION FOR SEQ ID NO: 103:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
PCT-US94-02631-103

Query Match 65.2%; Score 15; DB 5; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5  
||  
Db 4 LW 5

RESULT 33  
5171838-3  
; Patent No. 5171838  
; APPLICANT: CHIBA, YUKINOBU  
; TITLE OF INVENTION: LEUJA BINDING PEPTIDES  
; NUMBER OF SEQUENCES: 24  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/526,921  
; FILING DATE: 22-MAY-1990  
; SEQ ID NO:3:  
; LENGTH: 5  
5171838-3

Query Match 65.2%; Score 15; DB 6; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5  
||  
Db 3 LW 4

RESULT 34  
US-07-789-184-83  
; Sequence 83, Application US/07789184  
; Patent No. 5688768  
; GENERAL INFORMATION:  
; APPLICANT: COUGHLIN, SHAUN R.  
; APPLICANT: SCARBOROUGH, ROBERT M.  
; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND  
; TITLE OF INVENTION: RELATED PHARMACEUTICALS  
; NUMBER OF SEQUENCES: 223  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/789,184  
; FILING DATE: 19911107  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MURASHIGE, KATE H.  
; REGISTRATION NUMBER: 29,959  
; REFERENCE/DOCKET NUMBER: 22000-20502.20

; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 813-5600  
; TELEFAX: (415) 494-0792  
; TELEX: 34-0154  
; INFORMATION FOR SEQ ID NO: 83:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: AMINO ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-07-789-184-83

Query Match 60.9%; Score 14; DB 1; Length 5;  
Best Local Similarity 40.0%; Pred. No. 2e+05;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXLW 5  
| |  
Db 1 FEPFW 5

RESULT 35  
US-08-475-263-83  
; Sequence 83, Application US/08475263  
; Patent No. 5759994  
; GENERAL INFORMATION:  
; APPLICANT: COUGHLIN, SHAUN R.  
; APPLICANT: SCARBOROUGH, ROBERT M.  
; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND  
; TITLE OF INVENTION: RELATED PHARMACEUTICALS  
; NUMBER OF SEQUENCES: 223  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 2000 Pennsylvania Ave., NW  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20006-1812  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/475,263  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MURASHIGE, KATE H.  
; REGISTRATION NUMBER: 29,959  
; REFERENCE/DOCKET NUMBER: 22000-20502.03  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 887-1500  
; TELEFAX: (202) 887-0763  
; TELEX: 90-4030  
; INFORMATION FOR SEQ ID NO: 83:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-475-263-83

Query Match 60.9%; Score 14; DB 1; Length 5;  
Best Local Similarity 40.0%; Pred. No. 2e+05;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXLW 5  
| |  
Db 1 FEPFW 5

RESULT 36

US-08-485-886-83	OPERATING SYSTEM: PC-DOS/MS-DOS	PC-DOS/MS-DOS	Version #1.25
Sequence 83, Application US/08485886	CURRENT APPLICATION DATA:		
Patent No. 5798248	APPLICATION NUMBER: US/08/477,362		
GENERAL INFORMATION:	FILING DATE: 07-JUN-1995		
CLASSIFICATION: 435			
APPLICANT: COUGHLIN, SHAUN R.	PRIOR APPLICATION DATA:		
APPLICANT: SCARBOROUGH, ROBERT M.	APPLICATION NUMBER: US 07/789,184		
TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND RELATED PHARMACEUTICALS	FILING DATE: 07-NOV-1991		
TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND RELATED PHARMACEUTICALS	ATTORNEY/AGENT INFORMATION:		
NUMBER OF SEQUENCES: 223	NAME: MURASHIGE, KATE H.		
CORRESPONDENCE ADDRESS:	REGISTRATION NUMBER: 29,959		
ADDRESS: MORRISON & FOERSTER	REFERENCE/DOCKET NUMBER: 22000-20502.20		
STREET: 755 Page Mill Road	TELECOMMUNICATION INFORMATION:		
CITY: Palo Alto	TELEPHONE: (415) 813-5600		
STATE: California	TELEFAX: (415) 494-0792		
COUNTRY: USA	TELEX: 34-0154		
ZIP: 94304-1018	INFORMATION FOR SEQ ID NO: 83:		
COMPUTER READABLE FORM:	SEQUENCE CHARACTERISTICS:		
MEDIUM TYPE: Floppy disk	LENGTH: 5 amino acids		
COMPUTER: IBM PC compatible	TYPE: amino acid		
OPERATING SYSTEM: PC-DOS/MS-DOS	STRANDEDNESS: single		
SOFTWARE: PatentIn Release #1.0, Version #1.25	TOPOLOGY: linear		
CURRENT APPLICATION DATA:			
APPLICATION NUMBER: US/08/485,886			
FILING DATE: 07-JUN-1995			
CLASSIFICATION: 435			
PRIOR APPLICATION DATA:			
APPLICATION NUMBER: US 07/789,184			
FILING DATE: 07-NOV-1991			
ATTORNEY/AGENT INFORMATION:			
NAME: MURASHIGE, KATE H.			
REGISTRATION NUMBER: 29,959			
REFERENCE/DOCKET NUMBER: 22000-20502.20			
TELECOMMUNICATION INFORMATION:			
TELEPHONE: (415) 813-5600			
TELEFAX: (415) 494-0792			
TELEX: 34-0154			
INFORMATION FOR SEQ ID NO: 83:			
SEQUENCE CHARACTERISTICS:			
LENGTH: 5 amino acids			
TYPE: amino acid			
STRANDEDNESS: single			
TOPOLOGY: linear			
US-08-485-886-83			
Query Match	60.9%;	Score 14;	DB 1; Length 5;
Best Local Similarity	40.0%;	Pred. No. 2e+05;	
Matches	2;	Conservative	0; Mismatches 3; Indels 0; Gaps 0;
QY	1 FXXLW 5		
DB	1 PEPFW 5		
RESULT 37			
US-08-477-362-83			
Sequence 83, Application US/08477362			
Patent No. 5849507			
GENERAL INFORMATION:			
APPLICANT: COUGHLIN, SHAUN R.			
APPLICANT: SCARBOROUGH, ROBERT M.			
TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND RELATED PHARMACEUTICALS			
TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND RELATED PHARMACEUTICALS			
NUMBER OF SEQUENCES: 223			
CORRESPONDENCE ADDRESS:			
ADDRESS: MORRISON & FOERSTER			
STREET: 755 Page Mill Road			
CITY: Palo Alto			
STATE: California			
COUNTRY: USA			
ZIP: 94304-1018			
COMPUTER READABLE FORM:			
MEDIUM TYPE: Floppy disk			
COMPUTER: IBM PC compatible			
OPERATING SYSTEM: PC-DOS/MS-DOS			
SOFTWARE: PatentIn Release #1.0, Version #1.25			
CURRENT APPLICATION DATA:			
APPLICATION NUMBER: US/08/485,886			
FILING DATE: 07-JUN-1995			
CLASSIFICATION: 435			
PRIOR APPLICATION DATA:			
APPLICATION NUMBER: US 07/789,184			
FILING DATE: 07-NOV-1991			
ATTORNEY/AGENT INFORMATION:			
NAME: MURASHIGE, KATE H.			
REGISTRATION NUMBER: 29,959			
REFERENCE/DOCKET NUMBER: 22000-20502.20			
TELECOMMUNICATION INFORMATION:			
TELEPHONE: (415) 813-5600			
TELEFAX: (415) 494-0792			
TELEX: 34-0154			
INFORMATION FOR SEQ ID NO: 83:			
SEQUENCE CHARACTERISTICS:			
LENGTH: 5 amino acids			
TYPE: amino acid			
STRANDEDNESS: single			
TOPOLOGY: linear			
US-08-485-886-83			
Query Match	60.9%;	Score 14;	DB 1; Length 5;
Best Local Similarity	40.0%;	Pred. No. 2e+05;	
Matches	2;	Conservative	0; Mismatches 3; Indels 0; Gaps 0;
QY	1 FXXLW 5		
DB	1 PEPFW 5		
RESULT 37			
US-08-477-362-83			
Sequence 83, Application US/08477362			
Patent No. 5849507			
GENERAL INFORMATION:			
APPLICANT: COUGHLIN, SHAUN R.			
APPLICANT: SCARBOROUGH, ROBERT M.			
TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND RELATED PHARMACEUTICALS			
TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND RELATED PHARMACEUTICALS			
NUMBER OF SEQUENCES: 223			
CORRESPONDENCE ADDRESS:			
ADDRESS: MORRISON & FOERSTER			
STREET: 755 Page Mill Road			
CITY: Palo Alto			
STATE: California			
COUNTRY: USA			
ZIP: 94304-1018			
COMPUTER READABLE FORM:			
MEDIUM TYPE: Floppy disk			
COMPUTER: IBM PC compatible			
OPERATING SYSTEM: PC-DOS/MS-DOS			
SOFTWARE: PatentIn Release #1.0, Version #1.25			
CURRENT APPLICATION DATA:			
APPLICATION NUMBER: US/0			

;  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-477-134-83

Query Match 60.9%; Score 14; DB 2; Length 5;  
Best Local Similarity 40.0%; Pred. No. 2e+05;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXLW 5  
|  
Db 1 FEPFW 5

## RESULT 39

US-08-473-489A-83  
; Sequence 83, Application US/08473489A  
; Patent No. 6024936

;  
; GENERAL INFORMATION:  
; APPLICANT: COUGHLIN, SHAUN R.  
; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND  
; TITLE OF INVENTION: RELATED PHARMACEUTICALS  
; NUMBER OF SEQUENCES: 223

;  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1018

;  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION NUMBER: US/08/473.489A  
; FILING DATE: 07-NOV-1991

;  
; CLASSIFICATION:  
; PRIOR APPLICATION NUMBER: US/07/789,184  
; FILING DATE: 1991-11-07

;  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MURASHIGE, KATE H.  
; REGISTRATION NUMBER: 29,959  
; REFERENCE/DOCKET NUMBER: 22000-20502.20  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 813-5600  
; TELEFAX: (415) 494-0792  
; TELEX: 34-0154

;  
; INFORMATION FOR SEQ ID NO: 83:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-473-489A-83

Query Match 60.9%; Score 14; DB 3; Length 5;  
Best Local Similarity 40.0%; Pred. No. 2e+05;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXLW 5  
|  
Db 1 FEPFW 5

## RESULT 40

US-08-485-695-83  
; Sequence 83, Application US/08485695  
; Patent No. 6124101

;  
; GENERAL INFORMATION:  
; APPLICANT: COUGHLIN, SHAUN R.  
; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND  
; TITLE OF INVENTION: RELATED PHARMACEUTICALS  
; NUMBER OF SEQUENCES: 223

;  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1018

;  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION NUMBER: US/08/485,695  
; FILING DATE: 07-JUN-1995

;  
; CLASSIFICATION: 435  
; PRIOR APPLICATION NUMBER: US 07/789,184  
; FILING DATE: 07-NOV-1991

;  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MURASHIGE, KATE H.  
; REGISTRATION NUMBER: 29,959  
; REFERENCE/DOCKET NUMBER: 22000-20502.20  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 813-5600  
; TELEFAX: (415) 494-0792  
; TELEX: 34-0154

;  
; INFORMATION FOR SEQ ID NO: 83:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-485-695-83

Query Match 60.9%; Score 14; DB 3; Length 5;  
Best Local Similarity 40.0%; Pred. No. 2e+05;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXLW 5  
|  
Db 1 FEPFW 5

## RESULT 41

US-08-018-760-83  
; Sequence 83, Application US/08018760  
; Patent No. 6197541

;  
; GENERAL INFORMATION:  
; APPLICANT: COUGHLIN, SHAUN R.  
; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND  
; TITLE OF INVENTION: RELATED PHARMACEUTICALS  
; NUMBER OF SEQUENCES: 223

;  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1018

;  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:

```
; APPLICATION NUMBER: US/08/018,760
; FILING DATE: 17-FEB-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/789,184
; FILING DATE: 07-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22000-20502.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 34-0154
; INFORMATION FOR SEQ ID NO: 83:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-018-760-83

Query Match 60.9%; Score 14; DB 4; Length 5;
Best Local Similarity 40.0%; Pred. No. 2e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXLW 5
Db 1 FEPFW 5

RESULT 42
US-07-858-842-3
; Sequence 3, Application US/07858842
; Patent No. 5314807
; GENERAL INFORMATION:
; APPLICANT: Yoshikawa, Masaaki
; APPLICANT: Yokoyama, Keiichi
; APPLICANT: Hasegawa, Masayasu
; APPLICANT: Yasumoto, Ryouichi
; APPLICANT: Fujita, Hiroyuki
; TITLE OF INVENTION: METHOD FOR PRODUCING AN ANGIOTENSIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARMSTRONG & KUBOWCIK
; STREET: 1725 K Street N.W., Suite 1000
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: United States of America
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/858,842
; FILING DATE: 19920327
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 142283
; FILING DATE: 29-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 298060
; FILING DATE: 17-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Gormley, Mary E.
; REGISTRATION NUMBER: 34, 409
; REFERENCE/DOCKET NUMBER: 920247
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 659-2930
; TELEFAX: (202) 887-0357
; TELEX: 440142
```

```
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; US-07-858-842-3

Query Match 56.5%; Score 13; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5
Db 1 IW 2

RESULT 43
US-07-960-636B-2
; Sequence 2, Application US/07960636B
; Patent No. 5363015
; GENERAL INFORMATION:
; APPLICANT: Yoshikawa, Masaaki
; APPLICANT: Yokoyama, Keiichi
; APPLICANT: Hasegawa, Masayasu
; APPLICANT: Yasumoto, Ryouichi
; APPLICANT: Fujita, Hiroyuki
; TITLE OF INVENTION: Method for Producing an Angiotensin
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Armstrong, Westerman, Hattori, McLeland &
; ADDRESSEE: Naughton
; STREET: 1725 K Street, N.W., Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/960,636B
; FILING DATE: 14-OCT-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 298061/1991
; FILING DATE: 17-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Tockman, Albert
; REGISTRATION NUMBER: 19722
; REFERENCE/DOCKET NUMBER: P1161-2679-A920798
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 659-2930
; TELEFAX: (202) 887-0357
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Mammalian meat, fish, crustaceans
; US-07-960-636B-2

Query Match 56.5%; Score 13; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. No. 2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5
```

```

;
; Db 1 IW 2
;
; TITLE OF INVENTION: NEW HEXAPEPTIDIC
; TITLE OF INVENTION: DERIVATIVES, PREPARATION, METHOD AND
; TITLE OF INVENTION: APPLICATION AS MEDICAMENTS OF SAID NEW
; TITLE OF INVENTION: DERIVATIVES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN AND MUSERLIAN
; STREET: 600 THIRD AVE.
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORD PERFECT # 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/133,020
; FILING DATE: 03-DEC-1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 146.1195
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-661-8000
; TELEFAX: 212-661-8002
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5
; TYPE: AMINO ACID
; TOPOLOGY: UNKNOWN
; MOLECULE TYPE:
; DESCRIPTION: PEPTIDE
; US-08-133-020-4

Query Match 56.5%; Score 13; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. No. 2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0;

QY 4 LW 5
Db 4 IW 5

RESULT 46
US-07-802-667-19
; Sequence 19, Application US/07802667
; Patent No. 5504070
; GENERAL INFORMATION:
; APPLICANT: BIHOVSKY, RON H.
; APPLICANT: ERHARDT, PAUL W.
; APPLICANT: LAMPE, JOHN W.
; APPLICANT: MOHAN, RAJU
; APPLICANT: SHAW, KENNETH J.
; TITLE OF INVENTION: INHIBITORS OF THE CONVERSION OF BIG
; TITLE OF INVENTION: ENDOTHELIN TO ENDOTHELIN
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERLEX LABORATORIES, INC.
; STREET: 300 FAIRFIELD ROAD
; CITY: WAYNE
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07470-5472
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/802,667

;
; Db 1 IW 2
;
; TITLE OF INVENTION: NEW HEXAPEPTIDIC
; TITLE OF INVENTION: DERIVATIVES, PREPARATION, METHOD AND
; TITLE OF INVENTION: APPLICATION AS MEDICAMENTS OF SAID NEW
; TITLE OF INVENTION: DERIVATIVES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN AND MUSERLIAN
; STREET: 600 THIRD AVE.
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORD PERFECT # 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/133,020
; FILING DATE: 03-DEC-1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 146.1195
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-661-8000
; TELEFAX: 212-661-8002
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5
; TYPE: AMINO ACID
; TOPOLOGY: UNKNOWN
; MOLECULE TYPE:
; DESCRIPTION: PEPTIDE
; US-08-133-020-4

Query Match 56.5%; Score 13; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. No. 2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0;

QY 4 LW 5
Db 4 IW 5

RESULT 46
US-07-802-667-19
; Sequence 19, Application US/07802667
; Patent No. 5504070
; GENERAL INFORMATION:
; APPLICANT: BIHOVSKY, RON H.
; APPLICANT: ERHARDT, PAUL W.
; APPLICANT: LAMPE, JOHN W.
; APPLICANT: MOHAN, RAJU
; APPLICANT: SHAW, KENNETH J.
; TITLE OF INVENTION: INHIBITORS OF THE CONVERSION OF BIG
; TITLE OF INVENTION: ENDOTHELIN TO ENDOTHELIN
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERLEX LABORATORIES, INC.
; STREET: 300 FAIRFIELD ROAD
; CITY: WAYNE
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07470-5472
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/802,667

;
; Db 1 IW 2
;
; TITLE OF INVENTION: NEW HEXAPEPTIDIC
; TITLE OF INVENTION: DERIVATIVES, PREPARATION, METHOD AND
; TITLE OF INVENTION: APPLICATION AS MEDICAMENTS OF SAID NEW
; TITLE OF INVENTION: DERIVATIVES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN AND MUSERLIAN
; STREET: 600 THIRD AVE.
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORD PERFECT # 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/133,020
; FILING DATE: 03-DEC-1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 146.1195
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-661-8000
; TELEFAX: 212-661-8002
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5
; TYPE: AMINO ACID
; TOPOLOGY: UNKNOWN
; MOLECULE TYPE:
; DESCRIPTION: PEPTIDE
; US-08-133-020-4

Query Match 56.5%; Score 13; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. No. 2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0;

QY 4 LW 5
Db 4 IW 5

RESULT 46
US-07-802-667-19
; Sequence 19, Application US/07802667
; Patent No. 5504070
; GENERAL INFORMATION:
; APPLICANT: BIHOVSKY, RON H.
; APPLICANT: ERHARDT, PAUL W.
; APPLICANT: LAMPE, JOHN W.
; APPLICANT: MOHAN, RAJU
; APPLICANT: SHAW, KENNETH J.
; TITLE OF INVENTION: INHIBITORS OF THE CONVERSION OF BIG
; TITLE OF INVENTION: ENDOTHELIN TO ENDOTHELIN
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERLEX LABORATORIES, INC.
; STREET: 300 FAIRFIELD ROAD
; CITY: WAYNE
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07470-5472
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/802,667

;
; Db 1 IW 2
;
; TITLE OF INVENTION: NEW HEXAPEPTIDIC
; TITLE OF INVENTION: DERIVATIVES, PREPARATION, METHOD AND
; TITLE OF INVENTION: APPLICATION AS MEDICAMENTS OF SAID NEW
; TITLE OF INVENTION: DERIVATIVES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN AND MUSERLIAN
; STREET: 600 THIRD AVE.
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORD PERFECT # 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/133,020
; FILING DATE: 03-DEC-1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 146.1195
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-661-8000
; TELEFAX: 212-661-8002
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5
; TYPE: AMINO ACID
; TOPOLOGY: UNKNOWN
; MOLECULE TYPE:
; DESCRIPTION: PEPTIDE
; US-08-133-020-4

Query Match 56.5%; Score 13; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. No. 2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0;

QY 4 LW 5
Db 4 IW 5

RESULT 46
US-07-802-667-19
; Sequence 19, Application US/07802667
; Patent No. 5504070
; GENERAL INFORMATION:
; APPLICANT: BIHOVSKY, RON H.
; APPLICANT: ERHARDT, PAUL W.
; APPLICANT: LAMPE, JOHN W.
; APPLICANT: MOHAN, RAJU
; APPLICANT: SHAW, KENNETH J.
; TITLE OF INVENTION: INHIBITORS OF THE CONVERSION OF BIG
; TITLE OF INVENTION: ENDOTHELIN TO ENDOTHELIN
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERLEX LABORATORIES, INC.
; STREET: 300 FAIRFIELD ROAD
; CITY: WAYNE
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07470-5472
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/802,667

;
; Db 1 IW 2
;
; TITLE OF INVENTION: NEW HEXAPEPTIDIC
; TITLE OF INVENTION: DERIVATIVES, PREPARATION, METHOD AND
; TITLE OF INVENTION: APPLICATION AS MEDICAMENTS OF SAID NEW
; TITLE OF INVENTION: DERIVATIVES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN AND MUSERLIAN
; STREET: 600 THIRD AVE.
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORD PERFECT # 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/133,020
; FILING DATE: 03-DEC-1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 146.1195
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-661-8000
; TELEFAX: 212-661-8002
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5
; TYPE: AMINO ACID
; TOPOLOGY: UNKNOWN
; MOLECULE TYPE:
; DESCRIPTION: PEPTIDE
; US-08-133-020-4

Query Match 56.5%; Score 13; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. No. 2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0;

QY 4 LW 5
Db 4 IW 5

RESULT 46
US-07-802-667-19
; Sequence 19, Application US/07802667
; Patent No. 5504070
; GENERAL INFORMATION:
; APPLICANT: BIHOVSKY, RON H.
; APPLICANT: ERHARDT, PAUL W.
; APPLICANT: LAMPE, JOHN W.
; APPLICANT: MOHAN, RAJU
; APPLICANT: SHAW, KENNETH J.
; TITLE OF INVENTION: INHIBITORS OF THE CONVERSION OF BIG
; TITLE OF INVENTION: ENDOTHELIN TO ENDOTHELIN
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERLEX LABORATORIES, INC.
; STREET: 300 FAIRFIELD ROAD
; CITY: WAYNE
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07470-5472
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/802,667

;
; Db 1 IW 2
;
```



; LOCATION: 5  
; OTHER INFORMATION: /note= "C-TERMINAL AMIDE ESTER"  
; US-07-802-667-21

Query Match 56.5%; Score 13; DB 1; Length 5;  
Best Local Similarity 50.0%; Pred. No. 2e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5  
;:  
Db 3 IW 4

## RESULT 49

US-08-057-167-12  
; Sequence 12, Application US/08057167  
; Patent No. 5541095  
; GENERAL INFORMATION:  
; APPLICANT: Hirschberg, Carlos B.  
; APPLICANT: Orellana, Ariel  
; APPLICANT: Hashimoto, Yasuhiro  
; APPLICANT: Swiedler, Stuart J.  
; APPLICANT: Wei, Zheng  
; APPLICANT: Ishihara, Masayuki  
; TITLE OF INVENTION: GLYCOSAMINOGLYCAN SPECIFIC  
; TITLE OF INVENTION: SULFOTRANSFERASES  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02110-2804

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM PS/2 Model 502 or 555X  
OPERATING SYSTEM: MS-DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/057,167  
FILING DATE: 19930430

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/899,432  
FILING DATE: 16 June 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CLARK, PAUL T.

REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 04020/015002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154

INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5  
TYPE: AMINO ACID  
STRANDEDNESS: N/A  
TOPOLOGY: N/A  
US-08-057-167-12

Query Match 56.5%; Score 13; DB 1; Length 5;  
Best Local Similarity 50.0%; Pred. No. 2e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5  
;:  
Db 2 IW 3

## RESULT 50

US-08-269-257-9

; Sequence 9, Application US/08269257  
; Patent No. 5550110  
; GENERAL INFORMATION:  
; APPLICANT: Cody, Wayne L.  
; APPLICANT: Doherty, Annette M.  
; APPLICANT: Topliss, John G.  
; TITLE OF INVENTION: Endothelin Antagonists II  
; NUMBER OF SEQUENCES: 64  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Warner-Lambert Company  
; STREET: 2800 Plymouth Rd.  
; CITY: Ann Arbor  
; STATE: MI  
; COUNTRY: US  
; ZIP: 48105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Ver. #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/269,257  
; FILING DATE:

CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/033,515  
FILING DATE: 31-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Tinney, Francis J.  
REGISTRATION NUMBER: 33069  
REFERENCE/DOCKET NUMBER: PD-4334-P2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 313 996-7295  
TELEFAX: 313 996-1553

INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-269-257-9

Query Match 56.5%; Score 13; DB 1; Length 5;  
Best Local Similarity 50.0%; Pred. No. 2e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5  
;:  
Db 4 IW 5

## RESULT 51

US-08-373-911-5  
; Sequence 5, Application US/08373911  
; Patent No. 5663296  
; GENERAL INFORMATION:  
; APPLICANT: Doherty, Annette M.  
; APPLICANT: Kornberg, Brian E.  
; APPLICANT: Nikam, Sham S.  
; TITLE OF INVENTION: Hydroxamate Inhibitors of  
; TITLE OF INVENTION: Endothelin Converting Enzyme  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Warner-Lambert Company  
; STREET: 2800 Plymouth Rd.  
; CITY: Ann Arbor  
; STATE: MI  
; COUNTRY: US  
; ZIP: 48105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible

```
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/373,911
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/070,161
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Tinney, Francis J.
; REGISTRATION NUMBER: 33069
; REFERENCE/DOCKET NUMBER: PD-4435
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 313 996-7295
; TELEFAX: 313 996-1553
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-373-911-5

Query Match 56.5%; Score 13; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. No. 2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5
Db 4 IW 5

RESULT 52
US-08-373-911-6
; Sequence 6, Application US/08373911
; Patent No. 5663296
; GENERAL INFORMATION:
; APPLICANT: Doherty, Annette M.
; APPLICANT: Kornberg, Brian E.
; APPLICANT: Nikam, Sham S.
; TITLE OF INVENTION: Hydroxamate Inhibitors of
; TITLE OF INVENTION: Endothelin Converting Enzyme
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Warner-Lambert Company
; STREET: 2800 Plymouth Rd.
; CITY: Ann Arbor
; STATE: MI
; COUNTRY: US
; ZIP: 48105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/070,161
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Tinney, Francis J.
; REGISTRATION NUMBER: 33069
; REFERENCE/DOCKET NUMBER: PD-4435
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 313 996-7295
; TELEFAX: 313 996-1553
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
```

```
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-373-911-6

Query Match 56.5%; Score 13; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. No. 2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5
Db 4 IW 5

RESULT 53
US-08-483-506A-1
; Sequence 1, Application US/08483506A
; Patent No. 5925529
; GENERAL INFORMATION:
; APPLICANT: COUGHLIN, ET AL.
; TITLE OF INVENTION: METHOD FOR DISCOVERY OF PEPTIDE AGONISTS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOLEY GODWARD LLP
; STREET: FIVE PALO ALTO SQUARE
; STREET: 3000 EL CAMINO REAL
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,506A
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: NEELEY, RICHARD L. PhD
; REGISTRATION NUMBER: 30,092
; REFERENCE/DOCKET NUMBER: UCAL-239/00US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 843-5000
; TELEFAX: (415) 857-0663
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-483-506A-1

Query Match 56.5%; Score 13; DB 2; Length 5;
Best Local Similarity 50.0%; Pred. No. 2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5
Db 2 MW 3

RESULT 54
US-08-483-506A-2
; Sequence 2, Application US/08483506A
; Patent No. 5925529
; GENERAL INFORMATION:
; APPLICANT: COUGHLIN, ET AL.
; TITLE OF INVENTION: METHOD FOR DISCOVERY OF PEPTIDE AGONISTS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOLEY GODWARD LLP
```



```
/ STREET: FIVE PALO ALTO SQUARE
/ STREET: 3000 EL CAMINO REAL
/ CITY: PALO ALTO
/ STATE: CALIFORNIA
/ COUNTRY: USA
/ ZIP: 94306-2155
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/483,506A
/ FILING DATE: 7-JUN-1995
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: NEELEY, RICHARD L. PhD
/ REGISTRATION NUMBER: 30,092
/ REFERENCE/DOCKET NUMBER: UCAL-239/00US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 843-5000
/ TELEFAX: (415) 857-0663
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 5 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ FEATURE:
/ NAME/KEY: Modified-site
/ LOCATION: 1
/ OTHER INFORMATION: /note= "Should be Formyl-Met"
/ US-08-483-506A-2

Query Match 56.5%; Score 13; DB 2; Length 5;
Best Local Similarity 50.0%; Pred. No. 2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5
Db 2 MW 3

RESULT 55
US-08-437-607A-38
/ Sequence 38, Application US/08437607A
/ Patent No. 5955579
/ GENERAL INFORMATION:
/ APPLICANT: Leonard, James N. Montminy, Marc R.
/ TITLE OF INVENTION: ISLET-SPECIFIC HOMEOPROTEIN AND TRANSCRIPTIONAL
/ TITLE OF INVENTION: REGULATOR OF INSULIN GENE EXPRESSION
/ NUMBER OF SEQUENCES: 49
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Klauber & Jackson
/ STREET: 411 Hackensack Avenue
/ CITY: Hackensack
/ STATE: New Jersey
/ COUNTRY: USA
/ ZIP: 07601
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/437,607A
/ FILING DATE: MAY 9, 1995
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Jackson Esq., David A.
/ REGISTRATION NUMBER: 26,742
/ REFERENCE/DOCKET NUMBER: 1110-1-001
/ TELECOMMUNICATION INFORMATION:
```

```
/ TELEPHONE: 201 487-5800
/ TELEFAX: 201 343-1684
/ TELEX: 133521
/ INFORMATION FOR SEQ ID NO: 38:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 5 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ DESCRIPTION: amino acids 47-51 of the homeobox homeodomain
/ ORIGINAL SOURCE:
/ ORGANISM: Rat
/ US-08-437-607A-38

Query Match 56.5%; Score 13; DB 2; Length 5;
Best Local Similarity 50.0%; Pred. No. 2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5
Db 1 IW 2

RESULT 56
US-08-981-122-2
/ Sequence 2, Application US/08981122B
/ Patent No. 6127339
/ GENERAL INFORMATION:
/ APPLICANT: Hatanaka, Yoshihiro
/ APPLICANT: Aritomi, Masaharu
/ TITLE OF INVENTION: Peptide for binding thereto a low density lipoprotein
/ FILE REFERENCE:
/ CURRENT APPLICATION NUMBER: US/08/981,122B
/ CURRENT FILING DATE: 1997-12-18
/ PRIOR APPLICATION NUMBER: JP 7-176904
/ PRIOR FILING DATE: 1995-06-21
/ PRIOR APPLICATION NUMBER: PCT/JP96/01734
/ PRIOR FILING DATE: 1996-06-21
/ NUMBER OF SEQ ID NOS: 90
/ SOFTWARE: Patent In Ver. 2.0
/ SEQ ID NO 2
/ LENGTH: 5
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Sequence of a peptide synthesized in Example 1 from L-form
/ Patent No. 6127339
/ OTHER INFORMATION: F-moc amino acids by solid phase method using a multipetide
/ OTHER INFORMATION: synthesizing system (RAMPS)
/ US-08-981-122-2

Query Match 56.5%; Score 13; DB 3; Length 5;
Best Local Similarity 50.0%; Pred. No. 2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5
Db 3 IW 4

RESULT 57
US-08-981-122-19
/ Sequence 19, Application US/08981122B
/ Patent No. 6127339
/ GENERAL INFORMATION:
/ APPLICANT: Hatanaka, Yoshihiro
/ APPLICANT: Aritomi, Masaharu
/ TITLE OF INVENTION: Peptide for binding thereto a low density lipoprotein
/ FILE REFERENCE:
/ CURRENT APPLICATION NUMBER: US/08/981,122B
/ CURRENT FILING DATE: 1997-12-18
/ PRIOR APPLICATION NUMBER: JP 7-176904
/ PRIOR FILING DATE: 1995-06-21
```

; PRIOR APPLICATION NUMBER: PCT/JP96/01734  
; PRIOR FILING DATE: 1996-06-21  
; NUMBER OF SEQ ID NOS: 90  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 19  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Sequence of a peptide synthesized in Example 2 from L-form  
; Patent No. 6127339  
; OTHER INFORMATION: F-moc amino acids by solid phase method using a multi-peptide  
; OTHER INFORMATION: synthesizing system (RAMPS)  
US-08-981-122-19

Query Match 56.5%; Score 13; DB 3; Length 5;  
Best Local Similarity 50.0%; Pred. No. 2e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5  
:|  
Db 3 MW 4

RESULT 58  
US-08-981-122-37  
; Sequence 37, Application US/08981122B  
; Patent No. 6127339  
; GENERAL INFORMATION:  
; APPLICANT: Hatanaka, Yoshihiro  
; APPLICANT: Arimoto, Masaharu  
; TITLE OF INVENTION: Peptide for binding thereto a low density lipoprotein  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/08/981,122B  
; PRIOR FILING DATE: 1997-12-18  
; PRIOR APPLICATION NUMBER: JP 7-176904  
; PRIOR FILING DATE: 1995-06-21  
; PRIOR APPLICATION NUMBER: PCT/JP96/01734  
; PRIOR FILING DATE: 1996-06-21  
; NUMBER OF SEQ ID NOS: 90  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 37  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: AMIDATION  
; LOCATION: 5  
; OTHER INFORMATION: Sequence of peptides synthesized in Examples 11 and 12 from L-form  
; Patent No. 6127339  
; OTHER INFORMATION: F-moc amino acids by solid phase method using an automatic peptide  
; OTHER INFORMATION: synthesizer (9050 plus peptide synthesizer)  
US-08-981-122-37

Query Match 56.5%; Score 13; DB 3; Length 5;  
Best Local Similarity 40.0%; Pred. No. 2e+05;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXLW 5  
:|  
Db 1 FFFRW 5

RESULT 59  
US-08-981-122-53  
; Sequence 53, Application US/08981122B  
; Patent No. 6127339  
; GENERAL INFORMATION:  
; APPLICANT: Hatanaka, Yoshihiro  
; APPLICANT: Arimoto, Masaharu  
; TITLE OF INVENTION: Peptide for binding thereto a low density lipoprotein  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/08/981,122B

; CURRENT FILING DATE: 1997-12-18  
; PRIOR APPLICATION NUMBER: JP 7-176904  
; PRIOR FILING DATE: 1995-06-21  
; PRIOR APPLICATION NUMBER: PCT/JP96/01734  
; PRIOR FILING DATE: 1996-06-21  
; NUMBER OF SEQ ID NOS: 90  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 53  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: AMIDATION  
; LOCATION: 5  
; OTHER INFORMATION: Sequence of peptides synthesized in Examples 11 and 12 from L-form  
; Patent No. 6127339  
; OTHER INFORMATION: F-moc amino acids by solid phase method using an automatic peptide  
; OTHER INFORMATION: synthesizer (9050 plus peptide synthesizer)  
US-08-981-122-53

Query Match 56.5%; Score 13; DB 3; Length 5;  
Best Local Similarity 50.0%; Pred. No. 2e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5  
:|  
Db 4 IW 5

RESULT 60  
US-08-981-122-72  
; Sequence 72, Application US/08981122B  
; Patent No. 6127339  
; GENERAL INFORMATION:  
; APPLICANT: Hatanaka, Yoshihiro  
; APPLICANT: Arimoto, Masaharu  
; TITLE OF INVENTION: Peptide for binding thereto a low density lipoprotein  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/08/981,122B  
; CURRENT FILING DATE: 1997-12-18  
; PRIOR APPLICATION NUMBER: JP 7-176904  
; PRIOR FILING DATE: 1995-06-21  
; PRIOR APPLICATION NUMBER: PCT/JP96/01734  
; PRIOR FILING DATE: 1996-06-21  
; NUMBER OF SEQ ID NOS: 90  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 72  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Sequence of a peptide synthesized in Comparative Example 2 from  
; Patent No. 6127339  
; OTHER INFORMATION: L-form F-moc amino acids by solid phase method using a  
; OTHER INFORMATION: multi-peptide synthesizing system (RAMPS)  
US-08-981-122-72

Query Match 56.5%; Score 13; DB 3; Length 5;  
Best Local Similarity 20.0%; Pred. No. 2e+05;  
Matches 1; Conservative 2; Mismatches 2; Indels 0; Gaps 0.

Qy 1 FXXLW 5  
:|  
Db 1 YIQWV 5

RESULT 61  
US-08-871-600A-4  
; Sequence 4, Application US/08871600A  
; Patent No. 6222021  
; GENERAL INFORMATION:  
; APPLICANT: Wainwright, No. 6222021man R.  
; APPLICANT: No. 6222021itsky, Thomas J.

;; TITLE OF INVENTION: Endotoxin Binding and Neutralizing  
;; TITLE OF INVENTION: Protein and Uses Thereof  
;; NUMBER OF SEQUENCES: 4  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
;; STREET: 1100 New York Avenue, N.W., Suite 600  
;; CITY: Washington  
;; STATE: District of Columbia  
;; COUNTRY: United States of America  
;; ZIP: 20005-3934  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/871,600A  
;; FILING DATE: 09-JUN-1997  
;; CLASSIFICATION: 514  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/704,872  
;; FILING DATE: 30-AUG-1996  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/264,244  
;; FILING DATE: 22-JUN-1994  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/883,457  
;; FILING DATE: 15-MAY-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/701,501  
;; FILING DATE: 16-MAY-1991  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/480,957  
;; FILING DATE: 16-FEB-1990  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/210,575  
;; FILING DATE: 23-JUN-1988  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Esmond, Robert W.  
;; REGISTRATION NUMBER: 32,893  
;; REFERENCE/DOCKET NUMBER: 1413.001000A/RWE  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (202) 371-2600  
;; TELEFAX: (202) 371-2540  
;; TELEX: 248636 SSK  
;; INFORMATION FOR SEQ ID NO: 4:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 5 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: not relevant  
;; MOLECULE TYPE: peptide  
US-08-871-600A-4

Query Match 56.5%; Score 13; DB 4; Length 5;  
Best Local Similarity 50.0%; Pred. No. 2e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5  
;|  
DB 3 IW 4

RESULT 62  
US-09-216-295-26  
; Sequence 26, Application US/09216295  
; Patent No. 6268328  
; GENERAL INFORMATION:  
; APPLICANT: Mitchinson, Colin  
; APPLICANT: Wendt, Dan J.  
; TITLE OF INVENTION: No. 6268328el Variant EGIII-Like Cellulase Compositions  
; FILE REFERENCE: GC555  
; CURRENT APPLICATION NUMBER: US/09/216,295

;; CURRENT FILING DATE: 1998-12-18  
;; NUMBER OF SEQ ID NOS: 41  
;; SOFTWARE: FastSEQ for Windows Version 3.0  
;; SEQ ID NO 26  
;; LENGTH: 5  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Peptide  
;; NAME/KEY: VARIANT  
;; LOCATION: (1)...(5)  
;; OTHER INFORMATION: Xaa = Leu, Phe, or Ile  
US-09-216-295-26

Query Match 56.5%; Score 13; DB 4; Length 5;  
Best Local Similarity 50.0%; Pred. No. 2e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5  
;|  
DB 4 IW 5

RESULT 63  
US-09-638-202A-51  
; Sequence 51, Application US/09638202A  
; Patent No. 6462189  
; GENERAL INFORMATION:  
; APPLICANT: Koeda, Shohei  
; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES  
; NUMBER OF SEQUENCES: 118  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.  
; STREET: 121 South Eighth Street, Ste. 1600  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: USA  
; ZIP: 55402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/638,202A  
; FILING DATE: 11-Aug-2000  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/096,749  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ann S. Viksnins  
; REGISTRATION NUMBER: 37,748  
; REFERENCE/DOCKET NUMBER: 109.034US1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (612) 373-6900  
; TELEFAX: (612) 339-3061  
; INFORMATION FOR SEQ ID NO: 51:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal  
; ORIGINAL SOURCE:  
; SEQUENCE DESCRIPTION: SEQ ID NO: 51:

US-09-638-202A-51  
Query Match 56.5%; Score 13; DB 4; Length 5;  
Best Local Similarity 50.0%; Pred. No. 2e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5  
:|  
Db 2 MW 3

RESULT 64  
PCT-US93-05412-12  
; Sequence 12, Application PC/TUS9305412  
; GENERAL INFORMATION:  
; APPLICANT: Hirschberg, Carlos B.  
; APPLICANT: Orellana, Ariel  
; APPLICANT: Hashimoto, Yasuhiro  
; APPLICANT: Swiedler, Stuart J.  
; APPLICANT: Wei, Zheng  
; APPLICANT: Ishihara, Masayuki  
; TITLE OF INVENTION: GLYCOSAMINOGLYCAN SPECIFIC  
; TITLE OF INVENTION: SULFOTRANSFERASES  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; COMPUTER: IBM PS/2 Model 502 or 55SX  
; OPERATING SYSTEM: MS-DOS (Version 5.0)  
; SOFTWARE: WordPerfect (Version 5.1)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/05412  
; FILING DATE: 19930607  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/899,432  
; FILING DATE: 16 June 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CLARK, PAUL T.  
; REGISTRATION NUMBER: 30,162  
; REFERENCE/DOCKET NUMBER: 04020/015002  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 542-5070  
; TELEFAX: (617) 542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5  
; TYPE: amino acid  
; STRANDEDNESS: N/A  
; TOPOLOGY: N/A  
PCT-US93-05412-12

Query Match 56.5%; Score 13; DB 5; Length 5;  
Best Local Similarity 50.0%; Pred. No. 2e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5  
:|  
Db 2 IW 3

RESULT 65  
PCT-US95-04171-9  
; Sequence 9, Application PC/TUS9504171  
; GENERAL INFORMATION:  
; APPLICANT: Cody, Wayne L.  
; APPLICANT: Doherty, Annette M.  
; APPLICANT: Topliss, John G.  
; TITLE OF INVENTION: Endothelin Antagonists II  
; NUMBER OF SEQUENCES: 64  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Warner-Lambert Company  
; STREET: 2800 Plymouth Rd.  
; CITY: Ann Arbor  
; STATE: MI  
; COUNTRY: US  
; ZIP: 48105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Ver. #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/04171  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/033,515  
; FILING DATE: 31-MAR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Timney, Francis J.  
; REGISTRATION NUMBER: 33069  
; REFERENCE/DOCKET NUMBER: PD-4334-P2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 313 996-7295  
; TELEFAX: 313 996-1553  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
PCT-US95-04171-9

Query Match 56.5%; Score 13; DB 5; Length 5;  
Best Local Similarity 50.0%; Pred. No. 2e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5  
:|  
Db 4 IW 5

RESULT 66  
5217869-16  
; Patent No. 5217869  
; APPLICANT: KAUVAR, LAWRENCE M.  
; TITLE OF INVENTION: METHOD TO PRODUCE IMMUNODIAGNOSTIC  
; REAGENTS  
; NUMBER OF SEQUENCES: 121  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/255,906  
; FILING DATE: 11-OCT-1988  
; SEQ ID NO:16:  
; LENGTH: 5  
5217869-16

Query Match 56.5%; Score 13; DB 6; Length 5;  
Best Local Similarity 50.0%; Pred. No. 2e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5  
:|  
Db 2 MW 3

RESULT 67  
5217869-22  
; Patent No. 5217869  
; APPLICANT: KAUVAR, LAWRENCE M.  
; TITLE OF INVENTION: METHOD TO PRODUCE IMMUNODIAGNOSTIC  
; REAGENTS  
; NUMBER OF SEQUENCES: 121

; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/255.906  
; FILING DATE: 11-OCT-1988  
; SEQ ID NO:22:  
; LENGTH: 5  
5217869-22

Query Match 56.5%; Score 13; DB 6; Length 5;  
Best Local Similarity 50.0%; Pred. No. 2e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5  
;:  
Db 1 MW 2

RESULT 68  
5217869-24  
; Patent No. 5217869  
; APPLICANT: KAUVAR, LAWRENCE M.  
; TITLE OF INVENTION: METHOD TO PRODUCE IMMUNODIAGNOSTIC  
; REAGENTS  
; NUMBER OF SEQUENCES: 121  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/255.906  
; FILING DATE: 11-OCT-1988  
; SEQ ID NO:24:  
; LENGTH: 5  
5217869-24

Query Match 56.5%; Score 13; DB 6; Length 5;  
Best Local Similarity 50.0%; Pred. No. 2e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5  
;:  
Db 3 MW 4

RESULT 69  
5217869-34  
; Patent No. 5217869  
; APPLICANT: KAUVAR, LAWRENCE M.  
; TITLE OF INVENTION: METHOD TO PRODUCE IMMUNODIAGNOSTIC  
; REAGENTS  
; NUMBER OF SEQUENCES: 121  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/255.906  
; FILING DATE: 11-OCT-1988  
; SEQ ID NO:34:  
; LENGTH: 5  
5217869-34

Query Match 56.5%; Score 13; DB 6; Length 5;  
Best Local Similarity 50.0%; Pred. No. 2e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5  
;:  
Db 1 MW 2

RESULT 70  
US-07-946-237-4  
; Sequence 4, Application US/07946237  
; Patent No. 5348874  
; GENERAL INFORMATION:  
; APPLICANT: Savakis, Charalampos  
; APPLICANT: Franz, Gerald H  
; APPLICANT: Loukeris, Athanasios  
; TITLE OF INVENTION: Eukaryotic Transposable Element  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02173  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/946.237  
; FILING DATE: 19920914  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: David E. Brook  
; REGISTRATION NUMBER: 22,592  
; REFERENCE/DOCKET NUMBER: BT92-01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 861-6240  
; TELEFAX: (617) 861-9540  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: AMINO ACID  
; MOLECULE TYPE: peptide  
US-07-946-237-4

Query Match 52.2%; Score 12; DB 1; Length 5;  
Best Local Similarity 50.0%; Pred. No. 2e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5  
;:  
Db 2 VW 3

RESULT 71  
US-08-290-448A-3  
; Sequence 3, Application US/08290448A  
; Patent No. 5676954  
; GENERAL INFORMATION:  
; APPLICANT: Rogers, Bruce  
; APPLICANT: Klapper, David G.  
; APPLICANT: Rafnar, Thorunn  
; APPLICANT: Kuo, Mei-Chang  
; TITLE OF INVENTION: Allergenic Proteins From Ragweed and Uses  
; NUMBER OF SEQUENCES: 93  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 60 State Street, suite 510  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109-1875  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/290.448A  
; FILING DATE: August 15, 1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/529,951  
; FILING DATE: May 29, 1990  
; APPLICATION NUMBER: US 07/325,365  
; FILING DATE: March 17, 1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Amy E. Mandragouras  
; REGISTRATION NUMBER: 36,207  
; REFERENCE/DOCKET NUMBER: IMI-018CN

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-08-290-448A-3

Query Match 52.2%; Score 12; DB 1; Length 5;  
Best Local Similarity 50.0%; Pred. No. 2e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5  
Db 1 VW 2

RESULT 72  
US-08-290-448A-39  
Sequence 39, Application US/08290448A  
Patent No. 5676954  
GENERAL INFORMATION:  
APPLICANT: Rogers, Bruce  
APPLICANT: Klapper, David G.  
APPLICANT: Rafnar, Thorunn  
APPLICANT: Kuo, Mei-chang  
TITLE OF INVENTION: Allergenic Proteins From Ragweed and Uses  
NUMBER OF SEQUENCES: 93  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 State Street, suite 510  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875

COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/290,448A  
FILING DATE: August 15, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/529,951  
FILING DATE: May 29, 1990  
APPLICATION NUMBER: US 07/325,365  
FILING DATE: March 17, 1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Amy E. Mandragouras  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: IMI-018CN  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-08-290-448A-39

Query Match 52.2%; Score 12; DB 1; Length 5;  
Best Local Similarity 50.0%; Pred. No. 2e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5

Db 1 VW 2

RESULT 73  
US-08-064-111C-22  
Sequence 22, Application US/08064111C  
Patent No. 5688760  
GENERAL INFORMATION:  
APPLICANT: Kemp, Bruce E.  
APPLICANT: Nicholson, Geoffrey C.  
APPLICANT: Martin, Thomas J.  
APPLICANT: Fenton, Anna J.  
APPLICANT: Hammonds, R. Glenn  
TITLE OF INVENTION: COMPOUNDS AND COMPOSITIONS WHICH INHIBIT  
TITLE OF INVENTION: BONE RESORPTION  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert,  
ADDRESSEE: Attn: W.H. Dreger  
STREET: 4 Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: United States  
ZIP: 94111-4187  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/064,111C  
FILING DATE: 12-AUG-1993  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/AU91/00580  
FILING DATE: 13-DEC-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: AU PK9567  
FILING DATE: 19-NOV-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: AU PK3879  
FILING DATE: 13-DEC-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Dreger, Walter H.  
REGISTRATION NUMBER: 24,190  
REFERENCE/DOCKET NUMBER: A-58456/WHI  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 781-1989  
TELEFAX: (415) 398-3249  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-064-111C-22

Query Match 52.2%; Score 12; DB 1; Length 5;  
Best Local Similarity 20.0%; Pred. No. 2e+05;  
Matches 1; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXLW 5  
Db 1 YRSAM 5

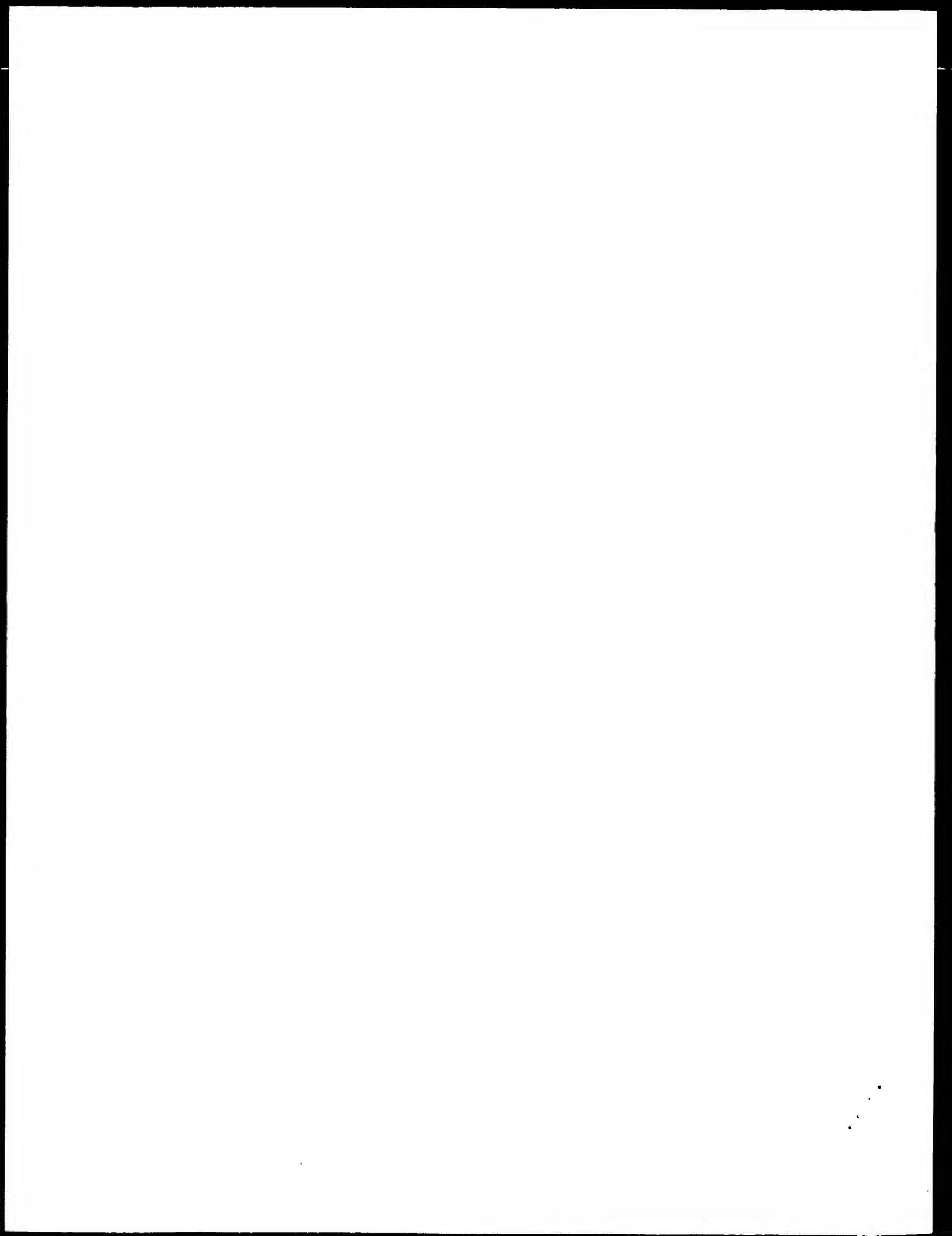
RESULT 74  
US-08-290-448A-3  
Sequence 3, Application US/08290448A  
Patent No. 5698204

GENERAL INFORMATION:  
APPLICANT: Rogers, Bruce  
APPLICANT: Klapper, David G.  
APPLICANT: Rafnar, Thorunn  
APPLICANT: Kuo, Mei-chang  
TITLE OF INVENTION: Allergenic Proteins From Ragweed and Uses  
NUMBER OF SEQUENCES: 93  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 State Street, suite 510  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/290,448A  
FILING DATE: August 15, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/529,951  
FILING DATE: May 29, 1990  
APPLICATION NUMBER: US 07/325,365  
FILING DATE: March 17, 1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Amy E. Mandragouras  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: IMI-018CN  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-08-290-448A-3

Query Match 52.2%; Score 12; DB 1; Length 5;  
Best Local Similarity 50.0%; Pred. No. 2e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 4 LW 5  
Db 1 VW 2

RESULT 75  
US-08-290-448A-39  
Sequence 39, Application US/08290448A  
Patent No. 5698204  
GENERAL INFORMATION:  
APPLICANT: Rogers, Bruce  
APPLICANT: Klapper, David G.  
APPLICANT: Rafnar, Thorunn  
APPLICANT: Kuo, Mei-chang  
TITLE OF INVENTION: Allergenic Proteins From Ragweed and Uses  
NUMBER OF SEQUENCES: 93  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 State Street, suite 510  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/290,448A  
FILING DATE: August 15, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/529,951  
FILING DATE: May 29, 1990  
APPLICATION NUMBER: US 07/325,365  
FILING DATE: March 17, 1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Amy E. Mandragouras  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: IMI-018CN  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-08-290-448A-39  
Query Match 52.2%; Score 12; DB 1; Length 5;  
Best Local Similarity 50.0%; Pred. No. 2e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 4 LW 5  
Db 1 VW 2  
Search completed: February 12, 2003, 10:53:11  
Job time : 15 secs





GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 12, 2003, 11:12:22 ; Search time 5.41667 Seconds  
(without alignments)  
88.739 Million cell updates/sec

Title: US-09-403-440A-1

Perfect score: 23

Sequence: 1 FXXLW 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 4984

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_73.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	87.0	15	2	PH1613
2	17	73.9	16	2	C37290
3	17	73.9	25	2	S68897
4	16	69.6	24	2	S38281
5	15	65.2	6	2	B34835
6	15	65.2	6	2	P70519
7	15	65.2	7	2	PH1602
8	15	65.2	8	2	A39308
9	15	65.2	9	2	A42444
10	15	65.2	9	2	S07241
11	15	65.2	10	2	E49033
12	15	65.2	10	2	F49033
13	15	65.2	11	1	LFTWE
14	15	65.2	11	2	C33652
15	15	65.2	12	2	A39169
16	15	65.2	12	2	I64829
17	15	65.2	12	2	A36093
18	15	65.2	12	2	I58273
19	15	65.2	13	2	PH1620
20	15	65.2	13	2	G37266
21	15	65.2	13	2	D37267
22	15	65.2	13	2	I51905
23	15	65.2	13	2	S54344
24	15	65.2	14	2	A35105
25	15	65.2	14	2	PH1625
26	15	65.2	14	2	PH1626
27	15	65.2	14	2	PH1627
28	15	65.2	14	2	PH1594
29	15	65.2	14	2	PH0801

Tcr delta chain V-  
T cell receptor al  
7 alpha-hydroxy-4-  
Ig H chain V-D-J r  
Ig H chain V-D-J r  
Ig H chain V-D-J r  
Tcr delta chain V-  
hydrogenase (SC 1.  
Ig H chain V-D-J r  
Ig H chain V-D-J r  
Tcr delta chain V-  
transforming prote  
caldesmon - rabbit  
Ig H chain V-D-J r  
T-cell receptor de  
shikimate 5-dehydr  
choline O-acetyltr

#### ALIGNMENTS

##### RESULT 1

PH1613

Ig H chain V-D-J region (clone B-less 17) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999

C;Accession: PH1613

R;Levinson, D.A.; Campos-Torres, J.; Leder, P.

J. Exp. Med. 178, 317-329, 1993

A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice

A;Reference number: PH1580; MUID:93301609; PMID:8315387

A;Accession: PH1613

A;Molecule type: DNA

A;Residues: 1-15 <LEV>

A;Experimental source: bone marrow pre-B lymphocyte

C;Keywords: immunoglobulin

Query Match 87.0%; Score 20; DB 2; Length 15;

Best Local Similarity 60.0%; Pred. No. 2.2e+02;

Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5

Db 10 FXXLW 14

##### RESULT 2

C37290

homeotic protein Gsh-3 - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jan-1992 #sequence\_revision 17-Jan-1992 #text\_change 17-Oct-1997

C;Accession: C37290; C38809

R;Singh, G.; Kaur, S.; Stock, J.L.; Jenkins, N.A.; Gilbert, D.J.; Copeland, N.G.; Potter

Proc. Natl. Acad. Sci. U.S.A. 88, 10706-10710, 1991

A;Title: Identification of 10 murine homeobox genes.

A;Reference number: A37290; MUID:92073356; PMID:1683707

A;Accession: C37290

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-16 <SIN>

C;Superfamily: unassigned homeobox proteins; homeobox homology

C;Keywords: DNA binding; homeobox; nucleus; transcription regulation

F;1-14/Domain: homeobox homology (fragment) <HOX>

Query Match 73.9%; Score 17; DB 2; Length 16;

Best Local Similarity 40.0%; Pred. No. 1e+03;

Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5

Db 12 FXXLW 16

```

RESULT 3
S68897
phospholipase A2 (EC 3.1.1.4), cytosolic - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 04-Dec-1997 #sequence_revision 12-Dec-1997 #text_change 17-Mar-1999
C;Accession: S68897
R;Gordon, R.D.; Leighton, I.A.; Campbell, D.G.; Cohen, P.; Creaney, A.; Wilton, D.C.; Ma
Eur. J. Biochem. 238, 690-697, 1996
A;Title: Cloning and expression of cytosolic phospholipase A(2) (cPLA(2)) and a natural
results in an increase in specific activity.
A;Reference number: S68897; MUID:96300233; PMID:8706669
A;Accession: S68897
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-25 <OR>
C;Keywords: carboxylic ester hydrolase; cytosol

Query Match      73.9%; Score 17; DB 2; Length 25;
Best Local Similarity 40.0%; Pred. No. 1.5e+03;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 FXXLW 5
      : ||
Db      13 YMSLW 17

RESULT 4
S38281
GTP-binding protein - clawed frog (fragments)
C;Species: Xenopus sp. (clawed frog)
C;Date: 19-May-1994 #sequence_revision 27-Feb-1997 #text_change 28-May-1999
C;Accession: S38281
R;Moore, M.S.; Blobel, G.
Nature 365, 661-663, 1993
A;Title: The GTP-binding protein Ran/TCA is required for protein import into the nucleus
A;Reference number: S38281; MUID:94019818; PMID:8413630
A;Accession: S38281
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-24 <MO>
C;Superfamily: ras transforming protein; translation elongation factor Tu homology
C;Keywords: GTP binding

Query Match      69.6%; Score 16; DB 2; Length 24;
Best Local Similarity 40.0%; Pred. No. 2.4e+03;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 FXXLW 5
      : ||
Db      13 FPNVW 17

RESULT 5
B34835
dnaA protein - Pseudomonas aeruginosa (fragment)
C;Species: Pseudomonas aeruginosa
C;Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 08-Oct-1999
C;Accession: B34835
R;Yee, T.W.; Smith, D.W.
Proc. Natl. Acad. Sci. U.S.A. 87, 1278-1282, 1990
A;Title: Pseudomonas chromosomal replication origins: a bacterial class distinct from Es
A;Reference number: A34835; MUID:90160310; PMID:2106132
A;Accession: B34835
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-6 <YEE>
A;Cross-references: GB:M30125; NID:G151419; PIDN:AAA25916.1; PID:G151421.
C;Keywords: DNA binding

Query Match      65.2%; Score 15; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2;
Db      2;

```

```

QY      4 LW 5
      ||
Db      5 LW 6

RESULT 6
PT0519
T-cell receptor beta chain V-D-J region (100-4C) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0519
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0519
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-6 <FEES>
A;Experimental source: adult thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match      65.2%; Score 15; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 LW 5
      ||
Db      4 LW 5

RESULT 7
PH1602
IG H chain V-D-J region (wild-type clone 313) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C;Accession: PH1602
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
A;Reference number: PH1580; MUID:93301609; PMID:8315387
A;Accession: PH1602
A;Molecule type: DNA
A;Residues: 1-7 <LEV>
A;Experimental source: bone marrow pre-B lymphocyte
C;Keywords: immunoglobulin

Query Match      65.2%; Score 15; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 LW 5
      ||
Db      5 LW 6

RESULT 8
A39308
glycine reductase (EC 1.4.99.-) sulphydryl protein C, alpha chain - Clostridium sticklan
C;Species: Clostridium sticklandii
C;Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 15-Aug-1997
C;Accession: A39308
R;Stadtman, T.C.; Davis, J.N.
J. Biol. Chem. 266, 22147-22153, 1991
A;Title: Glycine reductase protein C. Properties and characterization of its role in the
A;Reference number: A39308; MUID:92042141; PMID:1939235
A;Accession: A39308
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-8 <STA>
C;Function:
A;Description: glycine reductase complex catalyzes the reductive deamination of glycine
C;Keywords: ATP; oxido-reductase

```

Query Match 65.2%; Score 15; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5  
 ||  
 Db 5 LW 6

RESULT 9  
 A24244  
 adipokinetic hormone - bollworm  
 N;Alternate names: Hez-AKH  
 C;Species: Heliothis zea (bollworm, corn earworm, tomato fruitworm)  
 C;Date: 31-Mar-1998 #sequence\_revision 23-Mar-1995 #text\_change 31-Oct-1997  
 R;Jaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Holman, G.M.; Wagner, R.M.; Ridgway  
 Biochem. Biophys. Res. Commun. 135, 622-628, 1986  
 A;Title: Isolation and primary structure of a peptide from the corpora cardiaca of Helio  
 A;Reference number: A24244; MUID:86186794; PMID:3964263  
 A;Accession: A24244  
 A;Molecule type: protein  
 A;Residues: 1-9 <JAF>  
 C;Superfamily: adipokinetic hormone  
 C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic  
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F;9/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 65.2%; Score 15; DB 2; Length 9;  
 Best Local Similarity 40.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXLW 5  
 ||  
 Db 4 FTSSW 8

RESULT 10  
 S07241  
 litorin - Rohde's leaf frog  
 C;Species: Phyllomedusa rohdei (Rohde's leaf frog)  
 C;Date: 12-Feb-1993 #sequence\_revision 12-Mar-1993 #text\_change 18-Aug-2000  
 C;Accession: S07241  
 R;Barra, D.; Falconieri Erspamer, G.; Simmaco, M.; Bossa, F.; Melchiorri, P.; Erspamer,  
 FEBS Lett. 182, 53-56, 1985  
 A;Title: Rohdei-litorin: a new peptide from the skin of Phyllomedusa rohdei.  
 A;Reference number: S07241; MUID:85127560; PMID:3838283  
 A;Accession: S07241  
 A;Molecule type: protein  
 A;Residues: 1-9 <BAR>  
 C;Superfamily: gastrin-releasing peptide  
 C;Keywords: amidated carboxyl end; blocked amino end; neuropeptide; pyroglutamic acid  
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F;9/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 65.2%; Score 15; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5  
 ||  
 Db 2 LW 3

RESULT 11  
 E49033  
 T-cell receptor gamma chain V-D-J region - human (fragment)  
 C;Species: Homo sapiens (man)  
 C;Date: 19-Dec-1993 #sequence\_revision 25-Aug-1995 #text\_change 21-Jul-2000  
 C;Accession: E49033; D49033  
 R;Morita, C.T.; Verma, S.; Aparicio, P.; Martinez, C.; Spits, H.; Brenner, M.B.  
 Eur. J. Immunol. 21, 2999-3007, 1991

A;Title: Functionally distinct subsets of human gamma/delta T cells.

A;Reference number: A49033; MUID:92083926; PMID:1684157

A;Accession: E49033

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-10 <MOR>

A;Cross-references: GB:S72587; NID:g240696; PIDN:AAB20630.1; PID:g240697

A;Note: sequence extracted from NCBI backbone (NCBIN:72591, NCBIP:72595)

A;Accession: D49033

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-10 <MOR2>

A;Cross-references: GB:S72587; NID:g240696; PIDN:AAB20630.1; PID:g240697

A;Note: sequence extracted from NCBI backbone (NCBIN:72587, NCBIP:72589)

C;Keywords: T-cell receptor

Query Match 65.2%; Score 15; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5

||

Db 3 LW 4

#### RESULT 12

F49033

T-cell receptor gamma chain V-D-J region - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 19-Dec-1993 #sequence\_revision 17-Mar-2000 #text\_change 17-Mar-2000

C;Accession: F49033

R;Morita, C.T.; Verma, S.; Aparicio, P.; Martinez, C.; Spits, H.; Brenner, M.B.  
 Eur. J. Immunol. 21, 2999-3007, 1991

A;Title: Functionally distinct subsets of human gamma/delta T cells.

A;Reference number: A49033; MUID:92083926; PMID:1684157

A;Accession: F49033

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-10 <MOR>

A;Cross-references: GB:S72605; NID:g240700; PIDN:AAB20632.1; PID:g240701

A;Note: sequence extracted from NCBI backbone (NCBIN:72605, NCBIP:72606)

C;Keywords: T-cell receptor

Query Match 65.2%; Score 15; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5

||

Db 3 LW 4

#### RESULT 13

LFTWWE

probable trpEG leader peptide - Thermus aquaticus

C;Species: Thermus aquaticus

C;Date: 30-Jun-1991 #sequence\_revision 30-Jun-1991 #text\_change 16-Jul-1999

C;Accession: S03315

R;Sato, S.; Nakada, Y.; Kanaya, S.; Tanaka, T.

Biochim. Biophys. Acta 950, 303-312, 1988

A;Title: Molecular cloning and nucleotide sequence of Thermus thermophilus HB8 trpE and

A;Reference number: S03315; MUID:89000781; PMID:2844259

A;Accession: S03315

A;Molecule type: DNA

A;Residues: 1-11 <SAT>

A;Cross-references: EMBL:X07744; NID:g48261; PIDN:CAA30565.1; PID:g48262

A;Note: the source is designated as Thermus thermophilus HB8

C;Genetics:

A;Gene: trpL

C;Superfamily: probable trpEG leader peptide

Query Match 65.2%; Score 15; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 2e+03;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5  
||  
Db 7 LW 8

## RESULT 14

C53652  
rhlR protein - Pseudomonas aeruginosa (fragment)  
C;Species: Pseudomonas aeruginosa  
C;Date: 21-Jul-1995 #sequence\_revision 28-Jul-1995 #text\_change 21-Aug-1998  
C;Accession: C53652  
R;Ochser, U.A.; Flechter, A.; Reiser, J.  
J. Biol. Chem. 269, 19787-19795, 1994  
A;Title: Isolation, characterization, and expression in Escherichia coli of the Pseudomonas  
A;Reference number: A53652; MUID:94327521; PMID:8051059  
A;Accession: C53652  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-11 <OCH>  
A;Cross-references: GB:L28170  
C;Superfamily: sdiA regulatory protein

Query Match 65.2%; Score 15; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2e+03; 0; Indels 0; Gaps 0;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5  
||  
Db 9 LW 10

## RESULT 15

A29169  
phospholipase A2 (EC 3.1.1.4) precursor - sheep (fragment)  
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C;Date: 02-Jun-1988 #sequence\_revision 02-Jun-1988 #text\_change 31-Oct-1997  
C;Accession: A29169  
R;Dutilh, C.E.; Van Doren, P.J.; Verheul, F.E.A.M.; De Haas, G.H.  
Eur. J. Biochem. 53, 91-97, 1975  
A;Title: Isolation and properties of phospholipase A2 from ox and sheep pancreas.  
A;Reference number: A94661  
A;Accession: A29169  
A;Molecule type: protein  
A;Residues: 1-12 <DUT>  
C;Superfamily: phospholipase A2  
C;Keywords: carboxylic ester hydrolase; pyroglutamic acid  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 65.2%; Score 15; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5  
||  
Db 9 LW 10

Search completed: February 12, 2003, 11:15:30  
Job time : 5.41667 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 12, 2003, 11:11:31 ; Search time 2.70833 Seconds  
(without alignments)  
76.572 Million cell updates/sec

Title: US-09-403-440A-1  
Perfect score: 23  
Sequence: 1 FXXLW 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues  
Total number of hits satisfying chosen parameters: 1520

Minimum DB seq length: 0  
Maximum DB seq length: 25

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	69.6	6	1 E101_LITRU	P82096 litoria rub
2	16	69.6	24	1 RAN_XENLA	P52301 xenopus lae
3	15	65.2	9	1 LITR_PHYRO	P08946 phyllomedus
4	15	65.2	10	1 APE_CAPI	P80474 capnocytoph
5	15	65.2	11	1 LPW_TETH	P05624 thermus the
6	15	65.2	17	1 PH4_PERAM	P82697 periplaneta
7	15	65.2	20	1 AIBG_EQUNS	P39090 equus asinu
8	15	65.2	21	1 NDK_CANAL	Q9ur66 candida alb
9	15	65.2	22	1 CR31_LITSP	P56238 litoria spl
10	15	65.2	22	1 CR32_LITCE	P56239 litoria cae
11	15	65.2	22	1 CR33_LITCE	P56240 litoria cae
12	15	65.2	22	1 CR34_LITCE	P56241 litoria cae
13	15	65.2	23	1 CR41_LITCE	P56242 litoria cae
14	15	65.2	23	1 CR42_LITCE	P56243 litoria cae
15	15	65.2	23	1 CR43_LITCE	P56244 litoria cae
16	15	65.2	23	1 SODP_PICAB	P29427 picea abies
17	15	65.2	24	1 DMS6_PHYBI	P81490 phyllomedus
18	15	65.2	24	1 PCL1_PACGO	P82421 pachycondyl
19	15	65.2	24	1 PCL2_PACGO	P82422 pachycondyl
20	15	65.2	24	1 VGG_BPAL3	P08766 bacterioph
21	15	65.2	24	1 YJKD_NEUCR	P22702 neurospora
22	15	65.2	25	1 VGJ_BPG4	P03652 bacterioph
23	14	60.9	20	1 COXA_THUOB	P80972 thunnus obe
24	14	60.9	25	1 COXC_THUOB	P80973 thunnus obe
25	14	60.9	25	1 COX1_PARVE	Q00502 paracoccus
26	13	56.5	8	1 AKHG_GRYBI	P14086 gryllus bim
27	13	56.5	8	1 AKH_LIBAU	P25418 libellula a
28	13	56.5	10	1 HTF_HELZE	P16353 heliothis z
29	13	56.5	13	1 YPNP_PHOLI	P41122 photorhabdu
30	13	56.5	14	1 LPW_RHIME	P18854 rhizobium m
31	13	56.5	14	1 PKK6_PERAM	P82693 periplaneta
32	13	56.5	17	1 PKK5_PERAM	P82617 periplaneta
33	13	56.5	21	1 BTX_ATRBI	P80163 atractaspis

## ALIGNMENTS

## RESULT 1

E101\_LITRU STANDARD; PRT; 6 AA.  
AC P82096;  
DT 15-JUN-2002 (Rel. 41, Created)  
DT 15-JUN-2002 (Rel. 41, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Electrin 1.  
OS Litoria rubella (Desert tree frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;  
OC Pelodyadinae; Litoria.  
OX NCBI\_TaxID=104895;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Skin secretion;  
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;  
RT "Peptides from the skin glands of the Australian buzzing tree frog  
RT Litori electrica. Comparison with the skin peptides from Litoria  
RT rubella.";  
RL Aust. J. Chem. 52:639-645(1999).  
CC -!- SUBCELLULAR LOCATION: SECRETED.  
KW Amphibian skin; Amidation.  
FT MOD RES 6  
SQ SEQUENCE 6 AA; 792 MW; 668370472C9A000 CRC64;

Query Match 69.6%; Score 16; DB 1; Length 6;  
Best Local Similarity 40.0%; Pred. No. 1.1e+05;  
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXLW 5  
| : |  
DB 1 FVPIW 5

## RESULT 2

RAN\_XENLA STANDARD; PRT; 24 AA.  
AC P52301;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE GTP-binding nuclear protein RAN (TC4) (fragments).  
GN RAN.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Ovary;  
RX MEDLINE=94019818; PubMed=8413630;  
RA Moore M.S., Blobel G.;  
RT "The GTP-binding protein Ran/TC4 is required for protein import into  
RT the nucleus.";

```

RL Nature 365:661-663(1993).
CC -!- FUNCTION: GTP-BINDING PROTEIN INVOLVED IN NUCLEOCYTOPLASMIC
CC TRANSPORT. REQUIRED FOR THE IMPORT OF PROTEIN INTO THE NUCLEUS AND
CC ALSO FOR RNA EXPORT. INVOLVED IN CHROMATIN CONDENSATION AND
CC CONTROL OF CELL CYCLE (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: BELONGS TO THE RAN FAMILY IN THE RAS SUPERFAMILY.
CC HSP; P17080; IAK2K.
DR InterPro: IPR002041; RAN.
DR PROSITE: PS01115; RAN; PARTIAL.
KW GTP-binding; Nuclear protein; Protein transport.
FT NON_TER 1
FT NON_CONS 13 14 GTP (BY SIMILARITY).
FT NP_BIND 18 22
FT NON_TER 24 24
FT SEQUENCE 24 AA; 2657 MW; B69F83236247A250 CRC64;
SQ
Query Match 69.6%; Score 16; DB 1; Length 24;
Best Local Similarity 40.0%; Pred. No. 9.1e+02;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 FXXLM 5
DB 13 FNVW 17
RESULT 3
LITR PHYRO STANDARD; PRT; 9 AA.
AC P08946;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Rhodei-litorin.
OS Phyllomedusa rohdei (Rhode's leaf frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Phyllomedusinae; Phyllomedusa.
OX NCBI_TaxID=8394;
RN [1]
RP SEQUENCE.
RX MEDLINE=85127560; PubMed=3838283;
RA Barra D., Erspamer G.F., Simmaco M., Bossa F., Melchiorri P.,
RA Erspamer V.;
RT "Rhodei-litorin: a new peptide from the skin of Phyllomedusa rohdei.";
RL FEBS Lett. 182:53-56(1985).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN
CC FAMILY.
DR PIR; S07241; S07241.
DR InterPro: IPR000874; Bombesin.
DR Pfam; PF02044; Bombesin; 1.
DR PROSITE; PS00257; BOMBESIN; 1.
KW Bombesin family; Amidation.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 9 9 AMIDATION.
FT SEQUENCE 9 AA; 1090 MW; 4ECC1B861ADC377 CRC64;
SQ
Query Match 65.2%; Score 15; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 LW 5
DB 2 LW 3
RESULT 4
APE CAPGI 1
ID APE_CARGI STANDARD; PRT; 10 AA.
AC P80474;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)

```

```

DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Aminopeptidase (EC 3.4.11.-) (Fragment).
OS Capnocytophaga gingivalis.
OC Bacteria; Bacteroidetes; Flavobacteriia; Flavobacteriales;
OC Flavobacteriaceae; Capnocytophaga.
OX NCBI_TaxID=1017;
RN [1]
RP SEQUENCE.
RC STRAIN=ATCC 33624;
RX MEDLINE=96118234; PubMed=8574402;
RA Spratt D.A., Greenman J., Schaffer A.G.;
RT "Capnocytophaga gingivalis aminopeptidase: a potential virulence
RT factor.";
RL Microbiology 141:3087-3093(1995).
CC -!- FUNCTION: AMINOPEPTIDASE WHICH HYDROLYZES SUBSTRATES WITH FREE N-
CC TERMINAL AMINO ACID RESIDUES BUT NOT N-TERMINAL BLOCKED ONES.
CC OPTIMUM ACTIVITY IS MEASURED AT PH 7.5. MAY BE IMPORTANT IN THE
CC NUTRITION AND PATHOGENESIS OF THE ORGANISM IN THE HUMAN ORAL
CC CAVITY.
CC -!- COFACTOR: REQUIRES MAGNESIUM OR CALCIUM.
KW Hydrolase; Aminopeptidase; Magnesium; Calcium.
FT NON_TER 1 1
FT NON_TER 10 10
FT SEQUENCE 10 AA; 1306 MW; 00C0A6DB43772694 CRC64;
SQ
Query Match 65.2%; Score 15; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 LW 5
DB 5 LW 6
RESULT 5
LPW THETH STANDARD; PRT; 11 AA.
AC P05624;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Ttp operon leader peptide.
GN TRPL.
OS Thermus thermophilus.
OC Bacteria; Thermus/Deinococcus group; Deinococci; Thermales;
OC Thermaceae; Thermus.
OX NCBI_TaxID=274;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HB8 / ATCC 27634;
RX MEDLINE=89000781; PubMed=2844259;
RA Sato S., Nakada Y., Kanaya S., Tanaka T.;
RT "Molecular cloning and nucleotide sequence of Thermus thermophilus
RT HB8 tpe and trpg.";
RL Biochim. Biophys. Acta 950:303-312(1988).
CC -!- FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS
CC OF TRYPTOPHAN.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X07744; CAA30565.1; -.
DR PIR; S03315; LFTWWE.
KW Tryptophan biosynthesis; Leader peptide.
SQ SEQUENCE 11 AA; 1228 MW; 364B295A772DC5A7 CRC64;
Query Match 65.2%; Score 15; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;

```

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5  
Db 7 LW 8

RESULT 6  
PH4\_PERAM  
ID\_NDK\_CANAL STANDARD; PRT; 17 AA.  
AC P82697;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Peptide hormone 4 (Pea-VLS-amide).  
OS Periplaneta americana (American cockroach).  
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
OC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;  
OC Blattelloidea; Blattidae; Periplaneta.  
OX NCBI\_TaxID=6978;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RC TISSUE=Abdominal perisymphathetic organs;  
RX MEDLINE=20140865; PubMed=10676456;  
RA Predel R., Eckert M., Holman G.M.;  
RT "The unique neuropeptide pattern in abdominal perisymphathetic organs  
of insects.";  
RL Ann. N.Y. Acad. Sci. 897:282-290 (1999).  
CC -!- FUNCTION: UNKNOWN.  
CC -!- MASS SPECTROMETRY: MW=1966.48; METHOD=MALDI.  
KW Neuropeptide; Amidation.  
FT MOD RES 17  
SQ SEQUENCE 17 AA; 1968 MW; CAAPF57ECD8218A9 CRC64;

Query Match 65.2%; Score 15; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5  
Db 4 LW 5

RESULT 7  
A1BG\_EQUAS  
ID\_A1BG\_EQUAS STANDARD; PRT; 20 AA.  
AC P39090;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 01-FEB-1995 (Rel. 31, Last annotation update)  
DE Alpha-1B-glycoprotein (Postalbumin) (Fragment).  
OS Equus asinus (Donkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
OX NCBI\_TaxID=9793;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Plasma;  
RX MEDLINE=91330579; PubMed=1868686;  
RA Patterson S.D., Bell K., Shaw D.C.;  
RT "Donkey and horse alpha 1 B-glycoprotein: partial characterization  
and new alleles.";  
RL Comp. Biochem. Physiol. 98B:523-528 (1991).  
CC -!- FUNCTION: PLASMA GLYCOPROTEIN OF UNKNOWN FUNCTION.  
CC -!- SUBCELLULAR LOCATION: Extracellular.  
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.  
KW Immunoglobulin domain; Glycoprotein; Plasma.  
FT NON TER 20  
SQ SEQUENCE 20 AA; 2197 MW; 65857DFDA68EBD9F CRC64;

Query Match 65.2%; Score 15; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5  
Db 10 LW 11

RESULT 8  
NDK\_CANAL  
ID\_NDK\_CANAL STANDARD; PRT; 21 AA.  
AC Q9UR66;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Nucleoside diphosphate kinase (EC 2.7.4.6) (NDK) (NDP kinase) (NDPK)  
(Fragment).  
GN NDK1  
OS Candida albicans (Yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.  
OX NCBI\_TaxID=5476;  
RN [1]  
RP SEQUENCE, AND CHARACTERIZATION.  
RX MEDLINE=96019963; PubMed=7487065;  
RA Biondi R.M., Veron M., Walz K., Passeron S.;  
RT "Candida albicans nucleoside-diphosphate kinase: purification and  
characterization.";  
RL Arch. Biochem. Biophys. 323:187-194 (1995).  
CC -!- FUNCTION: MAJOR ROLE IN THE SYNTHESIS OF NUCLEOSIDE TRIPHOSPHATES  
OTHER THAN ATP (BY SIMILARITY).  
CC -!- CATALYTIC ACTIVITY: ATP + nucleoside diphosphate = ADP +  
nucleoside triphosphate.  
CC -!- SUBUNIT: HOMOHEXAMER.  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -!- SIMILARITY: BELONGS TO THE NDK FAMILY.  
HSP; P22887; 1LWX.  
DR InterPro; IPR001564; NDK.  
DR Pfam; PF00334; NDK; 1.  
DR PROSITE; PS00469; NDP\_KINASES; 1.  
KW Transferase; Kinase; ATP-binding.  
FT NON TER 1  
FT ACT\_SITE 4  
FT NON\_TER 21  
SQ SEQUENCE 21 AA; 2379 MW; 9DABB3A325947001 CRC64;

Query Match 65.2%; Score 15; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5  
Db 18 LW 19

RESULT 9  
CR31\_LITSP  
ID\_CR31\_LITSP STANDARD; PRT; 22 AA.  
AC P56238;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Caerin 3.1.  
OS Litoria splendida (Magnificent tree frog), and  
Litoria gilleni (Centralian tree frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;  
OC Pelodyadinae; Litoria.  
OX NCBI\_TaxID=30345, 39405;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RC SECTES=L.splendida; TISSUE=Parotoid gland;  
RA Stone D.J.M., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.;  
RT "Peptides from Australian frogs. Structures of the caerins and  
caeridin 1 from Litoria splendida.";

J. Chem. Soc. Perkin Trans. 1:3173-3178(1992).

[2]  
 RN SEQUENCE, AND MASS SPECTROMETRY.  
 RC SPECIES=L.gilleni; TISSUE=parotoid gland;  
 RA Waugh R.J., Stone D.J.M., Bowie J.H., Wallace J.C., Tyler M.J.;  
 RT "Peptides from Australian frogs. The structures of the caerins and  
 caeridins from Litoria gilleni."  
 RL J. Chem. Res. 139:937-961(1993).  
 CC -1- FUNCTION: ANTIBACTERIAL PEPTIDE, THAT ADOPTS AN ALPHA HELICAL  
 CONFORMATION WHICH CAN DISRUPT BACTERIAL MEMBRANES. EACH CAERIN  
 CC DISPLAYS A DIFFERENT ANTIMICROBIAL SPECIFICITY.  
 CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN PAROTOID AND/OR ROSTRAL  
 CC GLANDS.  
 CC -1- MASS SPECTROMETRY: MW=2382; METHOD=FAB.  
 CC Antibiotic; Amphibian skin; Amidation.  
 KW MOD RES 22 22  
 FT SEQUENCE 22 AA; 2385 MW; 1D4411E2E9D43739 CRC64;  
 SQ

Query Match 65.2%; Score 15; DB 1; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5  
 Db 2 LW 3

RESULT 10  
 CR32\_LITCE  
 ID CR32\_LITCE STANDARD; PRT; 22 AA.  
 AC P56239;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Caerin 3.2.  
 OS Litoria caerulea (Green tree frog).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;  
 CC Pelodyadinae; Litoria.  
 CC NCBI\_TaxID=30344;  
 OX [1]  
 RN SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Parotoid gland;  
 RA Stone D.J.M., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.;  
 RT "Peptides from Australian frogs. The structures of the caerins from  
 Litoria caerulea."  
 RL J. Chem. Res. 138:910-936(1993).  
 CC -1- FUNCTION: ANTIBACTERIAL PEPTIDE, THAT ADOPTS AN ALPHA HELICAL  
 CONFORMATION WHICH CAN DISRUPT BACTERIAL MEMBRANES. EACH CAERIN  
 CC DISPLAYS A DIFFERENT ANTIMICROBIAL SPECIFICITY.  
 CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN PAROTOID AND/OR ROSTRAL  
 CC GLANDS.  
 CC -1- MASS SPECTROMETRY: MW=2397; METHOD=FAB.  
 CC Antibiotic; Amphibian skin; Amidation.  
 KW MOD RES 22 22  
 FT SEQUENCE 22 AA; 2400 MW; 1D440B3829D4367C CRC64;  
 SQ

Query Match 65.2%; Score 15; DB 1; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5  
 Db 2 LW 3

RESULT 11  
 CR33\_LITCE  
 ID CR33\_LITCE STANDARD; PRT; 22 AA.  
 AC P56240;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE

DE Caerin 3.3.  
 OS Litoria caerulea (Green tree frog).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;  
 CC Pelodyadinae; Litoria.  
 CC NCBI\_TaxID=30344;  
 OX [1]  
 RN SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Parotoid gland;  
 RA Stone D.J.M., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.;  
 RT "Peptides from Australian frogs. The structures of the caerins from  
 Litoria caerulea."  
 RL J. Chem. Res. 138:910-936(1993).  
 CC -1- FUNCTION: ANTIBACTERIAL PEPTIDE, THAT ADOPTS AN ALPHA HELICAL  
 CONFORMATION WHICH CAN DISRUPT BACTERIAL MEMBRANES. EACH CAERIN  
 CC DISPLAYS A DIFFERENT ANTIMICROBIAL SPECIFICITY.  
 CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN PAROTOID AND/OR ROSTRAL  
 CC GLANDS.  
 CC -1- MASS SPECTROMETRY: MW=2424; METHOD=FAB.  
 CC Antibiotic; Amphibian skin; Amidation.  
 KW MOD RES 22 22  
 FT SEQUENCE 22 AA; 2427 MW; 1D440B2200D4367C CRC64;  
 SQ

Query Match 65.2%; Score 15; DB 1; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5  
 Db 2 LW 3

RESULT 12  
 CR34\_LITCE  
 ID CR34\_LITCE STANDARD; PRT; 22 AA.  
 AC P56241;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Caerin 3.4.  
 OS Litoria caerulea (Green tree frog).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;  
 CC Pelodyadinae; Litoria.  
 CC NCBI\_TaxID=30344;  
 OX [1]  
 RN SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Parotoid gland;  
 RA Stone D.J.M., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.;  
 RT "Peptides from Australian frogs. The structures of the caerins from  
 Litoria caerulea."  
 RL J. Chem. Res. 138:910-936(1993).  
 CC -1- FUNCTION: ANTIBACTERIAL PEPTIDE, THAT ADOPTS AN ALPHA HELICAL  
 CONFORMATION WHICH CAN DISRUPT BACTERIAL MEMBRANES. EACH CAERIN  
 CC DISPLAYS A DIFFERENT ANTIMICROBIAL SPECIFICITY.  
 CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN PAROTOID AND/OR ROSTRAL  
 CC GLANDS.  
 CC -1- MASS SPECTROMETRY: MW=2452; METHOD=FAB.  
 CC Antibiotic; Amphibian skin; Amidation.  
 KW MOD RES 22 22  
 FT SEQUENCE 22 AA; 2455 MW; 3AB40B2200D43663 CRC64;  
 SQ

Query Match 65.2%; Score 15; DB 1; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

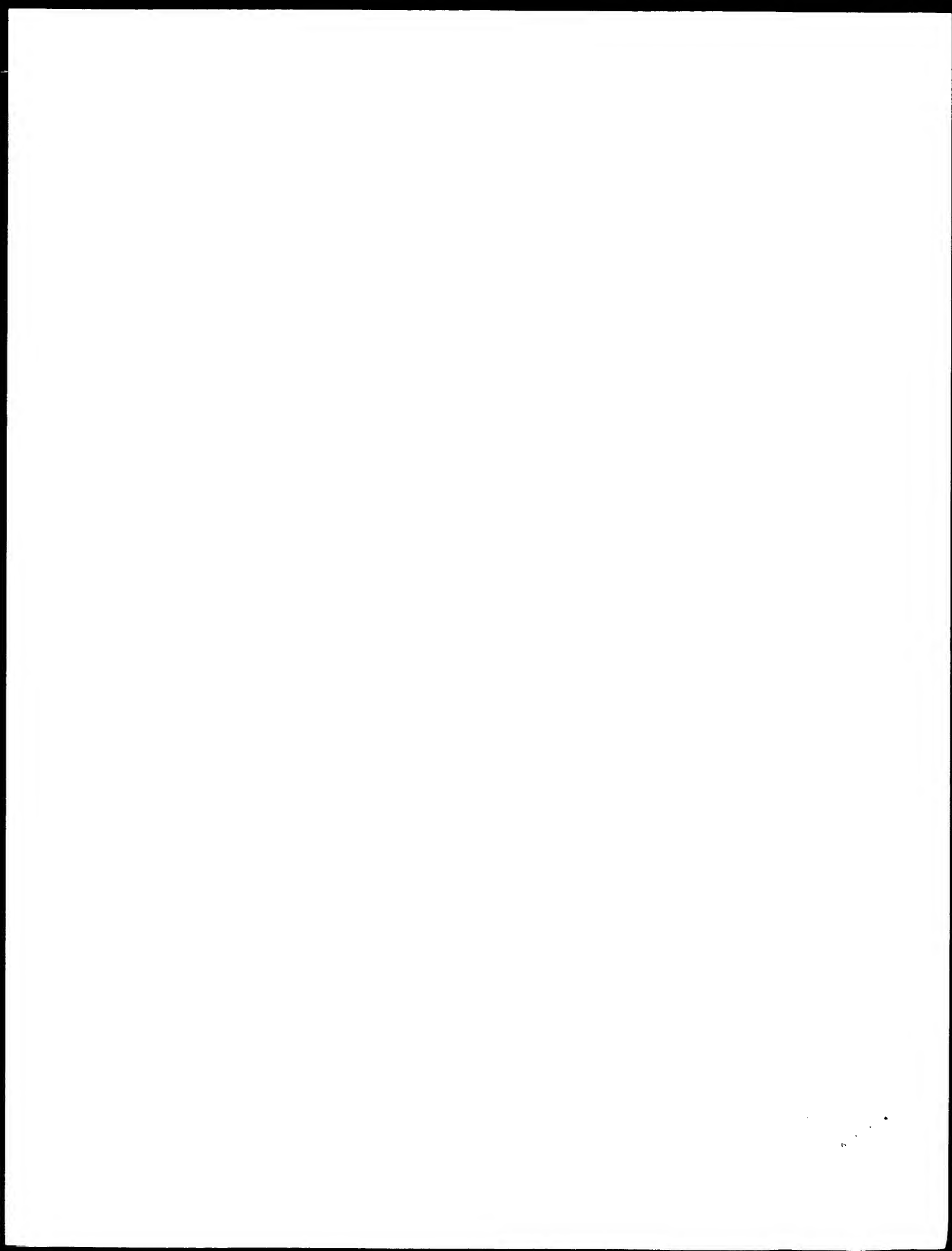
QY 4 LW 5  
 Db 2 LW 3

RESULT 13  
 CR41\_LITCE



ID CR41\_LITCE STANDARD; PRT; 23 AA.  
 AC P56242;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Caerin 4.1.  
 OS Litoria caerulea (Green tree frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;  
 OC Pelodyadinae; Litoria.  
 OX NCBI\_TaxID=30344;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Parotoid gland;  
 RA Stone D.J.M., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.;  
 RT "Peptides from Australian frogs. The structures of the caerins from  
 Litoria caerulea".  
 RL J. Chem. Res. 138:910-936(1993).  
 CC -1- FUNCTION: ANTIBACTERIAL PEPTIDE, THAT ADOPTS AN ALPHA HELICAL  
 CONFORMATION WHICH CAN DISRUPT BACTERIAL MEMBRANES. EACH CAERIN  
 DISPLAYS A DIFFERENT ANTIMICROBIAL SPECIFICITY.  
 CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN PAROTOID AND/OR ROSTRAL  
 GLANDS.  
 CC -1- MASS SPECTROMETRY: MW=2326; METHOD=FAB.  
 KW Antibiotic; Amphibian skin; Amidation.  
 FT MOD RES 23 23 AMIDATION.  
 SQ SEQUENCE 23 AA; 2329 MW; 83BFD80B6ADDC87 CRC64;  
  
 Query Match 65.2%; Score 15; DB 1; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 4 LW 5  
 DB 2 LW 3  
  
 RESULT 14  
 CR42\_LITCE STANDARD; PRT; 23 AA.  
 AC P56243;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Caerin 4.2.  
 OS Litoria caerulea (Green tree frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;  
 OC Pelodyadinae; Litoria.  
 OX NCBI\_TaxID=30344;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Parotoid gland;  
 RA Stone D.J.M., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.;  
 RT "Peptides from Australian frogs. The structures of the caerins from  
 Litoria caerulea".  
 RL J. Chem. Res. 138:910-936(1993).  
 CC -1- FUNCTION: ANTIBACTERIAL PEPTIDE, THAT ADOPTS AN ALPHA HELICAL  
 CONFORMATION WHICH CAN DISRUPT BACTERIAL MEMBRANES. EACH CAERIN  
 DISPLAYS A DIFFERENT ANTIMICROBIAL SPECIFICITY.  
 CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN PAROTOID AND/OR ROSTRAL  
 GLANDS.  
 CC -1- MASS SPECTROMETRY: MW=2340; METHOD=FAB.  
 KW Antibiotic; Amphibian skin; Amidation.  
 FT MOD RES 23 23 AMIDATION.  
 SQ SEQUENCE 23 AA; 2343 MW; 83BFD8516ADDC87 CRC64;  
  
 Query Match 65.2%; Score 15; DB 1; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 4 LW 5  
 DB 2 LW 3

Db 2 LW 3  
  
 RESULT 15  
 CR43\_LITCE STANDARD; PRT; 23 AA.  
 AC P56244;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Caerin 4.3.  
 OS Litoria caerulea (Green tree frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;  
 OC Pelodyadinae; Litoria.  
 OX NCBI\_TaxID=30344;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Parotoid gland;  
 RA Stone D.J.M., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.;  
 RT "Peptides from Australian frogs. The structures of the caerins from  
 Litoria caerulea".  
 RL J. Chem. Res. 138:910-936(1993).  
 CC -1- FUNCTION: ANTIBACTERIAL PEPTIDE, THAT ADOPTS AN ALPHA HELICAL  
 CONFORMATION WHICH CAN DISRUPT BACTERIAL MEMBRANES. EACH CAERIN  
 DISPLAYS A DIFFERENT ANTIMICROBIAL SPECIFICITY.  
 CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN PAROTOID AND/OR ROSTRAL  
 GLANDS.  
 CC -1- MASS SPECTROMETRY: MW=2353; METHOD=FAB.  
 KW Antibiotic; Amphibian skin; Amidation.  
 FT MOD RES 23 23 AMIDATION.  
 SQ SEQUENCE 23 AA; 2356 MW; B98FDD80B6ADDC9D CRC64;  
  
 Query Match 65.2%; Score 15; DB 1; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 4 LW 5  
 DB 2 LW 3  
  
 Search completed: February 12, 2003, 11:14:05  
 Job time : 3.70833 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 12, 2003, 11:12:02 ; Search time 9.79167 Seconds  
(without alignments)  
105.216 Million cell updates/sec

Title: US-09-403-440A-1

Perfect score: 23 FXXLW 5

Sequence: 1 FXXLW 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 segs, 206047115 residues

Total number of hits satisfying chosen parameters: 9297

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_21.\*  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phase.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_rvirus.\*  
16: sp\_bacteriap.\*  
17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	20	87.0	22	13	Q9W6D7	Q9W6D7 gallus gall
2	20	87.0	25	4	Q9NP68	Q9NP68 homo sapien
3	20	87.0	25	13	Q9UWV3	Q9UWV3 brachydanio
4	19	82.6	21	11	Q61943	Q61943 mus musculus
5	18	78.3	23	4	Q9BYM6	Q9BYM6 homo sapien
6	17	73.9	12	2	Q53579	Q53579 rhodobacter
7	17	73.9	15	2	Q53580	Q53580 rhodobacter
8	17	73.9	16	11	Q9QW76	Q9QW76 mus sp. hom
9	17	73.9	20	11	Q35353	Q35353 rattus norv
10	17	73.9	20	12	Q66548	Q66548 human herpe
11	16	69.6	17	15	Q72017	Q72017 human immun
12	16	69.6	25	2	Q9S0U6	Q9S0U6 shigella so
13	16	69.6	25	16	P72429	P72429 salmonella
14	15	65.2	8	2	O85406	O85406 coxiella bu
15	15	65.2	9	4	O95953	O95953 homo sapien
16	15	65.2	9	9	Q98366	Q98366 bacterioph

17	15	65.2	10	4	Q8WTT4	Q8WTT4 homo sapien
18	15	65.2	10	8	Q8SHF6	Q8SHF6 chameleleo m
19	15	65.2	10	11	Q9ESU5	Q9ESU5 mus musculus
20	15	65.2	11	2	Q47602	Q47602 escherichia
21	15	65.2	11	4	Q9UCR1	Q9UCR1 homo sapien
22	15	65.2	11	4	Q9UB69	Q9UB69 homo sapien
23	15	65.2	11	6	Q9GL48	Q9GL48 sus scrofa
24	15	65.2	11	7	O77895	O77895 oreochromis
25	15	65.2	11	7	O77896	O77896 oreochromis
26	15	65.2	11	8	Q9G649	Q9G649 otoecryptis
27	15	65.2	12	11	Q63579	Q63579 rattus norv
28	15	65.2	12	15	Q98240	Q98240 human immun
29	15	65.2	13	2	Q49230	Q49230 mycoplasma
30	15	65.2	13	8	Q9XLI2	Q9XLI2 bemisia tab
31	15	65.2	14	2	Q9R782	Q9R782 bacillus li
32	15	65.2	14	4	Q99902	Q99902 homo sapien
33	15	65.2	14	6	O77538	O77538 bos taurus
34	15	65.2	14	8	Q9MT61	Q9MT61 allium cepa
35	15	65.2	14	8	Q9MRV1	Q9MRV1 allium sati
36	15	65.2	14	8	Q9MRV4	Q9MRV4 allium port
37	15	65.2	14	8	Q9MT8	Q9MT8 alooe vera (
38	15	65.2	14	11	Q9JHK8	Q9JHK8 mus musculu
39	15	65.2	14	15	Q98Y97	Q98Y97 human immun
40	15	65.2	15	4	Q96RX1	Q96RX1 homo sapien
41	15	65.2	16	11	Q920J2	Q920J2 mus musculu
42	15	65.2	16	13	Q8UUF8	Q8UUF8 dendragapus
43	15	65.2	16	13	Q8UUF7	Q8UUF7 bonasa bona
44	15	65.2	16	13	Q8UUF6	Q8UUF6 pavo crista
45	15	65.2	16	13	Q8UUF5	Q8UUF5 alectoris c

## ALIGNMENTS

### RESULT 1

Q9W6D7 ID Q9W6D7 PRELIMINARY; PRT; 22 AA.  
AC Q9W6D7;  
DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE Hydroxyindole-O-methyltransferase isoform A (Fragment).  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archoeauria; Aves; Neognathae; Galliformes; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99067015; PubMed=9851690;  
RA Grechez-Cassiau A., Bernard M., Ladjali K., Rodriguez I.R., Voisin P.;  
RT "Structural analysis of the chicken hydroxyindole-O-methyltransferase gene.";  
RL Eur. J. Biochem. 258:44-52(1998).  
DR EMBL; AF116455; AAD23444.1; -.  
KW Methyltransferase; Transferase.  
FT NON TER 1 1  
SQ SEQUENCE 22 AA; 2783 MW; 35726EABF1E450C8 CRC64;

Query Match 87.0%; Score 20; DB 13; Length 22;  
Best Local Similarity 60.0%; Pred. No. 5.9e+02;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5  
Db 12 FADLW 16

### RESULT 2

Q9NP68 ID Q9NP68 PRELIMINARY; PRT; 25 AA.  
AC Q9NP68;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)

```

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Tumor suppressor p53 (Fragment).
GN TP53.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Thompson-Hehir J., Davies M.P.A., Green J.A., Halliwell N.,
RA Joyce K.A., Salisbury J., Sibson D.R., Vergote I., Walker C.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF209136; AAF36362.1; -
DR EMBL; AF209128; AAF36354.1; -
DR EMBL; AF209129; AAF36355.1; -
DR EMBL; AF209130; AAF36356.1; -
DR EMBL; AF209131; AAF36357.1; -
DR EMBL; AF209132; AAF36358.1; -
DR EMBL; AF209133; AAF36359.1; -
DR EMBL; AF209134; AAF36360.1; -
DR EMBL; AF209135; AAF36361.1; -
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
FT NON TER 25
SQ SEQUENCE 25 AA; 2890 MW; D7FA272EBFAB9798 CRC64;

Query Match 87.0%; Score 20; DB 4; Length 25;
Best Local Similarity 60.0%; Pred. No. 6.7e+02;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5
Db 19 FSDLW 23

RESULT 3
Q8UUVW3 PRELIMINARY; PRT; 25 AA.
AC Q8UUVW3;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE AMPA receptor subunit 2 (Fragment).
GN GLUR2B.
OS Brachydanio rerio (Zebrafish) (Zebra daniel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Kung S.-S., Chen C.-C., Chen Y.-C., Chen B.-Y., Lin W.-H., Chow W.-Y.;
RA "O/R RNA editing of the AMPA receptor subunit GluR2 transcript evolves
RT no later than the appearance of cartilaginous fishes.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF350049; AAL57191.1; -
DR InterPro; IPR001320; Ion_glu_receptor.
DR ProDom; PD000500; Ion_glu_receptor; 1.
KW Receptor.
FT NON TER 1
FT NON TER 25
SQ SEQUENCE 25 AA; 2837 MW; 9EBBA36B50DB17E CRC64;

Query Match 87.0%; Score 20; DB 13; Length 25;
Best Local Similarity 60.0%; Pred. No. 6.7e+02;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5
Db 6 FNSLW 10

```

```

RESULT 4
Q61943 PRELIMINARY; PRT; 21 AA.
AC Q61943;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Nicotinic acetylcholine receptor beta 2-subunit protein
DE (Fragment).
GN CHRN2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=D9A2;
RX MEDLINE=96164254; PubMed=8596650;
RA Bessis A., Salmon A.M., Zoli M., Le Novere N., Picciotto M.,
RA Changeux J.P.;
RT "Promoter elements conferring neuron-specific expression of the beta
RT 2-subunit of the neuronal nicotinic acetylcholine receptor studied in
RT vitro and in transgenic mice.";
RL Neuroscience 69:807-819 (1995).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=D9A2;
RA Bessis A.E.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; X82655; CAA57978.1; -
DR MGD; MGI:87891; Chrn2.
KW Receptor.
FT NON TER 21
FT NON TER 21
SQ SEQUENCE 21 AA; 2351 MW; 28E57E2BC2BC67FA CRC64;

Query Match 82.6%; Score 19; DB 11; Length 21;
Best Local Similarity 60.0%; Pred. No. 9.3e+02;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5
Db 14 FGLLW 18

RESULT 5
Q9BYM6 PRELIMINARY; PRT; 23 AA.
AC Q9BYM6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Dsrna adenosine deaminase (Fragment).
GN DSRAD.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Deblandre G., Marinx O., Nols C., Defrance P., Berr P., Huez G.;
RA Caput D.;
RC TISSUE=PLACENTA;
RT "The gene coding for the interferon-inducible human dsrna adenosine
RT deaminase is transcribed into several messengers specifying different
RT proteins.";
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; X98560; CAA67171.1; -
FT NON TER 23
FT NON TER 23
SQ SEQUENCE 23 AA; 2543 MW; CF29179B7DFC1395 CRC64;

Query Match 78.3%; Score 18; DB 4; Length 23;
Best Local Similarity 40.0%; Pred. No. 1.7e+03;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 1 FXXLW 5
Db 19 FAANV 23

RESULT 6
Q53579 PRELIMINARY; PRT; 12 AA.
AC Q53579;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Light-harvesting complex I alpha polypeptide (Fragment).
GN PUFa.
OS Rhodobacter capsulatus (Rhodospseudomonas capsulata).
OC Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
OC Rhodobacter.
OX NCBI_TaxID=1061;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92234963; PubMed=1569029;
RA Richter P., Brand M., Drews G.;
RT "Characterization of LHI- and LHI+ Rhodobacter capsulatus pufa
mutants.";
RL J. Bacteriol. 174:3030-3041(1992).
DR EMBL; S97551; AAC60405.1; -.
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1627 MW; 0F92F6E8A8A70532B CRC64;

Query Match 73.9%; Score 17; DB 2; Length 12;
Best Local Similarity 40.0%; Pred. No. 1.5e+03;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXLW 5
Db 4 FYKIW 8

RESULT 7
Q53580 PRELIMINARY; PRT; 15 AA.
AC Q53580;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Light-harvesting complex I alpha polypeptide (Fragment).
GN PUFa.
OS Rhodobacter capsulatus (Rhodospseudomonas capsulata).
OC Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
OC Rhodobacter.
OX NCBI_TaxID=1061;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92234963; PubMed=1569029;
RA Richter P., Brand M., Drews G.;
RT "Characterization of LHI- and LHI+ Rhodobacter capsulatus pufa
mutants.";
RL J. Bacteriol. 174:3030-3041(1992).
DR EMBL; S97552; AAC60406.1; -.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 2054 MW; 3561FE413591D31A CRC64;

Query Match 73.9%; Score 17; DB 2; Length 15;
Best Local Similarity 40.0%; Pred. No. 1.8e+03;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXLW 5
Db 4 FYKIW 8

RESULT 8
Q53579 PRELIMINARY; PRT; 16 AA.
AC Q53579;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Homeobox GSH-3 (Fragment).
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92073356; PubMed=1683707;
RA Singh G., Kaur S., Stock J.L., Jenkins N.A., Gilbert D.J.,
Copoland N.G., Potter S.S.;
RT "Identification of 10 murine homeobox genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:10706-10710(1991).
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; Homeobox; 1.
DR PROSITE; PS50071; HOMEBOX_2; 1.
FT NON_TER 1 16
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 2183 MW; BE902130A4525041 CRC64;

Query Match 73.9%; Score 17; DB 11; Length 16;
Best Local Similarity 40.0%; Pred. No. 1.9e+03;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXLW 5
Db 12 FKKMW 16

RESULT 9
Q53553 PRELIMINARY; PRT; 20 AA.
AC Q53553;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Guanine nucleotide-binding protein beta subunit 4 (Transducin beta
chain 4) (Fragment).
GN GNB4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., AND DISTRIBUTION IN BRAIN.
RX STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;
MEDLINE=98283588; PubMed=9622245;
RA Betty M., Harnish S.W., Rhodes K.J., Cockett M.I.;
RT "Distribution of heterotrimeric G-protein beta and gamma subunits in
the rat brain.";
RL Neuroscience 85:475-486(1998).
CC -1- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE
INVOLVED AS A MODULATOR OR TRANSDUCER IN VARIOUS TRANSMEMBRANE
SIGNALING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE
GTPASE ACTIVITY, FOR REPLACEMENT OF GDP BY GTP, AND FOR G PROTEIN-
EFFECTOR INTERACTION.
CC -1- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED IN THE BRAIN. HIGHEST LEVELS
FOUND IN THE HIPPOCAMPUS AND LAYERS V AND VI OF THE NEOCORTIX.
CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
DR EMBL; AF022085; AB82552.1; -.
DR InterPro; IPR001680; WD40.
DR PROSITE; PS00678; WD REPEATS_1; PARTIAL.
DR PROSITE; PS00082; WD REPEATS_2; 1.
DR PROSITE; PS50294; WD REPEATS_REGION; 1.
DR Transducer; Repeat; WD repeat; Multigene family.
FT NON_TER 1 1
FT REPEAT <1 20 WD7.

```

SQ SEQUENCE 20 AA; 2242 MW; C143688295AE0BE0 CRC64;

Query Match 73.9%; Score 17; DB 11; Length 20;  
 Best Local Similarity 40.0%; Pred. No. 2.4e+03;  
 Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXLW 5  
 Db 15 FLRIW 19

RESULT 10

Q66548 PRELIMINARY; PRT; 20 AA.  
 AC Q66548;  
 DT 01-NOV-1996 (TReMBLrel. 01, Created)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 DE EBV B95-8 Cl(g) DNA with antigen-coding ORF (Fragment).  
 OS Human herpesvirus 4 (Epstein-Barr virus).  
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 OC Gammaherpesvirinae; Lymphocryptovirus.  
 NCBI\_TaxID=10376;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=B95-8;  
 RX MEDLINE=88217505; PubMed=2835748;  
 RA Walls D., Perricaudet M., Gannon F.;  
 RT "The analysis of EBV proteins which are antigenic in vivo."  
 RL Nucleic Acids Res. 16:2859-2872(1988).  
 DR EMBL; X07531; CAA30406.1; -.  
 FT NON TER 20  
 SQ SEQUENCE 20 AA; 2576 MW; 05F877676B235F95 CRC64;

Query Match 73.9%; Score 17; DB 12; Length 20;  
 Best Local Similarity 40.0%; Pred. No. 2.4e+03;  
 Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXLW 5  
 Db 11 FRFIW 15

RESULT 11

Q72017 PRELIMINARY; PRT; 17 AA.  
 AC Q72017;  
 DT 01-NOV-1996 (TReMBLrel. 01, Created)  
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 DE Env protein (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
 ON NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Michael N.L.;  
 RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U24486; AAA79676.1; -.  
 FT NON TER 17  
 SQ SEQUENCE 17 AA; 2072 MW; BOAEB4D30DE21302 CRC64;

Query Match 69.6%; Score 16; DB 15; Length 17;  
 Best Local Similarity 40.0%; Pred. No. 3.4e+03;  
 Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXLW 5  
 Db 10 YQHLW 14

RESULT 12

Q9S0U6 PRELIMINARY; PRT; 25 AA.  
 ID Q9S0U6;  
 DT 01-MAY-2000 (TReMBLrel. 13, Created)  
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 DE ORF10S (Fragment).  
 OS Shigella sonnei.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Shigella.  
 NCBI\_TaxID=624;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=HW383;  
 RX MEDLINE=20248365; PubMed=10789503;  
 RA Chida T., Okamura N., Ohtani K., Yoshida Y., Arakawa E., Watanabe H.;  
 RT "The complete DNA sequence of the O antigen gene region of Plesiomonas  
 shigelloides serotype O17 which is identical to Shigella sonnei form  
 I antigen."  
 RL Microbiol. Immunol. 44:161-172(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=HW383;  
 RX MEDLINE=99036814; PubMed=9817819;  
 RA Hough H.H., Venkatesan M.M.;  
 RT "Genetic analysis of Shigella sonnei form I antigen: identification of  
 a novel 18630 as an essential element for the form I antigen  
 expression."  
 RL Microb. Pathog. 25:165-173(1998).  
 DR EMBL; AB028134; BAA85070.1; -.  
 FT NON TER 25  
 SQ SEQUENCE 25 AA; 2726 MW; A6CC5D24211CDAAD CRC64;

Query Match 69.6%; Score 16; DB 2; Length 25;  
 Best Local Similarity 40.0%; Pred. No. 4.8e+03;  
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXLW 5  
 Db 10 FGTFW 14

RESULT 13

P72429 PRELIMINARY; PRT; 25 AA.  
 ID P72429;  
 DT 01-FEB-1997 (TReMBLrel. 02, Created)  
 DT 01-FEB-1997 (TReMBLrel. 02, Last sequence update)  
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)  
 DE TAP/REPC (Replication of plasmid).  
 GN TAP/REPC OR TAP OR PSLT005.  
 OS Salmonella enteritidis.  
 OS Salmonella enterica subsp. enterica serovar Choleraesuis, and  
 OS Salmonella typhimurium.  
 OG Plasmid virulence, Plasmid 50k virulence, and Plasmid pSLT.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Salmonella.  
 NCBI\_TaxID=592, 119912, 602;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=S.enteritidis; STRAIN=82139; PLASMID=VIRULENCE;  
 RX MEDLINE=97254449; PubMed=9099859;  
 RA Rodriguez-Pena J.M., Buisan M., Ibanez M., Rotger R.;  
 RT "Genetic map of the virulence plasmid of Salmonella enteritidis and  
 nucleotide sequence of its replicons."  
 RL Gene 188:53-61(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=S.enterica subsp. enterica serovar Choleraesuis; STRAIN=RF-1;  
 RC PLASMID=50K VIRULENCE;  
 RA Okada N., Haneda T.;  
 RT "50 kb virulence plasmid of Salmonella enterica serovar  
 Choleraesuis.";

RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RC SEQUENCE FROM N.A.  
 RC SPECIES=S.typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720;  
 RC PLASMID=PSLT;  
 RX MEDLINE=21534948; PubMed=11677609;  
 RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,  
 RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,  
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,  
 RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,  
 RA Waterston R., Wilson R.K.;  
 RT "Complete genome sequence of Salmonella enterica serovar Typhimurium  
 LT2.";  
 RL Nature 413:852-856(2001).  
 DR EMBL; U64797; AAB53038.1; -.  
 DR EMBL; AB040415; BAB20531.1; -.  
 DR EMBL; AE006471; AAL23447.1; -.  
 KW Plasmid; Complete proteome.  
 SQ SEQUENCE 25 AA; 3008 MW; B21F596B6DBFABE7 CRC64;

Query Match 69.6%; Score 16; DB 16; Length 25;  
 Best Local Similarity 40.0%; Pred. No. 4.8e+03;  
 Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXLW 5  
 : ||  
 Db 7 YLFLW 11

## RESULT 14

O85406  
 ID O85406 PRELIMINARY; PRT; 8 AA.  
 AC O85406;  
 DT 01-NOV-1998 (TREMELrel. 08, Created)  
 DT 01-NOV-1998 (TREMELrel. 08, Last sequence update)  
 DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)  
 DE Hypothetical 1.0 kDa protein (Fragment).  
 OS Coccidia burnetii.  
 OC Bacteria; Proteobacteria; gamma subdivision; Legionellaceae group;  
 OC Coccidia group; Coccidia.  
 OX NCBI\_TaxID=777;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NINE MILE PHASE I;  
 RX MEDLINE=98348442; PubMed=9683477;  
 RA Willems H., Jaeger C., Baljer G.;  
 RT "Physical and genetic map of the obligate intracellular bacterium  
 RT Coccidia burnetii.";  
 RL J. Bacteriol. 180:3816-3822(1998).  
 DR EMBL; AF064963; AAD09947.1; -.  
 KW Hypothetical protein.  
 FT NON\_TER 1  
 SQ SEQUENCE 8 AA; 993 MW; 045B5AA45372727 CRC64;

Query Match 65.2%; Score 15; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5  
 : ||  
 Db 3 LW 4

## RESULT 15

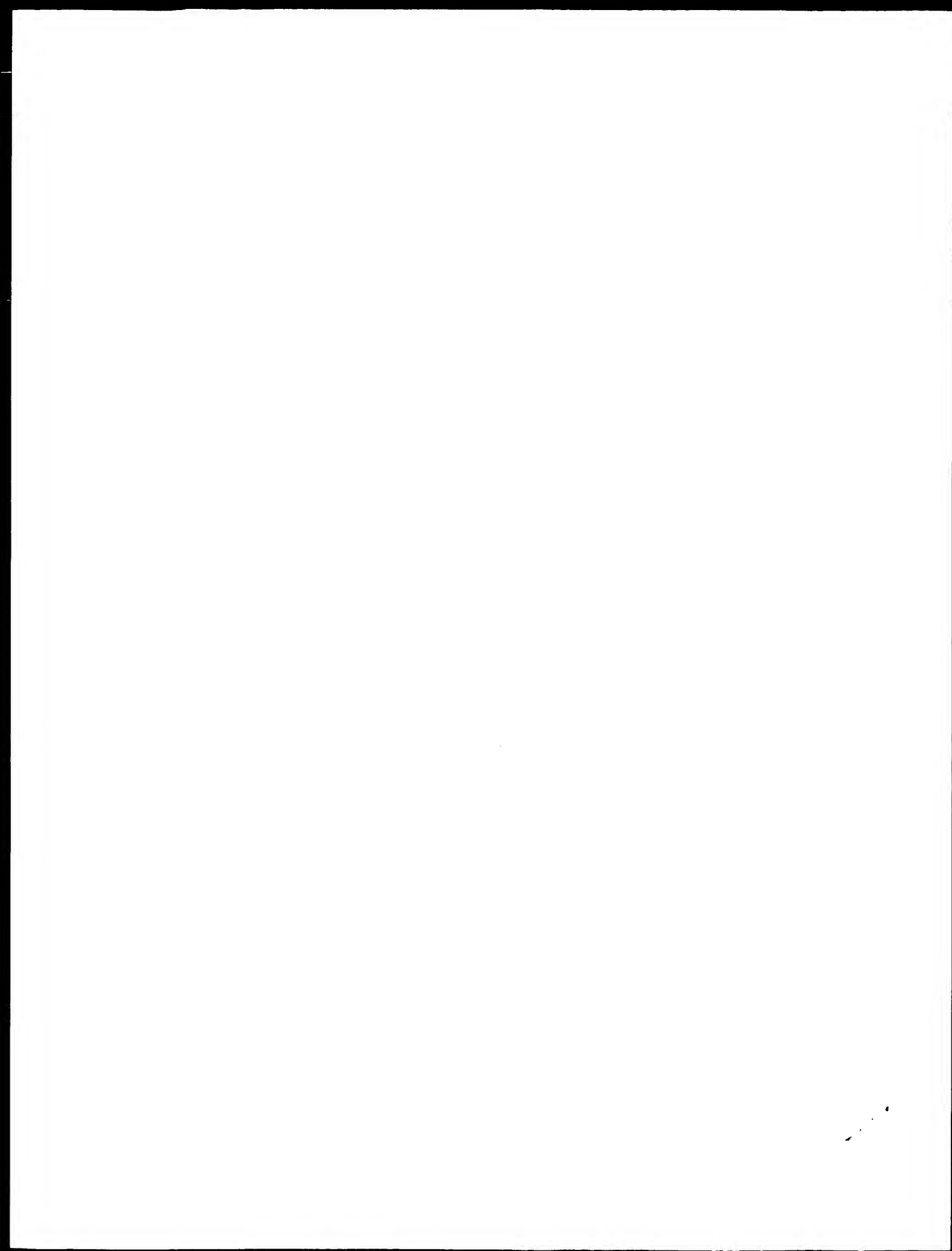
O85953  
 ID O85953 PRELIMINARY; PRT; 9 AA.  
 AC O85953;  
 DT 01-MAY-1999 (TREMELrel. 10, Created)  
 DT 01-MAY-1999 (TREMELrel. 10, Last sequence update)  
 DT 01-MAR-2002 (TREMELrel. 20, Last annotation update)  
 DE Galactocerebrosidase (EC 3.2.1.46) (Fragment).  
 GN GALC.  
 OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=BRAIN;  
 RA Lulli L., Torchiana E., Finocchiaro G.;  
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U77631; AAD15626.1; -.  
 KW Glycosidase; Hydrolase.  
 FT NON\_TER 9  
 SQ SEQUENCE 9 AA; 1069 MW; 374E2AAD2C2C699C8 CRC64;

Query Match 65.2%; Score 15; DB 4; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5  
 : ||  
 Db 8 LW 9

Search completed: February 12, 2003, 11:14:58  
 Job time : 10.7917 secs





GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 12, 2003, 11:10:52 ; Search time 12.5 Seconds  
(without alignments)  
53.300 Million cell updates/sec

Title: US-09-403-440A-1

Perfect score: 23

Sequence: 1 FXXLW 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 320064

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_101002.\*

```

1: /SID22/gcgdata/geneseq/geneseqp-embl/AA1980.DAT.*
2: /SID22/gcgdata/geneseq/geneseqp-embl/AA1981.DAT.*
3: /SID22/gcgdata/geneseq/geneseqp-embl/AA1982.DAT.*
4: /SID22/gcgdata/geneseq/geneseqp-embl/AA1983.DAT.*
5: /SID22/gcgdata/geneseq/geneseqp-embl/AA1984.DAT.*
6: /SID22/gcgdata/geneseq/geneseqp-embl/AA1985.DAT.*
7: /SID22/gcgdata/geneseq/geneseqp-embl/AA1986.DAT.*
8: /SID22/gcgdata/geneseq/geneseqp-embl/AA1987.DAT.*
9: /SID22/gcgdata/geneseq/geneseqp-embl/AA1988.DAT.*
10: /SID22/gcgdata/geneseq/geneseqp-embl/AA1989.DAT.*
11: /SID22/gcgdata/geneseq/geneseqp-embl/AA1990.DAT.*
12: /SID22/gcgdata/geneseq/geneseqp-embl/AA1991.DAT.*
13: /SID22/gcgdata/geneseq/geneseqp-embl/AA1992.DAT.*
14: /SID22/gcgdata/geneseq/geneseqp-embl/AA1993.DAT.*
15: /SID22/gcgdata/geneseq/geneseqp-embl/AA1994.DAT.*
16: /SID22/gcgdata/geneseq/geneseqp-embl/AA1995.DAT.*
17: /SID22/gcgdata/geneseq/geneseqp-embl/AA1996.DAT.*
18: /SID22/gcgdata/geneseq/geneseqp-embl/AA1997.DAT.*
19: /SID22/gcgdata/geneseq/geneseqp-embl/AA1998.DAT.*
20: /SID22/gcgdata/geneseq/geneseqp-embl/AA1999.DAT.*
21: /SID22/gcgdata/geneseq/geneseqp-embl/AA2000.DAT.*
22: /SID22/gcgdata/geneseq/geneseqp-embl/AA2001.DAT.*
23: /SID22/gcgdata/geneseq/geneseqp-embl/AA2002.DAT.*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	91.3	15	21 AAB29164	Peptide #8. Unide
2	20	87.0	5	21 AAB29164	Carbohydrate anti
3	20	87.0	5	21 AAB29164	Motif binding to a
4	20	87.0	6	17 AAR89913	p53/MDM2 binding i
5	20	87.0	6	17 AAR89913	p53 minimal MDM2 b
6	20	87.0	6	18 AAW13606	p53 protein amino
7	20	87.0	6	21 AAB17074	Mdm/hdm antagonist
8	20	87.0	6	23 ABB73169	Mdm/hdm antagonist
9	20	87.0	7	17 AAR89921	Antibody DO-1 epit
10	20	87.0	7	17 AAR89925	p53 binding site k

11	20	87.0	7	20 AAW94141	FG loop sequence o
12	20	87.0	7	21 AAY57789	TRAM-interaction m
13	20	87.0	7	23 ABB94392	Ubiquitin binding
14	20	87.0	8	21 AAB09130	Hepatitis GB virus
15	20	87.0	8	22 AAB62220	Glycine max homogl
16	20	87.0	9	19 AAW37199	Human oncogenic pr
17	20	87.0	9	19 AAW46349	Amino acid sequenc
18	20	87.0	9	19 AAW46350	Amino acid sequenc
19	20	87.0	9	19 AAW46351	Amino acid sequenc
20	20	87.0	9	21 AAB34807	Human secreted pro
21	20	87.0	10	17 AAR89917	Human p53 MDM2-con
22	20	87.0	10	17 AAR89918	Mouse p53 MDM2-con
23	20	87.0	10	18 AAW13605	p53 protein amino
24	20	87.0	10	19 AAW37198	Human oncogenic pr
25	20	87.0	11	18 AAW11231	Peptide A, used in
26	20	87.0	11	22 AAU26842	Human Leukocyte An
27	20	87.0	11	22 AAU27152	Human Leukocyte An
28	20	87.0	11	23 AAW52269	Miniature protein
29	20	87.0	12	19 AAW37181	Human p53 wild-typ
30	20	87.0	12	19 AAW37188	Human oncogenic pr
31	20	87.0	12	19 AAW37189	Human oncogenic pr
32	20	87.0	12	21 AAB17075	Mdm/hdm antagonist
33	20	87.0	12	21 AAB17076	Mdm/hdm antagonist
34	20	87.0	12	21 AAB17087	Mdm/hdm antagonist
35	20	87.0	12	21 AAB17088	Mdm/hdm antagonist
36	20	87.0	12	22 AAB86005	DCM-associated pep
37	20	87.0	12	23 ABB73170	Mdm/hdm antagonist
38	20	87.0	12	23 ABB73171	Mdm/hdm antagonist
39	20	87.0	12	23 ABB73182	Mdm/hdm antagonist
40	20	87.0	12	23 ABB73183	Mdm/hdm antagonist
41	20	87.0	13	21 AAY57799	TRAM-interaction m
42	20	87.0	13	22 AAB86006	DCM-associated pep
43	20	87.0	14	22 AAG98212	Human SNP associat
44	20	87.0	14	22 AAB86012	DCM-associated pep
45	20	87.0	14	22 AAB86020	DCM autoantibody-a

#### ALIGNMENTS

RESULT 1  
AAB29164  
ID AAB29164 standard; Peptide; 15 AA.  
XX  
AC AAB29164;  
XX  
DT 02-FEB-2001 (first entry)  
XX  
DE Peptide #8.  
XX  
KW Fork head associated; FHA; domain; transcriptional control;  
KW DNA replication; DNA repair; cell cycle control.  
XX  
OS Unidentified.  
XX  
PN WO200057184-A2.  
XX  
PD 28-SEP-2000.  
XX  
PF 17-MAR-2000; 2000WO-GB01024.  
XX  
PR 19-MAR-1999; 99GB-0006432.  
PR 28-JUN-1999; 99GB-0015075.  
XX  
PA (KUDO-) KUDOS PHARM LTD.  
XX  
PI Jackson SP, Durocher D;  
XX  
DR WPI; 2000-664872/64.  
XX  
PT Assays and screening methods based on direct interaction between FHA  
PT domains and phosphopeptides, useful for characterizing binding and to  
PT identify binding partners and modulators of FHA domain-phosphopeptide

PT binding -  
XX Disclosure; Fig 2; 92pp; English.  
XX  
CC The present invention relates to assays and screening methods based on  
CC a direct interaction between fork head associated (FHA) domains and  
CC phosphorylated polypeptides, for characterizing the binding of these  
CC molecules. FHA peptides may be useful for treating medical conditions,  
CC associated with defects in transcriptional control, DNA replication,  
CC DNA repair, cell cycle control or other cellular processes. The method  
CC may provide valuable insights into checkpoint signalling, has important  
CC implications for the functions of other FHA domain-containing  
CC proteins and provides basis for new lines of therapy. The present  
CC sequence is a peptide used in the present invention.  
XX  
SQ Sequence 15 AA;  
Query Match 91.3%; Score 21; DB 21; Length 15;  
Best Local Similarity 60.0%; Pred. No. 5.3e+02;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Oy 1 FXXLW 5  
| |  
Db 9 FSALW 13  
RESULT 2  
AAY33038  
ID AAY33038 standard; peptide; 5 AA.  
AC AAY33038;  
XX  
DT 03-NOV-1999 (first entry)  
XX  
DE Carbohydrate antigen peptide mimotope 11.  
XX  
KW Mimotope; antigen; carbohydrate; antibody; mimic; vaccine; adjuvant;  
KW tumour immunity; cancer therapy; antibacterial; immune response;  
KW immunogenicity; anti-idiotype; T cell response manipulation.  
XX  
OS Synthetic.  
XX  
XX WO9940433-A1.  
XX  
XX 12-AUG-1999.  
XX  
XX 04-FEB-1999; 99WO-US02405.  
XX  
XX 04-FEB-1998; 98US-0073690.  
XX  
XX (UYPE-) UNIV PENNSYLVANIA.  
XX  
XX Kieber-Emmons T;  
XX  
XX WPI; 1999-527317/44.  
XX  
XX Peptides and recombinant antibody mimics of carbohydrate antigens,  
XX used for, e.g. treatment of cancer and infection  
XX  
XX Claim 21; Page 72; 88pp; English.  
XX  
CC This invention describes a novel method for preparing a peptide or  
CC recombinant antibody, which mimics an antigenic carbohydrate. The  
CC peptides and recombinant antibodies prepared to mimic antigenic  
CC carbohydrates can be used to enhance binding of anti-antigenic  
CC carbohydrate antibodies to the antigenic carbohydrate, e.g. as vaccine  
CC adjuvants. The peptides can be used to inhibit binding of a ligand to a  
CC receptor, which is an antigenic carbohydrate. The methods are used to  
CC prepare the peptides and antigenic antibodies, which mimic the antigenic  
CC carbohydrates. Carbohydrate-conjugate vaccines could be used in tumour  
CC immunity and cancer therapy. The peptides and antibodies can also be  
CC used as antibacterials. Peptides that mimic carbohydrate antigens can be  
CC formulated to develop a longer lasting immune response. Other advantages

CC of the peptide mimics are: (1) the chemical composition and purity of  
CC synthesized peptides can be precisely defined; (2) the immunogenicity  
CC of the peptides can be significantly enhanced by polymerization or  
CC addition of relatively small carrier molecules that reduce the total  
CC amount of antigen required for immunization; (3) peptide synthesis may  
CC be more practical than synthesis of carbohydrate-protein conjugates or  
CC the production of anti-idiotypes; (4) peptide mimicking sequences can  
CC be engineered into DNA plasmids for DNA vaccination to further  
CC manipulate T cell responses. AAY33028-Y33087 represent the carbohydrate  
CC antigen peptide mimotopes described in the invention.  
XX  
SQ Sequence 5 AA;  
Query Match 87.0%; Score 20; DB 20; Length 5;  
Best Local Similarity 60.0%; Pred. No. 7.8e+05;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0.  
Oy 1 FXXLW 5  
| |  
Db 1 FSLW 5  
RESULT 3  
AAB07280  
ID AAB07280 standard; peptide; 5 AA.  
AC AAB07280;  
XX  
DT 17-OCT-2000 (first entry)  
XX  
DE Motif binding to anti-Lewis antigen antibody BR55-2.  
XX  
KW Human; peptido-mimetic; tumour metastasis; E-selectin;  
KW adhesion molecule; Lewis antigen; anti-adhesion therapy.  
XX  
XX Unidentified.  
XX  
XX WO200027420-A1.  
XX  
XX 18-MAY-2000.  
XX  
XX 05-NOV-1999; 99WO-US26277.  
XX  
XX 06-NOV-1998; 98US-0107478.  
XX  
XX (WIST-) WISTAR INST ANATOMY & BIOLOGY.  
XX (UYPE-) UNIV PENNSYLVANIA.  
XX  
XX Blaszczyk-Thurin M, Kieber-Emmons T;  
XX  
XX WPI; 2000-376309/32.  
XX  
XX Peptidomimetics of carbohydrate Lewis ligands useful for modulating  
XX inflammation, metastasis and angiogenesis -  
XX  
XX Example 5; Page 37; 107pp; English.  
XX  
CC Tumour metastasis requires detachment of malignant cells from the primary  
CC tumour, penetration of blood or lymph vessels and attachment to the  
CC endothelium of distant organs, ultimately resulting in the formation of  
CC new tumours. The selectin family of adhesion molecules is implicated in  
CC this process. E-selectin is a calcium-dependent molecule expressed by  
CC activated vascular endothelium. E-selectins bind to glycoconjugates  
CC carrying a terminal tetrasaccharide Lewis antigen, which are found on  
CC tumour cell surfaces. One such Lewis antigen is Lewis X (LeX). The  
CC binding of selectin molecules to their ligands is thought to be an  
CC important step in metastasis. Therefore, inhibition of  
CC E-selectin-dependent carbohydrate-mediated interactions is thought to  
CC be a target for anti-cancer therapy. The present sequence is a non  
CC planar-X planar type motif. This motif is thought to bind to anti-LeX  
CC antibody BR55-2. BR55-2 is a peptido-mimetic of E-selectins. Peptides  
CC that block E-selectin-LeX binding and therefore adhesion of tumour cells  
CC and leukocytes to endothelial cells inhibit metastasis.

```

XX SQ Sequence 5 AA;
Query Match 87.0%; Score 20; DB 21; Length 5;
Best Local Similarity 60.0%; Pred. No. 7.8e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXLW 5
DB 1 FSLWL 5

RESULT 4
AAR89913
ID AAR89913 standard; peptide; 6 AA.
XX AC AAR89913;
XX DT 10-SEP-1996 (first entry)
XX DE p53/MDM2 binding inhibitor #3.
XX KW Interference; binding; p53; tumour suppressor; MDM2; oncogene; cancer;
XX KW inhibition; diagnosis; treatment; malignancy; consensus.
XX OS Synthetic.
XX PN WO9602642-A1.
XX PD 01-FEB-1996.
XX PF 20-JUL-1995; 95WO-GB01719.
XX PR 19-APR-1995; 95US-0424957.
XX PR 20-JUL-1994; 94US-0277660.
XX PA (UYDU-) UNIV DUNDEE.
XX PI Lane DP, Picklesley SM;
XX DR WPI; 1996-105905/11.
XX PS New cpds. which interfere with binding of MDM2 and p53 - used to
PT develop prods. for use in the diagnosis and treatment of cancer and
PT other malignancies
XX Claim 4; Page 29; 46pp; English.
XX CC New peptides of the invention which interfere with the binding of the
CC p53 tumour suppressor protein and the MDM2 oncogene protein contain
CC the peptide sequences AAR89911-3 which form part of the p53 protein
CC binding motif between amino acids 16-33 (AAR89914). The peptides were
CC identified by modifying the p53 consensus binding sequence by
CC substitution of an Alanine at each pos. and identifying which amino
CC acid changes altered binding to expressed MDM2. The peptides and
CC methods of identifying similar inhibitory peptides can be used to
CC diagnose and treat e.g. cancer and other malignancies.
XX SQ Sequence 6 AA;
Query Match 87.0%; Score 20; DB 17; Length 6;
Best Local Similarity 60.0%; Pred. No. 7.8e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXLW 5
DB 2 FSDLW 6

RESULT 5
AAR89915
ID AAR89915 standard; peptide; 6 AA.
XX AC AAR89915;
XX DT 10-SEP-1996 (first entry)
XX DE p53 minimal MDM2 binding site #1.
XX KW Interference; binding; p53; tumour suppressor; MDM2; oncogene; cancer;
XX KW inhibition; diagnosis; treatment; malignancy; consensus.
XX OS Synthetic.
XX PN WO9602642-A1.
XX PD 01-FEB-1996.
XX PF 20-JUL-1995; 95WO-GB01719.
XX PR 19-APR-1995; 95US-0424957.
XX PR 20-JUL-1994; 94US-0277660.
XX PA (UYDU-) UNIV DUNDEE.
XX PI Lane DP, Picklesley SM;
XX DR WPI; 1996-105905/11.
XX PS New cpds. which interfere with binding of MDM2 and p53 - used to
PT develop prods. for use in the diagnosis and treatment of cancer and
PT other malignancies
XX Disclosure; Page 15; 46pp; English.
XX CC This is the sequence of the p53 tumour suppressor protein minimal MDM2
CC oncogene protein binding site. The sequence is used to generate peptides
CC binding motif between amino acids 16-33 (AAR89914). The peptides were
CC identified by modifying the p53 consensus binding sequence by
CC substitution of an Alanine at each pos. and identifying which amino
CC acid changes altered binding to expressed MDM2. The peptides and
CC methods of identifying similar inhibitory peptides can be used to
CC diagnose and treat e.g. cancer and other malignancies.
XX SQ Sequence 6 AA;
Query Match 87.0%; Score 20; DB 17; Length 6;
Best Local Similarity 60.0%; Pred. No. 7.8e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXLW 5
DB 2 FSGLW 6

RESULT 6
AAW13606
ID AAW13606 standard; peptide; 6 AA.
XX AC AAW13606;
XX DT 16-JAN-1998 (first entry)
XX DE p53 protein amino acids 18-23.
XX KW Mouse; Mdm2; murine double minute; phosphoprotein; binding; modulation;
XX KW tumour suppressor; p53; oncogene; cell cycle arrest; p107; antagonist;
XX KW inhibition; transcription factor; adenocarcinoma; colon; cancer; breast;
XX KW lung; stomach; myeloid leukaemia; lymphoma; hyperproliferative;
XX KW restenosis.
XX OS Homo sapiens.
XX PN WO9709343-A2.
XX XX

```

```

AC AAR89915;
XX DT 10-SEP-1996 (first entry)
XX DE p53 minimal MDM2 binding site #1.
XX KW Interference; binding; p53; tumour suppressor; MDM2; oncogene; cancer;
XX KW inhibition; diagnosis; treatment; malignancy; consensus.
XX OS Synthetic.
XX PN WO9602642-A1.
XX PD 01-FEB-1996.
XX PF 20-JUL-1995; 95WO-GB01719.
XX PR 19-APR-1995; 95US-0424957.
XX PR 20-JUL-1994; 94US-0277660.
XX PA (UYDU-) UNIV DUNDEE.
XX PI Lane DP, Picklesley SM;
XX DR WPI; 1996-105905/11.
XX PS New cpds. which interfere with binding of MDM2 and p53 - used to
PT develop prods. for use in the diagnosis and treatment of cancer and
PT other malignancies
XX Disclosure; Page 15; 46pp; English.
XX CC This is the sequence of the p53 tumour suppressor protein minimal MDM2
CC oncogene protein binding site. The sequence is used to generate peptides
CC binding motif between amino acids 16-33 (AAR89914). The peptides were
CC identified by modifying the p53 consensus binding sequence by
CC substitution of an Alanine at each pos. and identifying which amino
CC acid changes altered binding to expressed MDM2. The peptides and
CC methods of identifying similar inhibitory peptides can be used to
CC diagnose and treat e.g. cancer and other malignancies.
XX SQ Sequence 6 AA;
Query Match 87.0%; Score 20; DB 17; Length 6;
Best Local Similarity 60.0%; Pred. No. 7.8e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXLW 5
DB 2 FSGLW 6

RESULT 6
AAW13606
ID AAW13606 standard; peptide; 6 AA.
XX AC AAW13606;
XX DT 16-JAN-1998 (first entry)
XX DE p53 protein amino acids 18-23.
XX KW Mouse; Mdm2; murine double minute; phosphoprotein; binding; modulation;
XX KW tumour suppressor; p53; oncogene; cell cycle arrest; p107; antagonist;
XX KW inhibition; transcription factor; adenocarcinoma; colon; cancer; breast;
XX KW lung; stomach; myeloid leukaemia; lymphoma; hyperproliferative;
XX KW restenosis.
XX OS Homo sapiens.
XX PN WO9709343-A2.
XX XX

```

PD 13-MAR-1997.  
 XX  
 PF 02-SEP-1996; 96WO-FR01340.  
 XX  
 PR 04-SEP-1995; 95FR-0010331.  
 XX  
 PA (INRM ) INST NAT SANTE & RECH MEDICALE.  
 PA (RHON ) RHONE POULENC RORER SA.  
 XX  
 PI Dubs-Poterezman M, Tocque B, Waslylyk B;  
 XX  
 DR WPI; 1997-192837/17.  
 XX  
 PT Treating cancer with antagonist of oncogenic activity of protein  
 PT Mdm2 - or nucleic acid encoding an antagonist, also viral vectors  
 PT contg. this nucleic acid  
 XX  
 PS Claim 4; Page -; 43pp; French.  
 XX  
 CC The peptides AAW13602-6 represent peptide fragments derived from the  
 CC wild type human p53 protein. This peptide corresponds to amino acids  
 CC 18-23 of the p53 sequence. The peptides are claimed peptides which are  
 CC able to bind the N-terminal amino acids (1-134) of the murine double  
 CC minute-2 (mdm2) protein (AAW13600). Mdm2 protein is a 90 kD  
 CC phosphoprotein which binds and modulates the activity of the tumour  
 CC suppressor protein p53. It has now been shown that the mdm2 protein  
 CC itself has oncogenic properties, especially in a p53-null background.  
 CC Mdm2 is observed to unblock cell cycle arrest in G1 caused by  
 CC over-expression of the p107 protein. The p53 peptides are examples of  
 CC antagonists of the invention which are able to inhibit the oncogenic  
 CC activity of mdm2. The antagonists are used to treat e.g. adenocarcinoma  
 CC of the colon; cancer of the breast, lung or stomach; myeloid leukaemia; B  
 CC cell lymphoma, or other hyperproliferative conditions such as  
 CC restenosis. Note: this sequence is not given in the specification but is  
 CC constructed from the wild type human p53 sequence.  
 XX  
 SQ Sequence 6 AA;  
 Query Match 87.0%; Score 20; DB 18; Length 6;  
 Best Local Similarity 60.0%; Pred. No. 7.8e+05;  
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 FXXLW 5  
 | | |  
 Db 2 FSDLW 6  
 RESULT 7  
 AAB17074  
 ID AAB17074 standard; Peptide; 6 AA.  
 XX  
 AC AAB17074;  
 XX  
 DT 31-OCT-2000 (first entry)  
 XX  
 DE Mdm/hdm antagonist peptide sequence SEQ ID NO:130.  
 XX  
 KW Modified peptide; therapeutic agent; fusion; Fc domain; cancer;  
 KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;  
 KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist;  
 KW MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;  
 KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;  
 KW vascular endothelial growth factor; matrix metalloproteinase;  
 KW asthma; thrombosis; pharmaceutical.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200024782-A2.  
 XX  
 PD 04-MAY-2000.  
 XX  
 PF 25-OCT-1999; 99WO-US25044.  
 XX  
 XX

PR 23-OCT-1998; 98US-0105371.  
 PR 22-OCT-1999; 99US-0428082.  
 XX  
 PA (AMGE-) AMGEN INC.  
 XX  
 PI Feige U, Liu C, Cheetham J, Boone TC;  
 XX  
 DR WPI; 2000-350702/30.  
 XX  
 PT Novel composition of matter comprising an Fc domain and  
 PT pharmacologically active peptides, useful for treating cancer and  
 PT autoimmune diseases -  
 XX  
 PS Claim 39; Page 240; 608pp; English.  
 XX  
 CC The present invention describes composition of matter (I) comprising an  
 CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:  
 CC (X1)-a-P1-(X2)b, where: P1 = an Fc domain; X1 and X2 = are each  
 CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, (L4)f-P4  
 CC where P1, P2, P3, and P4 = are each independently sequences of  
 CC pharmacologically active peptides; L1, L2, L3, and L4 = are each  
 CC independently linkers; and a, b, c, d, e, and f = are each independently  
 CC 0 or 1, provided that at least 1 of a and b is 1. The composition can  
 CC have cytostatic, antiasthmatic, thrombolytic and immunosuppressive  
 CC activities. DNAs, vectors and host cells from the present invention can  
 CC be used for producing pharmaceutical compositions. The compositions are  
 CC useful for treating cancer, asthma, thrombosis, or autoimmune diseases.  
 CC The use of an Fc domain (rather than a Fab domain) can provide a longer  
 CC half-life or incorporate functions such as Fc receptor binding, protein  
 CC A binding, complement fixation, and possibly placental transfer. AAA69443  
 CC to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid  
 CC sequences used in the exemplification of the present invention.  
 XX  
 SQ Sequence 6 AA;  
 Query Match 87.0%; Score 20; DB 21; Length 6;  
 Best Local Similarity 60.0%; Pred. No. 7.8e+05;  
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 FXXLW 5  
 | | |  
 Db 2 FSDLW 6  
 RESULT 8  
 ABB73169  
 ID ABB73169 standard; Peptide; 6 AA.  
 XX  
 AC ABB73169;  
 XX  
 DT 05-APR-2002 (first entry)  
 XX  
 DE Mdm/hdm antagonist peptide SEQ ID NO:130.  
 XX  
 KW Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG;  
 KW EPO; erythropoietin; TPO; tumour necrosis factor alpha inhibitor;  
 KW TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP;  
 KW TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;  
 KW MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;  
 KW cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;  
 KW antianaemic; anorectic; antifertility; haemostatic; dermatological;  
 KW neuroprotective; inflammatory disease; autoimmune disease; tumour growth;  
 KW cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;  
 KW sleep disorder; neurological degenerative disease; anaemia;  
 KW thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;  
 KW Fanconi's syndrome.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200183525-A2.  
 XX  
 XX

PD 08-NOV-2001.  
XX  
PF 02-MAY-2001; 2001WO-US14310.  
XX  
PR 03-MAY-2000; 2000US-0563286.  
XX  
PA (AMGE-) AMGEN INC.  
XX  
PI Feige U, Liu C, Cheetham JC, Boone TC, Gudas JM;  
XX  
DR WPI; 2002-130313/17.  
XX  
PT Novel vehicle-peptide molecule or its multimers useful for treating  
PT inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,  
PT diabetic retinopathy, obesity, sleep disorders and infertility -  
XX  
PS Claim 39; Page 53; 176pp; English.  
XX  
CC The present invention describes a vehicle-peptide molecule (I) or its  
CC multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,  
CC cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,  
CC antinaemic, anorectic, antiinfertility, haemostatic, dermatological and  
CC neuroprotective activities. (I) can be used as a therapeutic or  
CC prophylactic agent as well as for screening purposes. (I) is useful for  
CC diagnosing diseases characterised by dysfunction of their associated  
CC protein of interest, for identifying normal or abnormal proteins of  
CC interest, as a part of diagnostic kit to detect the presence of their  
CC proteins of interest in a biological sample. Additionally, (I) is useful  
CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,  
CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,  
CC infertility, and neurological degenerative diseases. (I), comprising  
CC EPO-mimetic compounds are useful for treating disorders characterised by  
CC low red blood cell levels such as anaemia. The TPO-mimetic comprising  
CC compounds are useful for treating conditions that involve an existing  
CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet  
CC deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic  
CC tumour which result in thrombocytopaenia, systemic lupus erythematosus,  
CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777  
CC represent amino acid and nucleic acid sequences used in the  
CC exemplification of the present invention.  
XX  
SQ Sequence 6 AA;  
Query Match 87.0%; Score 20; DB 23; Length 6;  
Best Local Similarity 60.0%; Pred. No. 7.8e+05;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 FXXLW 5  
| | |  
Db 2 FSDLW 6  
RESULT 9  
AAR89921  
ID AAR89921 standard; peptide; 7 AA.  
XX  
AC AAR89921;  
XX  
DT 10-SEP-1996 (first entry)  
XX  
DE Antibody DO-1 epitope on human p53 protein.  
XX  
KW Interference; binding; p53; tumour suppressor; MDM2; oncogene; cancer;  
KW inhibition; diagnosis; treatment; malignancy; consensus; antibody.  
XX  
OS Synthetic.  
XX  
PN WO9602642-A1.  
XX  
PD 01-FEB-1996.  
XX  
PF 20-JUL-1995; 95WO-GB01719.  
XX

PR 19-APR-1995; 95US-0424957.  
PR 20-JUL-1994; 94US-0277660.  
PA (UYDU-) UNIV DUNDEE.  
XX  
PI Lane DP, Picklesley SM;  
XX  
DR WPI; 1996-105905/11.  
XX  
PT New cpds. which interfere with binding of MDM2 and p53 - used to  
PT develop prods. for use in the diagnosis and treatment of cancer and  
PT other malignancies  
XX  
PS Example 3; Page 26; 46pp; English.  
XX  
CC New peptides of the invention which interfere with the binding of the  
CC p53 tumour suppressor protein and the MDM2 oncogene protein contain  
CC the peptide sequences AAR89911-3 which form part of the p53 protein  
CC binding motif between amino acids 16-33 (AAR89914). Peptides contg. (15  
CC these sequence were identified by immobilising a library of peptides (15  
CC amino acids long) covering the mouse or human p53 protein and adding an  
CC extract contg. expressed MDM2 protein. The interaction was identified by  
CC the antibody DO-1. This is the sequence of a human p53 epitope for the  
CC antibody. The peptides and methods of identifying similar inhibitory  
CC peptides can be used to diagnose and treat e.g. cancer and other  
CC malignancies.  
XX  
SQ Sequence 7 AA;  
Query Match 87.0%; Score 20; DB 17; Length 7;  
Best Local Similarity 60.0%; Pred. No. 7.8e+05;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 FXXLW 5  
| | |  
Db 1 FSDLW 5  
RESULT 10  
AAR89925  
ID AAR89925 standard; peptide; 7 AA.  
XX  
AC AAR89925;  
XX  
DT 10-SEP-1996 (first entry)  
XX  
DE p53 binding site key amino acid for binding mouse MDM2.  
XX  
KW Interference; binding; p53; tumour suppressor; MDM2; oncogene; cancer;  
KW inhibition; diagnosis; treatment; malignancy; consensus; antibody.  
XX  
OS Synthetic.  
XX  
PN WO9602642-A1.  
XX  
PD 01-FEB-1996.  
XX  
PF 20-JUL-1995; 95WO-GB01719.  
XX  
PR 19-APR-1995; 95US-0424957.  
PR 20-JUL-1994; 94US-0277660.  
XX  
PS (UYDU-) UNIV DUNDEE.  
XX  
PI Lane DP, Picklesley SM;  
XX  
DR WPI; 1996-105905/11.  
XX  
PT New cpds. which interfere with binding of MDM2 and p53 - used to  
PT develop prods. for use in the diagnosis and treatment of cancer and  
PT other malignancies  
XX  
PS Example 4; Page 27; 46pp; English.

XX CC New peptides of the invention which interfere with the binding of the  
 CC p53 tumour suppressor protein and the MDM2 oncogene protein contain  
 CC the peptide sequences AAR8911-3 which form part of the p53 protein  
 CC binding motif between amino acids 16-33 (AAR8914). Peptides contg.  
 CC these sequence were identified by immobilising a library of peptides (15  
 CC amino acids long) covering the mouse or human p53 protein and adding an  
 CC extract contg. expressed MDM2 protein. This sequence represent the key  
 CC amino acids in the p53 binding site required for mouse MDM2 binding.  
 CC The peptides and methods of identifying similar inhibitory peptides can  
 CC be used to diagnose and treat e.g. cancer and other malignancies.  
 XX SQ Sequence 7 AA;

Query Match 87.0%; Score 20; DB 17; Length 7;  
 Best Local Similarity 60.0%; Pred. No. 7.8e+05;  
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 FXXLW 5  
 | | |  
 DB 3 FSDLW 7

RESULT 11  
 AAW94141  
 ID AAW94141 standard; peptide; 7 AA.  
 AC AAW94141;  
 XX  
 DT 14-APR-1999 (first entry)  
 XX  
 DE FG loop sequence of ubiquitin-binding monobody clone 213.  
 XX  
 KW Fibronectin type III; Fn3; monobody; beta-strand domain; loop region;  
 KW specific binding partner; SBP; catalysis; LRS; ubiquitin.  
 XX  
 OS Saccharomyces cerevisiae.  
 XX  
 FN WO9856915-A2.  
 XX  
 PD 17-DEC-1998.  
 XX  
 PF 12-JUN-1998; 98WO-US12099.  
 XX  
 PR 12-JUN-1997; 97US-0049410.  
 XX  
 PA (RESE ) RESEARCH CORP TECHNOLOGIES INC.  
 XX  
 PI Koide S;  
 XX  
 DR WPI; 1999-060331/05.  
 XX  
 PT Production of antibody compounds, particularly catalytic antibodies  
 PT - using a fibronectin type III molecular scaffolding comprising  
 PT beta-strand domain sequences and modified in one or more loop  
 PT sequences  
 XX  
 PS Example 10; Page 41; 96pp; English.  
 XX

The invention relates to a synthetic fibronectin type III (Fn3)  
 CC polypeptide monobody that comprises Fn3 beta-strand domain sequences  
 CC that are linked to loop region sequences (LRSs). One or more of the loop  
 CC sequences in the synthetic Fn3 vary by deletion, insertion, or  
 CC replacement of at least 2 amino acids from the corresponding LRS in  
 CC wild-type Fn3. Host cells containing an expression vector comprising the  
 CC synthetic Fn3 nucleic acid are used for the production of the Fn3  
 CC monobody. The invention also provides methods of identifying the amino  
 CC acid sequence of a polypeptide molecule (i) capable of binding to a  
 CC specific binding partner (SBP) so as to form a polypeptide:SBP complex;  
 CC (ii) capable of catalysing a chemical reaction with a catalysed rate  
 CC constant, Kcat, and an uncatalysed rate constant, Kuncat, such that the  
 CC ratio of the Kcat/Kuncat is greater than 10. Sequences AAW94139-46  
 CC represent FG loop sequences of yeast ubiquitin-binding monobodies.

XX SQ Sequence 7 AA;  
 Query Match 87.0%; Score 20; DB 21; Length 7;  
 Best Local Similarity 60.0%; Pred. No. 7.8e+05;  
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 FXXLW 5  
 | | |  
 DB 1 FADLW 5

RESULT 12  
 AAY57789  
 ID AAY57789 standard; peptide; 7 AA.  
 AC AAY57789;  
 XX  
 DT 20-MAR-2000 (first entry)  
 XX  
 DE TRAM-interaction motif derived from p53 SEQ ID NO:12.  
 XX  
 KW Transcriptional adaptor motif; TRAM; TRAM interaction motif; TRIM;  
 KW cAMP binding protein; transcriptional regulation; cytosolic; antiviral;  
 KW cell cycle inhibitor; viral transcription inhibitor; cancer; tumour;  
 KW viral disease; viral infection; cell cycle; apoptosis; growth arrest.  
 XX  
 OS Unidentified.  
 XX  
 PN WO9961608-A2.  
 XX  
 PD 02-DEC-1999.  
 XX  
 PF 26-MAY-1999; 99WO-GB01668.  
 XX  
 PR 26-MAY-1998; 98GB-0011303.  
 PR 05-JAN-1999; 99GB-0000157.  
 XX  
 PA (MOLE-) INST MOLECULAR & CELL BIOLOGY.  
 XX  
 PI O'Connor MJ, Zimmermann H;  
 XX  
 DR WPI; 2000-072620/06.  
 XX  
 PT Novel polypeptides cells useful for treating viral disease and cancer  
 PS Disclosure; Page 7; 73pp; English.  
 XX

The present invention describes a polypeptide comprising a  
 CC transcriptional adaptor motif (TRAM) or a TRAM-interaction motif  
 CC (TRIM) (I). (I) can be used for identifying compounds (II) comprising a  
 CC polypeptide capable of disrupting an interaction between a TRAM sequence  
 CC and/or a TRIM sequence. Polypeptides which bind to a TRAM sequence or a  
 CC TRIM sequence are identified by incubating, the polypeptide with (I) and  
 CC determining if the polypeptide interacts with (I). Compound (II) is  
 CC useful for preparing a pharmaceutical composition and for disrupting an  
 CC interaction between TRAM sequence and TRIM sequence in vitro, thereby  
 CC inhibiting viral transcription or cell cycle progression in mammalian  
 CC cells especially cancer cell. Compounds which disrupt interaction  
 CC between TRIM/TRAM containing polypeptides can be used therapeutically to  
 CC prevent or treat viral diseases and tumours. The polypeptides reduce  
 CC susceptibility of cells to viral infection and regulate cell cycle  
 CC including apoptosis and growth arrest and can be used to produce  
 CC antibodies against the TRIM or TRAM sequences. HPV types associated  
 CC with high risk or low risk of cervical cancer can be distinguished  
 CC based on the ability of E6 polypeptides to bind to cAMP binding protein  
 CC (CBP) TRAM sequences. The present sequence represents a TRIM sequence  
 CC given in the present invention.



XX 29-MAR-2001.  
XX 18-SEP-2000; 2000WO-GB03573.  
XX 21-SEP-1999; 99GB-0022346.  
XX (ZENE ) ZENECA LTD.  
XX Andrews CJ, Jepson I, Townson JK, Edwards R, Cummins I, Skipsey M;  
XX WPI; 2001-257978/26.  
XX Novel glutathione-S-transferase and homogluthathione synthetase  
XX sequences from soybean for producing plants which are resistant and  
XX tolerant to herbicide comprising fomesafen and/or acifluorfen -  
XX Claim 9; Page 39; 64pp; English.  
XX  
XX The invention relates to new soybean glutathione-S-transferase (GST) and  
XX a homogluthathione synthetase (HGS). The HGS is capable of catalyzing the  
XX addition of beta-alanine onto gamma-glutamylcysteine. Polynucleotides  
XX encoding the proteins of the invention are useful for producing plants  
XX which are resistant and/or tolerant to a herbicide comprising fomesafen  
XX and/or acifluorfen. Methods of the invention are useful for providing  
XX plants with further desired agronomic trait, especially resistant to a  
XX herbicide, comprising glyphosate or its salt. Further desired agronomic  
XX traits include insect resistance, nematode resistance, stress tolerance,  
XX altered field, altered nutritional value, altered quality or any other  
XX desirable agronomic trait. GST or its variant is also useful as a  
XX selectable marker gene. The present sequence represents a Glycine max  
XX HGS protein fragment.  
XX  
XX Sequence 8 AA;  
XX  
XX Query Match 87.0%; Score 20; DB 22; Length 8;  
XX Best Local Similarity 60.0%; Pred. No. 7.8e+05;  
XX Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
XX  
XX QY 1 FXXLW 5  
XX Db 2 FAGLW 6

Search completed: February 12, 2003, 11:13:44  
Job time : 13.5 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 12, 2003, 11:15:02 ; Search time 3.33333 Seconds  
(without alignments)  
38.323 Million cell updates/sec

Title: US-09-403-440A-1

Perfect score: 23

Sequence: 1 FXXLW 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 140259 seqs, 25548876 residues

Total number of hits satisfying chosen parameters: 42882

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Published Applications AA:\*  
1: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*  
8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*  
12: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep.\*  
13: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
14: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	20	87.0	6	10	US-09-214-371-83
2	20	87.0	6	10	US-09-732-384-4
3	20	87.0	6	10	US-09-732-384-5
4	20	87.0	6	12	US-10-155-059-1
5	20	87.0	7	9	US-09-903-412-36
6	20	87.0	7	10	US-09-096-749A-36
7	20	87.0	8	8	US-08-424-550B-252
8	20	87.0	9	9	US-09-884-456-8
9	20	87.0	9	9	US-09-884-456-11
10	20	87.0	9	9	US-09-884-456-14
11	20	87.0	9	10	US-09-214-371-37
12	20	87.0	9	10	US-09-214-371-38
13	20	87.0	10	10	US-09-214-371-35
14	20	87.0	10	10	US-09-214-371-36
15	20	87.0	12	10	US-09-214-371-17
16	20	87.0	12	10	US-09-214-371-24
17	20	87.0	12	10	US-09-214-371-25
18	20	87.0	15	10	US-09-950-692-6
19	20	87.0	15	10	US-09-732-384-6

## ALIGNMENTS

### RESULT 1

US-09-214-371-83

; Sequence 83, Application US/09214371B

; Patent No. US2001001851A1

; GENERAL INFORMATION:

; APPLICANT: Lane, David

; APPLICANT: Bottger, Volker

; APPLICANT: Bottger, Angelica

; APPLICANT: Pickalev, Stephen

; APPLICANT: Chene, Patrick

; APPLICANT: Hochkeppel, Heinz-Kurt

; APPLICANT: Garcia-Echeverria, Carlos

; APPLICANT: Furet, Pascal

; TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2

; FILE REFERENCE: 4-20937/A/PCT

; CURRENT APPLICATION NUMBER: US/09/214,371B

; CURRENT FILING DATE: 1999-03-26

; PRIOR APPLICATION NUMBER: PCT/EP97/03549

; PRIOR FILING DATE: 1997-07-04

; NUMBER OF SEQ ID NOS: 83

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 83

; LENGTH: 6

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:peptide, amin

; OTHER INFORMATION: acid residues 18-23 of human p53

US-09-214-371-83

Query Match 87.0%; Score 20; DB 10; Length 6;

Best Local Similarity 60.0%; Pred. No. 1.2e+05;

Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXLW 5

Db 2 FSDLW 6

### RESULT 2

US-09-732-384-4

; Sequence 4, Application US/09732384

```

; Patent No. US20020132977A1
; GENERAL INFORMATION:
; APPLICANT: Yuan, Zhi-Min
; TITLE OF INVENTION: Inhibition of p53 Degradation
; FILE REFERENCE: 21508-044
; CURRENT APPLICATION NUMBER: US/09/732,384
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 60/169,816
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Protein
; OTHER INFORMATION: fragment not in inhibitory p53 polypeptide
US-09-732-384-4

Query Match      87.0%; Score 20; DB 10; Length 6;
Best Local Similarity 60.0%; Pred. No. 1.2e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXLW 5
   |  |  |
Db 2 FSDLW 6

RESULT 3
US-09-732-384-5
; Sequence 5, Application US/09732384
; Patent No. US20020132977A1
; GENERAL INFORMATION:
; APPLICANT: Yuan, Zhi-Min
; TITLE OF INVENTION: Inhibition of p53 Degradation
; FILE REFERENCE: 21508-044
; CURRENT APPLICATION NUMBER: US/09/732,384
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 60/169,816
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Protein
; OTHER INFORMATION: fragment not in inhibitory p53 polypeptide
US-09-732-384-5

Query Match      87.0%; Score 20; DB 10; Length 6;
Best Local Similarity 60.0%; Pred. No. 1.2e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXLW 5
   |  |  |
Db 2 FSGLW 6

RESULT 4
US-10-155-059-1
; Sequence 1, Application US/10155059
; Patent No. US20020147173A1
; GENERAL INFORMATION:
; APPLICANT: Kaelin, William
; TITLE OF INVENTION: METHODS OF TREATMENT USING
; NBS-1, ANTIBODIES AND PROTEINS THERE TO, AND USES OF THE
; ANTIBODIES

```

```

; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon Peabody LLP
; STREET: 101 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/155,059
; FILING DATE: 24-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/081,975
; FILING DATE: 12-MAY-1998
; APPLICATION NUMBER: 60/046,207
; FILING DATE: 12-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Eisenstein, Ronald I
; REGISTRATION NUMBER: 30,628
; REFERENCE/DOCKET NUMBER: 47400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-345-6054
; TELEFAX: 617-345-1300
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-155-059-1

Query Match      87.0%; Score 20; DB 12; Length 6;
Best Local Similarity 60.0%; Pred. No. 1.2e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXLW 5
   |  |  |
Db 2 FSDLW 6

RESULT 5
US-09-903-412-36
; Sequence 36, Application US/09903412
; Publication No. US20030027319A1
; GENERAL INFORMATION:
; APPLICANT: Koide, Shohei
; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
; FILE REFERENCE: 109.050US1
; CURRENT APPLICATION NUMBER: US/09/903,412
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US 60/217,474
; PRIOR FILING DATE: 2000-07-11
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The sequence of the FG loop of ubiquitin-binding
; OTHER INFORMATION: monobody clone 213.
US-09-903-412-36

Query Match      87.0%; Score 20; DB 9; Length 7;
Best Local Similarity 60.0%; Pred. No. 1.2e+05;

```

Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLM 5  
| |  
Db 1 FADLM 5

## RESULT 6

US-09-096-749A-36  
; Sequence 36, Application US/09096749A  
; Patent No. US20020019517A1  
; GENERAL INFORMATION:  
; APPLICANT: Koieda, Shohei  
; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES  
; NUMBER OF SEQUENCES: 118  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.  
; STREET: 121 South Eighth Street, Ste. 1600  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: USA  
; ZIP: 55402

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/096,749A  
; FILING DATE: June 12, 1998  
; PRIOR APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ann S. Viksnins

REGISTRATION NUMBER: 37,748  
REFERENCE/DOCKET NUMBER: 109,034US1  
TELEPHONE: (612) 373-6900  
TELEFAX: (612) 339-3061

INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
US-09-096-749A-36

Query Match 87.0%; Score 20; DB 10; Length 7;  
Best Local Similarity 60.0%; Pred. No. 1.2e+05;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLM 5  
| |  
Db 1 FADLM 5

## RESULT 7

US-08-424-550B-252  
; Sequence 252, Application US/08424550B  
; Patent No. US2002011947A1  
; GENERAL INFORMATION:

APPLICANT: JOHN N. SIMONS  
APPLICANT: TAMI J. PILOT-MATTIAS  
APPLICANT: GEORGE J. DAWSON  
APPLICANT: GEORGE G. SCHLAUDER  
APPLICANT: SURESH M. DESAI  
APPLICANT: THOMAS P. LEARY

APPLICANT: ANTHONY SCOTT MUERHOFF  
APPLICANT: JAMES C. ERKER  
APPLICANT: SHERI L. BUIJK  
APPLICANT: ISA K. MUSHAWAR  
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS  
REAGENTS AND METHODS FOR THEIR USE  
NUMBER OF SEQUENCES: 716  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D  
STREET: 100 ABBOTT PARK ROAD  
CITY: ABBOTT PARK  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/424,550B  
; FILING DATE:  
; CLASSIFICATION: 435435

ATTORNEY/AGENT INFORMATION:  
NAME: FOREMSKI, PRISCILLA E.  
REGISTRATION NUMBER: 33,207  
REFERENCE/DOCKET NUMBER: 5527.PC.01

TELEPHONE: 708-937-6365  
TELEFAX: 708-938-2623

INFORMATION FOR SEQ ID NO: 252:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-424-550B-252

Query Match 87.0%; Score 20; DB 8; Length 8;  
Best Local Similarity 60.0%; Pred. No. 1.2e+05;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLM 5  
| |  
Db 1 FSHLM 5

## RESULT 8

US-09-884-456-8  
; Sequence 8, Application US/09884456  
; Publication No. US20030027317A1  
; GENERAL INFORMATION:  
; APPLICANT: Houghton, Michael  
; APPLICANT: Choo, Oul-Lim  
; APPLICANT: Kuo, George  
TITLE OF INVENTION: Hepatitis C virus protease  
FILE REFERENCE: 223002010005  
CURRENT APPLICATION NUMBER: US/09/884,456  
CURRENT FILING DATE: 2001-06-18  
PRIOR APPLICATION NUMBER: 09/253,230  
PRIOR FILING DATE: 1999-02-19  
PRIOR APPLICATION NUMBER: 08/709,177  
PRIOR FILING DATE: 1996-09-06  
PRIOR APPLICATION NUMBER: 08/440,548  
PRIOR FILING DATE: 1995-05-12  
PRIOR APPLICATION NUMBER: 08/350,884  
PRIOR FILING DATE: 1994-12-06  
PRIOR APPLICATION NUMBER: 07/680,296  
PRIOR FILING DATE: 1991-04-04  
PRIOR APPLICATION NUMBER: 07/505,433  
PRIOR FILING DATE: 1990-04-04  
NUMBER OF SEQ ID NOS: 90  
SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 8  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: West Nile Fever virus  
; FEATURE:  
; OTHER INFORMATION: West Nile Fever virus protease  
US-09-884-456-8

Query Match 87.0%; Score 20; DB 9; Length 9;  
Best Local Similarity 60.0%; Pred. No. 1.2e+05;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5  
| | |  
Db 1 FHTLW 5

## RESULT 9

US-09-884-456-11  
; Sequence 11, Application US/09884456  
; Publication No. US20030027317A1  
; GENERAL INFORMATION:

; APPLICANT: Houghton, Michael  
; APPLICANT: Choo, Oui-Lim  
; TITLE OF INVENTION: Hepatitis C virus protease  
; FILE REFERENCE: 223002010005  
; CURRENT APPLICATION NUMBER: US/09/884,456  
; CURRENT FILING DATE: 2001-06-18  
; PRIOR APPLICATION NUMBER: 09/253,230  
; PRIOR FILING DATE: 1999-02-19  
; PRIOR APPLICATION NUMBER: 08/709,177  
; PRIOR FILING DATE: 1996-09-06  
; PRIOR APPLICATION NUMBER: 08/440,548  
; PRIOR FILING DATE: 1995-05-12  
; PRIOR APPLICATION NUMBER: 08/350,884  
; PRIOR FILING DATE: 1994-12-06  
; PRIOR APPLICATION NUMBER: 07/680,296  
; PRIOR FILING DATE: 1991-04-04  
; PRIOR APPLICATION NUMBER: 07/505,433  
; PRIOR FILING DATE: 1990-04-04  
; NUMBER OF SEQ ID NOS: 90  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Murray Valley virus  
; FEATURE:  
; OTHER INFORMATION: Murray Valley virus protease  
US-09-884-456-11

Query Match 87.0%; Score 20; DB 9; Length 9;  
Best Local Similarity 60.0%; Pred. No. 1.2e+05;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5  
| | |  
Db 1 FHTLW 5

## RESULT 10

US-09-884-456-14  
; Sequence 14, Application US/09884456  
; Publication No. US20030027317A1  
; GENERAL INFORMATION:

; APPLICANT: Houghton, Michael  
; APPLICANT: Choo, Oui-Lim  
; TITLE OF INVENTION: Hepatitis C virus protease  
; FILE REFERENCE: 223002010005  
; CURRENT APPLICATION NUMBER: US/09/884,456  
; CURRENT FILING DATE: 2001-06-18  
; PRIOR APPLICATION NUMBER: 09/253,230

; PRIOR FILING DATE: 1999-02-19  
; PRIOR APPLICATION NUMBER: 08/709,177  
; PRIOR FILING DATE: 1996-09-06  
; PRIOR APPLICATION NUMBER: 08/440,548  
; PRIOR FILING DATE: 1995-05-12  
; PRIOR APPLICATION NUMBER: 08/350,884  
; PRIOR FILING DATE: 1994-12-06  
; PRIOR APPLICATION NUMBER: 07/680,296  
; PRIOR FILING DATE: 1991-04-04  
; PRIOR APPLICATION NUMBER: 07/505,433  
; NUMBER OF SEQ ID NOS: 90  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Kunjin virus  
; FEATURE:  
; OTHER INFORMATION: Kunjin virus protease  
US-09-884-456-14

Query Match 87.0%; Score 20; DB 9; Length 9;  
Best Local Similarity 60.0%; Pred. No. 1.2e+05;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5  
| | |  
Db 1 FHTLW 5

## RESULT 11

US-09-214-371-37  
; Sequence 37, Application US/09214371B  
; Patent No. US20010018511A1  
; GENERAL INFORMATION:  
; APPLICANT: Lane, David  
; APPLICANT: Bottger, Volker  
; APPLICANT: Bottger, Angelica  
; APPLICANT: Pickseley, Stephen  
; APPLICANT: Chene, Patrick  
; APPLICANT: Hochkeppel, Heinz-Kurt  
; APPLICANT: Garcia-Echeverria, Carlos  
; APPLICANT: Furet, Pascal  
; TITLE OF INVENTION: Inhibitors of the interaction of P53 and MDM2  
; FILE REFERENCE: 4-20937/A/PCT  
; CURRENT APPLICATION NUMBER: US/09/214,371B  
; CURRENT FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: PCT/EP97/03549  
; PRIOR FILING DATE: 1997-07-04  
; NUMBER OF SEQ ID NOS: 83  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 37  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:peptide  
; NAME/KEY: VARIANT  
; LOCATION: (1)  
; OTHER INFORMATION: X = Ac=Cys (Acrd)  
; NAME/KEY: VARIANT  
; LOCATION: (9)  
; OTHER INFORMATION: X = Pro-NH2  
US-09-214-371-37

Query Match 87.0%; Score 20; DB 10; Length 9;  
Best Local Similarity 60.0%; Pred. No. 1.2e+05;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5  
| | |  
Db 4 FSDLW 8

RESULT 12  
US-09-214-371-38  
; Sequence 38, Application US/09214371B  
; Patent No. US20010018511A1  
; GENERAL INFORMATION:  
; APPLICANT: Lane, David  
; APPLICANT: Bottger, Volker  
; APPLICANT: Bottger, Angelica  
; APPLICANT: Picksley, Stephen  
; APPLICANT: Chene, Patrick  
; APPLICANT: Hochkeppel, Heinz-Kurt  
; APPLICANT: Garcia-Echeverria, Carlos  
; APPLICANT: Furet, Pascal  
; TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2  
; FILE REFERENCE: 4-20937/A/PCT  
; CURRENT APPLICATION NUMBER: US/09/214,371B  
; CURRENT FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: PCT/EP97/03549  
; PRIOR FILING DATE: 1997-07-04  
; NUMBER OF SEQ ID NOS: 83  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 38  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:peptide  
; NAME/KEY: VARIANT  
; LOCATION: (1)  
; OTHER INFORMATION: x = Ac-Cys  
; NAME/KEY: VARIANT  
; LOCATION: (9)  
; OTHER INFORMATION: X = Pro-NH2  
US-09-214-371-38

Query Match 87.0%; Score 20; DB 10; Length 9;  
Best Local Similarity 60.0%; Pred. No. 1.2e+05;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5  
Db 4 FSDLW 8

RESULT 13  
US-09-214-371-35  
; Sequence 35, Application US/09214371B  
; Patent No. US20010018511A1  
; GENERAL INFORMATION:  
; APPLICANT: Lane, David  
; APPLICANT: Bottger, Volker  
; APPLICANT: Bottger, Angelica  
; APPLICANT: Picksley, Stephen  
; APPLICANT: Chene, Patrick  
; APPLICANT: Hochkeppel, Heinz-Kurt  
; APPLICANT: Garcia-Echeverria, Carlos  
; APPLICANT: Furet, Pascal  
; TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2  
; FILE REFERENCE: 4-20937/A/PCT  
; CURRENT APPLICATION NUMBER: US/09/214,371B  
; CURRENT FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: PCT/EP97/03549  
; PRIOR FILING DATE: 1997-07-04  
; NUMBER OF SEQ ID NOS: 83  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 35  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:peptide  
; NAME/KEY: VARIANT

; LOCATION: (1)  
; OTHER INFORMATION: X = Ac-Cys (Acrid)  
; NAME/KEY: VARIANT  
; LOCATION: (10)  
; OTHER INFORMATION: X = Pro-NH2  
US-09-214-371-35

Query Match 87.0%; Score 20; DB 10; Length 10;  
Best Local Similarity 60.0%; Pred. No. 1.4e+02;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5  
Db 5 FSDLW 9

RESULT 14  
US-09-214-371-36  
; Sequence 36, Application US/09214371B  
; Patent No. US20010018511A1  
; GENERAL INFORMATION:  
; APPLICANT: Lane, David  
; APPLICANT: Bottger, Volker  
; APPLICANT: Bottger, Angelica  
; APPLICANT: Picksley, Stephen  
; APPLICANT: Chene, Patrick  
; APPLICANT: Hochkeppel, Heinz-Kurt  
; APPLICANT: Garcia-Echeverria, Carlos  
; APPLICANT: Furet, Pascal  
; TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2  
; FILE REFERENCE: 4-20937/A/PCT  
; CURRENT APPLICATION NUMBER: US/09/214,371B  
; CURRENT FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: PCT/EP97/03549  
; PRIOR FILING DATE: 1997-07-04  
; NUMBER OF SEQ ID NOS: 83  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 36  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:peptide  
; NAME/KEY: VARIANT  
; LOCATION: (1)  
; OTHER INFORMATION: X = Ac-Cys  
; NAME/KEY: VARIANT  
; LOCATION: (10)  
; OTHER INFORMATION: x = Pro-NH2  
US-09-214-371-36

Query Match 87.0%; Score 20; DB 10; Length 10;  
Best Local Similarity 60.0%; Pred. No. 1.4e+02;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5  
Db 5 FSDLW 9

RESULT 15  
US-09-214-371-17  
; Sequence 17, Application US/09214371B  
; Patent No. US20010018511A1  
; GENERAL INFORMATION:  
; APPLICANT: Lane, David  
; APPLICANT: Bottger, Volker  
; APPLICANT: Bottger, Angelica  
; APPLICANT: Picksley, Stephen  
; APPLICANT: Chene, Patrick  
; APPLICANT: Hochkeppel, Heinz-Kurt  
; APPLICANT: Garcia-Echeverria, Carlos  
; APPLICANT: Furet, Pascal

; TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2  
; FILE REFERENCE: 4-20937/A/PCT  
; CURRENT APPLICATION NUMBER: US/09/214,371B  
; CURRENT FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: PCT/EP97/03549  
; PRIOR FILING DATE: 1997-07-04  
; NUMBER OF SEQ ID NOS: 83  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 17  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:peptide  
US-09-214-371-17

Query Match 87.0%; Score 20; DB 10; Length 12;  
Best Local Similarity 60.0%; Pred. No. 1.7e+02;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXLW 5  
Db 4 FSDLW 8

Search completed: February 12, 2003, 11:25:07  
Job time : 4.33333 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 12, 2003, 11:13:52 ; Search time 99.375 Seconds  
(without alignments)  
32.439 Million cell updates/sec

Title: US-09-403-440A-1

Perfect score: 23  
Sequence: 1 FXXILW 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters: 2260083

Minimum DB seq length: 0  
Maximum DB seq length: 25

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending\_Patents\_AA\_Main.\*

1: /cgn2\_6/ptodata/1/paa/PCRTUS\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/paa/US06\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/paa/US07\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/paa/US080\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/paa/US081\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/paa/US082\_COMB.pep.\*  
7: /cgn2\_6/ptodata/1/paa/US083\_COMB.pep.\*  
8: /cgn2\_6/ptodata/1/paa/US084\_COMB.pep.\*  
9: /cgn2\_6/ptodata/1/paa/US085\_COMB.pep.\*  
10: /cgn2\_6/ptodata/1/paa/US086\_COMB.pep.\*  
11: /cgn2\_6/ptodata/1/paa/US087\_COMB.pep.\*  
12: /cgn2\_6/ptodata/1/paa/US088\_COMB.pep.\*  
13: /cgn2\_6/ptodata/1/paa/US089\_COMB.pep.\*  
14: /cgn2\_6/ptodata/1/paa/US090\_COMB.pep.\*  
15: /cgn2\_6/ptodata/1/paa/US091\_COMB.pep.\*  
16: /cgn2\_6/ptodata/1/paa/US092\_COMB.pep.\*  
17: /cgn2\_6/ptodata/1/paa/US093\_COMB.pep.\*  
18: /cgn2\_6/ptodata/1/paa/US094\_COMB.pep.\*  
19: /cgn2\_6/ptodata/1/paa/US095\_COMB.pep.\*  
20: /cgn2\_6/ptodata/1/paa/US096\_COMB.pep.\*  
21: /cgn2\_6/ptodata/1/paa/US097\_COMB.pep.\*  
22: /cgn2\_6/ptodata/1/paa/US098\_COMB.pep.\*  
23: /cgn2\_6/ptodata/1/paa/US099\_COMB.pep.\*  
24: /cgn2\_6/ptodata/1/paa/US100\_COMB.pep.\*  
25: /cgn2\_6/ptodata/1/paa/US101\_COMB.pep.\*  
26: /cgn2\_6/ptodata/1/paa/US102\_COMB.pep.\*  
27: /cgn2\_6/ptodata/1/paa/US60\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	91.3	11	6	US-08-277-660-16
2	21	91.3	15	23	US-09-936-956-10
3	20	87.0	5	1	PCT-US99-02405-11
4	20	87.0	5	1	PCT-US99-26277-114
5	20	87.0	5	20	US-09-601-558-11
6	20	87.0	5	22	US-09-831-047B-114

7	20	87.0	5	22	US-09-831-047C-114	Sequence 114, App
8	20	87.0	5	22	US-09-894-594-11	Sequence 11, Appl
9	20	87.0	6	1	PCT-US99-25044-130	Sequence 130, App
10	20	87.0	6	6	US-08-277-660-2	Sequence 2, Appli
11	20	87.0	6	6	US-08-277-660-3	Sequence 3, Appli
12	20	87.0	6	16	US-09-214-371-83	Sequence 83, Appl
13	20	87.0	6	18	US-09-428-082-130	Sequence 130, App
14	20	87.0	6	18	US-09-428-082B-130	Sequence 130, App
15	20	87.0	6	19	US-09-563-286B-130	Sequence 130, App
16	20	87.0	6	19	US-09-563-286C-130	Sequence 130, App
17	20	87.0	6	21	US-09-732-384-4	Sequence 4, Appli
18	20	87.0	6	21	US-09-732-384-5	Sequence 5, Appli
19	20	87.0	6	25	US-10-155-059-1	Sequence 1, Appli
20	20	87.0	7	6	US-08-277-660-27	Sequence 27, Appl
21	20	87.0	7	14	US-09-096-749A-36	Sequence 36, Appl
22	20	87.0	7	20	US-09-637-614-36	Sequence 24, Appl
23	20	87.0	7	21	US-09-701-080A-24	Sequence 24, Appl
24	20	87.0	7	23	US-09-903-412-36	Sequence 36, Appl
25	20	87.0	7	25	US-10-165-155-36	Sequence 36, Appl
26	20	87.0	7	25	US-10-190-162-36	Sequence 36, Appl
27	20	87.0	8	1	PCT-US02-09105-304	Sequence 304, App
28	20	87.0	8	1	PCT-US02-09135-206	Sequence 206, App
29	20	87.0	8	1	PCT-US02-09188-604	Sequence 604, App
30	20	87.0	8	1	PCT-US02-09257-393	Sequence 393, App
31	20	87.0	8	1	PCT-US02-09370-621	Sequence 621, App
32	20	87.0	8	1	PCT-US02-09922-382	Sequence 382, App
33	20	87.0	8	7	US-08-344-185B-123	Sequence 123, App
34	20	87.0	8	7	US-08-344-185C-123	Sequence 123, App
35	20	87.0	8	8	US-08-424-550A-252	Sequence 252, App
36	20	87.0	8	8	US-08-424-550B-252	Sequence 252, App
37	20	87.0	8	8	US-08-467-344A-252	Sequence 252, App
38	20	87.0	8	8	US-08-486-749-252	Sequence 252, App
39	20	87.0	8	8	US-08-488-445A-252	Sequence 252, App
40	20	87.0	8	8	US-08-488-446-252	Sequence 252, App
41	20	87.0	8	18	US-09-458-297-203	Sequence 203, App
42	20	87.0	8	18	US-09-458-297-345	Sequence 345, App
43	20	87.0	8	18	US-09-458-297-475	Sequence 475, App
44	20	87.0	8	18	US-09-458-297-690	Sequence 690, App
45	20	87.0	8	18	US-09-458-297-902	Sequence 902, App

#### ALIGNMENTS

RESULT 1  
US-08-277-660-16  
; Sequence 16, Application US/08277660  
; GENERAL INFORMATION:  
; APPLICANT: Picklesley, Steven M.  
; APPLICANT: Lane, David P.  
; TITLE OF INVENTION: Interruption of Binding of MDM2 and p53  
; TITLE OF INVENTION: Protein and Therapeutic Application Thereof  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert  
; STREET: Four Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States  
; ZIP: 94111-4187  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/277,660  
; FILING DATE: 20-JUL-1994  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dreger, Walter H.  
; REGISTRATION NUMBER: 24,190  
; REFERENCE/DOCKET NUMBER: A-60244/WHD

; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (415) 781-1989  
 ; TELEFAX: (415) 398-3249  
 ; TELEX: 910 277299  
 ; INFORMATION FOR SEQ ID NO: 16:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 11 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS:  
 ; TOPOLOGY: linear  
 ; US-08-277-660-16

Query Match 91.3%; Score 21; DB 6; Length 11;  
 Best Local Similarity 60.0%; Pred. No. 6.1e+03;  
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5  
 | |  
 Db 5 FSALW 9

RESULT 2  
 US-09-936-956-10  
 ; Sequence 10, Application US/09936956  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kudos Pharmaceuticals Limited  
 ; APPLICANT: Jackson, Stephen P  
 ; APPLICANT: Durocher, Daniel  
 ; TITLE OF INVENTION: Screening Methods Based on FHA Domains  
 ; FILE REFERENCE: MEWE014  
 ; CURRENT APPLICATION NUMBER: US/09/936,956  
 ; CURRENT FILING DATE: 2001-09-17  
 ; PRIOR APPLICATION NUMBER: GB 9906432.1  
 ; PRIOR FILING DATE: 1999-03-19  
 ; PRIOR APPLICATION NUMBER: GB 9915075.7  
 ; PRIOR FILING DATE: 1999-06-28  
 ; NUMBER OF SEQ ID NOS: 57  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 10  
 ; LENGTH: 15  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthesised  
 ; NAME/KEY: MOD\_RES  
 ; LOCATION: (8)  
 ; OTHER INFORMATION: PHOSPHORYLATION  
 ; US-09-936-956-10

Query Match 91.3%; Score 21; DB 23; Length 15;  
 Best Local Similarity 60.0%; Pred. No. 7.7e+03;  
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5  
 | |  
 Db 9 FSALW 13

RESULT 3  
 PCT-US99-02405-11  
 ; Sequence 11, Application PC/TUS9902405  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Trustees of the University of Pennsylvania  
 ; TITLE OF INVENTION: Peptide Mimotopes of Carbohydrate Antigens  
 ; FILE REFERENCE: UPN3544  
 ; CURRENT APPLICATION NUMBER: PCT/US99/02405  
 ; CURRENT FILING DATE: 1999-02-04  
 ; EARLIER APPLICATION NUMBER: 60/073,690  
 ; PRIOR FILING DATE: 1998-02-04  
 ; NUMBER OF SEQ ID NOS: 60  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 11  
 ; LENGTH: 5

; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Novel Sequence  
 ; PCT-US99-02405-11

Query Match 87.0%; Score 20; DB 1; Length 5;  
 Best Local Similarity 60.0%; Pred. No. 4.2e+06;  
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5  
 | |  
 Db 1 FSLW 5

RESULT 4  
 PCT-US99-26277-114  
 ; Sequence 114, Application PC/TUS9926277  
 ; GENERAL INFORMATION:  
 ; APPLICANT: The Wistar Institute of Anatomy and Biology  
 ; APPLICANT: The Trustees of the University of Pennsylvania  
 ; APPLICANT: Blaszczyk-Thurin, Magdalena  
 ; APPLICANT: Keiber-Emmons, Thomas  
 ; TITLE OF INVENTION: Compositions and Methods For Treatment of Cancer  
 ; FILE REFERENCE: WST93PCT  
 ; CURRENT APPLICATION NUMBER: PCT/US99/26277  
 ; CURRENT FILING DATE: 1999-11-05  
 ; EARLIER APPLICATION NUMBER: 60/107,478  
 ; EARLIER FILING DATE: 1998-11-06  
 ; NUMBER OF SEQ ID NOS: 121  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 114  
 ; LENGTH: 5  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence:  
 ; OTHER INFORMATION: peptido-mimetic of a Lewis antigen  
 ; PCT-US99-26277-114

Query Match 87.0%; Score 20; DB 1; Length 5;  
 Best Local Similarity 60.0%; Pred. No. 4.2e+06;  
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5  
 | |  
 Db 1 FSLW 5

RESULT 5  
 US-09-601-558-11  
 ; Sequence 11, Application US/09601558  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kieber-Emmons, Thomas  
 ; APPLICANT: The Trustees of the University of Pennsylvania  
 ; TITLE OF INVENTION: Peptide Mimotopes Of Carbohydrate Antigens  
 ; FILE REFERENCE: UPN3567  
 ; CURRENT APPLICATION NUMBER: US/09/601,558  
 ; CURRENT FILING DATE: 2000-08-03  
 ; PRIOR APPLICATION NUMBER: PCT/US99/02405  
 ; PRIOR FILING DATE: 1999-02-04  
 ; PRIOR APPLICATION NUMBER: 60/073,690  
 ; PRIOR FILING DATE: 1998-02-04  
 ; NUMBER OF SEQ ID NOS: 60  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 11  
 ; LENGTH: 5  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Novel Sequence  
 ; US-09-601-558-11



Query Match 87.0%; Score 20; DB 20; Length 5;  
Best Local Similarity 60.0%; Pred. No. 4.2e+06;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXLW 5  
|  
|  
|  
DB 1 FSLWL 5

RESULT 6  
US-09-831-047B-114  
; Sequence 114, Application US/09831047B  
; GENERAL INFORMATION:  
; APPLICANT: The Wistar Institute of Anatomy and Biology  
; APPLICANT: The Trustees of the University of Pennsylvania  
; APPLICANT: Blaszczyk-Thurin, Magdalena  
; APPLICANT: Kiebert-Emmons, Thomas  
; TITLE OF INVENTION: Compositions and Methods For Treatment of Cancer  
; FILE REFERENCE: WST93AUSA  
; CURRENT APPLICATION NUMBER: US/09/831,047B  
; PRIOR FILING DATE: 2001-08-14  
; PRIOR FILING DATE: 2001-08-14  
; PRIOR FILING DATE: 1998-11-06  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 114  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: peptido-mimetic of a Lewis antigen  
US-09-831-047B-114

Query Match 87.0%; Score 20; DB 22; Length 5;  
Best Local Similarity 60.0%; Pred. No. 4.2e+06;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXLW 5  
|  
|  
|  
DB 1 FSLWL 5

RESULT 7  
US-09-831-047C-114  
; Sequence 114, Application US/09831047C  
; GENERAL INFORMATION:  
; APPLICANT: The Wistar Institute of Anatomy and Biology  
; APPLICANT: The Trustees of the University of Pennsylvania  
; APPLICANT: Blaszczyk-Thurin, Magdalena  
; APPLICANT: Kiebert-Emmons, Thomas  
; TITLE OF INVENTION: Compositions and Methods For Treatment of Cancer  
; FILE REFERENCE: WST93AUSA  
; CURRENT APPLICATION NUMBER: US/09/831,047C  
; PRIOR FILING DATE: 2001-05-03  
; PRIOR FILING DATE: 2001-05-03  
; PRIOR FILING DATE: 1998-11-06  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 114  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: peptido-mimetic of a Lewis antigen  
US-09-831-047C-114

Query Match 87.0%; Score 20; DB 22; Length 5;  
Best Local Similarity 60.0%; Pred. No. 4.2e+06;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXLW 5  
|  
|  
|  
DB 1 FSLWL 5

## RESULT 8

US-09-894-594-11  
; Sequence 11, Application US/09894594  
; GENERAL INFORMATION:  
; APPLICANT: Kiebert-Emmons, Thomas  
; APPLICANT: Weiner, David B.  
; APPLICANT: Monzavi-Karbassi, Behjatolah  
; TITLE OF INVENTION: Peptide Mimotopes of Carbohydrate Antigens and DNA Molecules Encoded by Peptide Mimotopes  
; TITLE OF INVENTION: Same  
; FILE REFERENCE: UPN-3984  
; CURRENT APPLICATION NUMBER: US/09/894,594  
; CURRENT FILING DATE: 2001-06-28  
; PRIOR FILING DATE: 2000-11-07  
; PRIOR FILING DATE: 2000-11-07  
; PRIOR FILING DATE: 1999-02-04  
; PRIOR FILING DATE: 1998-02-04  
; PRIOR FILING DATE: 1998-02-04  
; PRIOR FILING DATE: 2000-06-28  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 11  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Novel Sequence  
US-09-894-594-11

Query Match 87.0%; Score 20; DB 22; Length 5;  
Best Local Similarity 60.0%; Pred. No. 4.2e+06;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXLW 5  
|  
|  
|  
DB 1 FSLWL 5

RESULT 9  
PCT-US99-25044-130  
; Sequence 130, Application PC/TUS9925044  
; GENERAL INFORMATION:  
; APPLICANT: LIU, CHUAN-FA  
; APPLICANT: PEIGE, ULRICH  
; APPLICANT: CHEETHAM, JANET  
; APPLICANT: BOONE, THOMAS CHARLES  
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS  
; FILE REFERENCE: A-527  
; CURRENT APPLICATION NUMBER: PCT/US99/25044  
; CURRENT FILING DATE: 1999-10-25  
; EARLIER APPLICATION NUMBER: 60/105,371  
; EARLIER FILING DATE: 1998-10-23  
; NUMBER OF SEQ ID NOS: 1133  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 130  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:MDM/HDM  
; OTHER INFORMATION: ANTAGONIST PEPTIDE  
PCT-US99-25044-130

Query Match 87.0%; Score 20; DB 1; Length 6;  
Best Local Similarity 60.0%; Pred. No. 4.2e+06;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXLW 5  
|  
|  
|  
DB 2 FSLWL 6

```

RESULT 10
US-08-277-660-2
; Sequence 2, Application US/08277660
; GENERAL INFORMATION:
; APPLICANT: Picksley, Steven M.
; APPLICANT: Lane, David P.
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/277,660
; FILING DATE: 20-JUL-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-60244/WHID
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-277-660-2

Query Match 87.0%; Score 20; DB 6; Length 6;
Best Local Similarity 60.0%; Pred. No. 4.2e+06;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5
Db 2 FSGLW 6

RESULT 11
US-08-277-660-3
; Sequence 3, Application US/08277660
; GENERAL INFORMATION:
; APPLICANT: Picksley, Steven M.
; APPLICANT: Lane, David P.
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30

```

```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/277,660
; FILING DATE: 20-JUL-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-60244/WHID
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-277-660-3

Query Match 87.0%; Score 20; DB 6; Length 6;
Best Local Similarity 60.0%; Pred. No. 4.2e+06;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5
Db 2 FSGLW 6

RESULT 12
US-09-214-371-83
; Sequence 83, Application US/09214371B
; GENERAL INFORMATION:
; APPLICANT: Lane, David
; APPLICANT: Bottger, Volker
; APPLICANT: Bottger, Angelica
; APPLICANT: Picksley, Stephen
; APPLICANT: Chene, Patrick
; APPLICANT: Hochkeppel, Heinz-Kurt
; APPLICANT: Garcia-Echeverria, Carlos
; APPLICANT: Furet, Pascal
; TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2
; FILE REFERENCE: 4-20937/A/PCT
; CURRENT APPLICATION NUMBER: US/09/214,371B
; CURRENT FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: PCT/EP97/03549
; PRIOR FILING DATE: 1997-07-04
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 83
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:peptide, amin
; OTHER INFORMATION: acid residues 18-23 of human p53
US-09-214-371-83

Query Match 87.0%; Score 20; DB 16; Length 6;
Best Local Similarity 60.0%; Pred. No. 4.2e+06;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5
Db 2 FSGLW 6

RESULT 13
US-09-428-082-130
; Sequence 130, Application US/09428082
; GENERAL INFORMATION:
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: FEIGE, ULRICH

```

; APPLICANT: CHEETHAM, JANET  
; APPLICANT: BOONE, THOMAS CHARLES  
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS  
; FILE REFERENCE: A-527  
; CURRENT APPLICATION NUMBER: US/09/428,082  
; CURRENT FILING DATE: 1999-10-22  
; EARLIER APPLICATION NUMBER: 60/105,371  
; EARLIER FILING DATE: 1998-10-23  
; NUMBER OF SEQ ID NOS: 1133  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 130  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:MDM/HDM  
; OTHER INFORMATION: ANTAGONIST PEPTIDE  
US-09-428-082B-130

Query Match 87.0%; Score 20; DB 18; Length 6;  
Best Local Similarity 60.0%; Pred. No. 4.2e+06;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5  
| | |  
Db 2 FSDLW 6

RESULT 14  
US-09-428-082B-130  
; Sequence 130, Application US/09428082B  
; GENERAL INFORMATION:  
; APPLICANT: FEIGE, ULRICH  
; APPLICANT: LIU, CHUAN-FA  
; APPLICANT: CHEETHAM, JANET C.  
; APPLICANT: BOONE, THOMAS CHARLES  
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS  
; FILE REFERENCE: A-527  
; CURRENT APPLICATION NUMBER: US/09/428,082B  
; CURRENT FILING DATE: 1999-10-22  
; PRIOR APPLICATION NUMBER: 60/105,371  
; PRIOR FILING DATE: 1998-10-23  
; NUMBER OF SEQ ID NOS: 1133  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 130  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: MDM/HDM ANTAGONIST PEPTIDE  
US-09-428-082B-130

Query Match 87.0%; Score 20; DB 18; Length 6;  
Best Local Similarity 60.0%; Pred. No. 4.2e+06;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5  
| | |  
Db 2 FSDLW 6

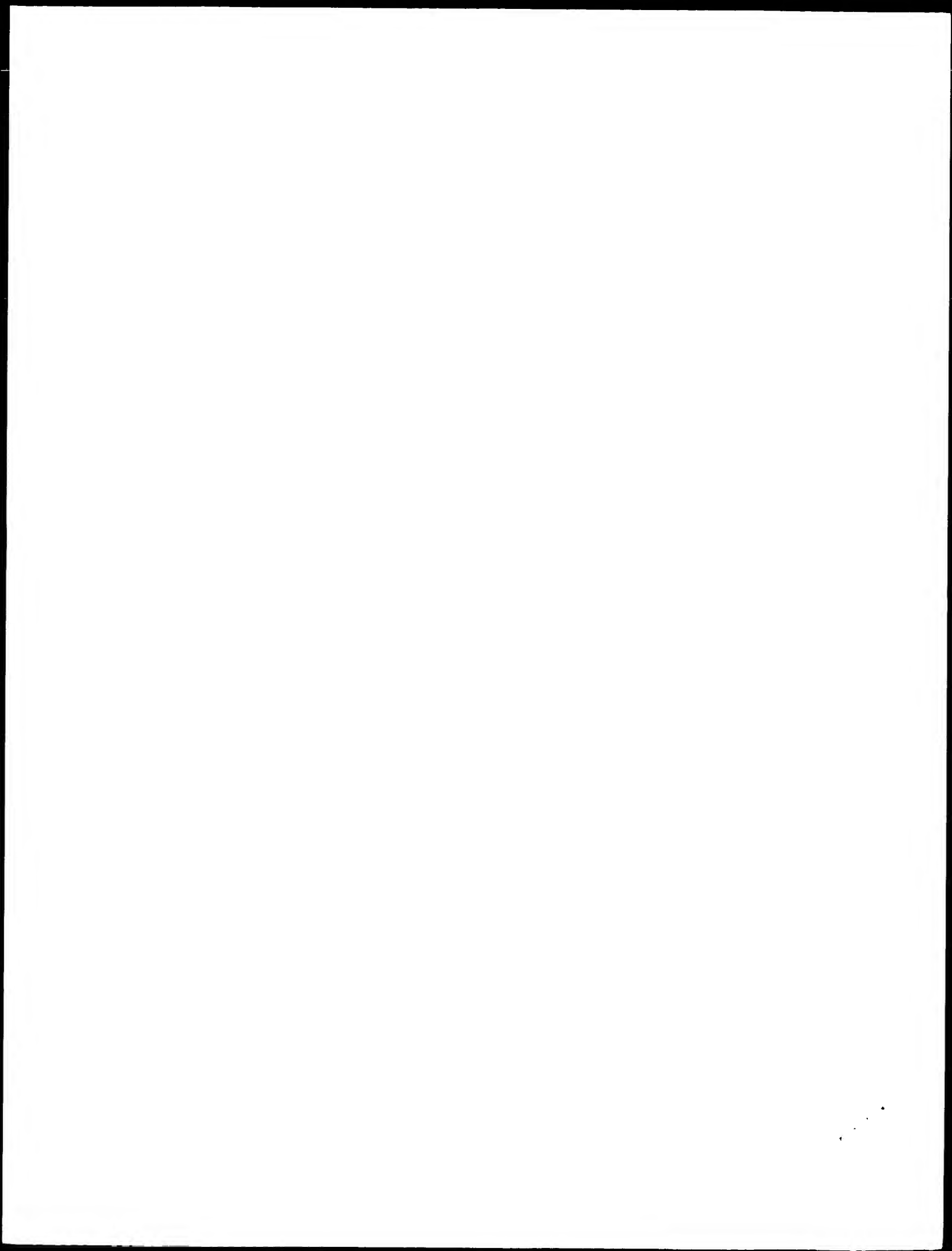
RESULT 15  
US-09-563-286B-130  
; Sequence 130, Application US/09563286B  
; GENERAL INFORMATION:  
; APPLICANT: FEIGE, ULRICH  
; APPLICANT: LIU, CHUAN-FA  
; APPLICANT: CHEETHAM, JANET C.  
; APPLICANT: BOONE, THOMAS CHARLES  
; APPLICANT: GUDAS, JEAN MARIE  
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS  
; FILE REFERENCE: A-527A  
; CURRENT APPLICATION NUMBER: US/09/563,286B

; CURRENT FILING DATE: 2000-05-03  
; PRIOR APPLICATION NUMBER: 09/428,082  
; PRIOR FILING DATE: 1999-10-22  
; PRIOR APPLICATION NUMBER: 60/105,371  
; PRIOR FILING DATE: 1998-10-23  
; NUMBER OF SEQ ID NOS: 1151  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 130  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Mdm/hdm antagonist peptide  
US-09-563-286B-130

Query Match 87.0%; Score 20; DB 19; Length 6;  
Best Local Similarity 60.0%; Pred. No. 4.2e+06;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5  
| | |  
Db 2 FSDLW 6

Search completed: February 12, 2003, 11:24:04  
Job time : 100.375 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

# OM protein - protein search, using sw model

Run on: February 12, 2003, 11:14:12 ; Search time 7.08333 Seconds  
(without alignments)  
59.144 Million cell updates/sec

Title: US-09-403-440A-1  
Perfect score: 23  
Sequence: 1 FXXLW 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 425801 seqs, 83787487 residues

Total number of hits satisfying chosen parameters: 159213

Minimum DB seq length: 0  
Maximum DB seq length: 25

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending Patents AA New: \*  
1: /cgn2\_6/ptodata/1/paa/PCT\_NEW\_COMB.psp.\*  
2: /cgn2\_6/ptodata/1/paa/US06\_NEW\_COMB.psp.\*  
3: /cgn2\_6/ptodata/1/paa/US07\_NEW\_COMB.psp.\*  
4: /cgn2\_6/ptodata/1/paa/US08\_NEW\_COMB.psp.\*  
5: /cgn2\_6/ptodata/1/paa/US09\_NEW\_COMB.psp.\*  
6: /cgn2\_6/ptodata/1/paa/US10\_NEW\_COMB.psp.\*  
7: /cgn2\_6/ptodata/1/paa/US60\_NEW\_COMB.psp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	87.0	7	5	US-09-701-080C-12
2	20	87.0	7	6	US-10-174-717A-36
3	20	87.0	11	5	US-09-189-702A-286
4	20	87.0	13	5	US-09-701-080C-22
5	20	87.0	13	5	US-09-701-080C-27
6	20	87.0	15	6	US-10-211-088-141
7	20	87.0	19	7	US-60-438-805-9
8	20	87.0	20	1	PCT-US02-34021-343
9	20	87.0	22	6	US-10-203-138A-12722
10	19	82.6	5	5	US-09-281-717A-3
11	19	82.6	12	6	US-10-225-567A-2041
12	19	82.6	14	6	US-10-225-567A-2196
13	19	82.6	15	6	US-10-225-567A-1920
14	19	82.6	18	6	US-10-283-599-199
15	19	82.6	20	6	US-10-319-786-54
16	19	82.6	21	6	US-10-203-138A-12994
17	19	82.6	22	6	US-10-283-599-15
18	19	82.6	22	6	US-10-283-599-139
19	19	82.6	22	6	US-10-283-599-149
20	19	82.6	22	6	US-10-283-599-155
21	18	78.3	8	6	US-10-258-144-37
22	18	78.3	8	6	US-10-258-147-8
23	18	78.3	8	6	US-10-171-734-4
24	18	78.3	8	6	US-10-053-498B-144
25	18	78.3	10	5	US-09-863-054-27
26	18	78.3	10	6	US-10-099-056-2094

Sequence 1318, Ap  
Sequence 316, App  
Sequence 399, App  
Sequence 13, Appl  
Sequence 20, Appl  
Sequence 39, Appl  
Sequence 31, Appl  
Sequence 129, App  
Sequence 372, App  
Sequence 380, App  
Sequence 372, App  
Sequence 380, App  
Sequence 16, Appl  
Sequence 73, Appl  
Sequence 14, Appl  
Sequence 95, Appl  
Sequence 251, Appl  
Sequence 7, Appl

## ALIGNMENTS

RESULT 1  
US-09-701-080C-12  
; Sequence 12, Application US/09701080C  
; GENERAL INFORMATION:  
; APPLICANT: INSTITUTE OF MOLECULAR AND CELL BIOLOGY  
; TITLE OF INVENTION: POLYPEPTIDES FROM CREB BINDING PROTEIN AND RELATED PROTEIN P300 F  
; FILE REFERENCE: N73477C GCM  
; CURRENT APPLICATION NUMBER: US/09/701,080C  
; CURRENT FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: GB 9811303.8  
; PRIOR FILING DATE: 1998-05-26  
; PRIOR APPLICATION NUMBER: GB 9900157.0  
; PRIOR FILING DATE: 1999-01-05  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 12  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: derived from p53  
US-09-701-080C-12

Query Match 87.0%; Score 20; DB 5; Length 7;  
Best Local Similarity 60.0%; Pred. No. 3.5e+05;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXLW 5  
Db 1 FSDLW 5

RESULT 2  
US-10-174-717A-36  
; Sequence 36, Application US/10174717A  
; APPLICANT: Koide, Shohei  
; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES  
; NUMBER OF SEQUENCES: 118  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: Schwegman, Lundberg, Woessner & Kluth P.A.  
; STREET: 121 South Eighth Street, St. 1600  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: USA  
; ZIP: 55402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible

OPERATING SYSTEM: WINDOWS  
SOFTWARE: FastSeq Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/174,717A  
FILING DATE: 18-Jun-2002  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/096,749  
FILING DATE: June 12, 1998  
APPLICATION NUMBER: 60/049,410  
FILING DATE: June 12, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Ann S. Vikenins  
REGISTRATION NUMBER: 37,748  
REFERENCE/DOCKET NUMBER: 109.034US4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (612) 373-6900  
TELEFAX: (612) 339-3061  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
SEQUENCE DESCRIPTION: SEQ ID NO: 36:  
US-10-174-717A-36

Query Match 87.0%; Score 20; DB 6; Length 7;  
Best Local Similarity 60.0%; Pred. No. 3.5e+05;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5  
|  
|  
Db 1 FADLW 5

RESULT 3  
US-09-189-702A-286  
Sequence 286, Application US/09189702A  
GENERAL INFORMATION:  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Kast, W. Martin  
APPLICANT: Southwood, Scott  
APPLICANT: Epimmune, Inc.  
TITLE OF INVENTION: HLA Binding Peptides and Their Uses  
FILE REFERENCE: 39963-20019.20  
CURRENT APPLICATION NUMBER: US/09/189,702A  
CURRENT FILING DATE: 1998-11-10  
PRIOR APPLICATION NUMBER: US 08/205,713  
PRIOR FILING DATE: 1994-03-04  
NUMBER OF SEQ ID NOS: 360  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 286  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: p53.14 peptide 34.0324  
US-09-189-702A-286

Query Match 87.0%; Score 20; DB 5; Length 11;  
Best Local Similarity 60.0%; Pred. No. 4e+02;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5  
|  
|  
Db 6 FSDLW 10

RESULT 4  
US-09-701-080C-22  
Sequence 22, Application US/09701080C  
GENERAL INFORMATION:  
APPLICANT: INSTITUTE OF MOLECULAR AND CELL BIOLOGY  
TITLE OF INVENTION: POLYPEPTIDES FROM CREB BINDING PROTEIN AND RELATED PROTEIN P300 F  
TITLE OF INVENTION: TRANSCRIPTIONAL REGULATION  
FILE REFERENCE: N73477C GCW  
CURRENT APPLICATION NUMBER: US/09/701,080C  
CURRENT FILING DATE: 2001-02-27  
PRIOR APPLICATION NUMBER: GB 9811303.8  
PRIOR FILING DATE: 1998-05-26  
PRIOR APPLICATION NUMBER: GB 9900157.0  
PRIOR FILING DATE: 1999-01-05  
NUMBER OF SEQ ID NOS: 36  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 22  
LENGTH: 13  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: derived from p53  
US-09-701-080C-22

Query Match 87.0%; Score 20; DB 5; Length 13;  
Best Local Similarity 60.0%; Pred. No. 4.5e+02;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5  
|  
|  
Db 5 FSDLW 9

RESULT 5  
US-09-701-080C-27  
Sequence 27, Application US/09701080C  
GENERAL INFORMATION:  
APPLICANT: INSTITUTE OF MOLECULAR AND CELL BIOLOGY  
TITLE OF INVENTION: POLYPEPTIDES FROM CREB BINDING PROTEIN AND RELATED PROTEIN P300 F  
TITLE OF INVENTION: TRANSCRIPTIONAL REGULATION  
FILE REFERENCE: N73477C GCW  
CURRENT APPLICATION NUMBER: US/09/701,080C  
CURRENT FILING DATE: 2001-02-27  
PRIOR APPLICATION NUMBER: GB 9811303.8  
PRIOR FILING DATE: 1998-05-26  
PRIOR APPLICATION NUMBER: GB 9900157.0  
PRIOR FILING DATE: 1999-01-05  
NUMBER OF SEQ ID NOS: 36  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 27  
LENGTH: 13  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: derived from p53  
US-09-701-080C-27

Query Match 87.0%; Score 20; DB 5; Length 13;  
Best Local Similarity 60.0%; Pred. No. 4.5e+02;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5  
|  
|  
Db 5 FSDLW 9

RESULT 6  
US-10-211-088-141  
Sequence 141, Application US/10211088  
GENERAL INFORMATION:  
APPLICANT: Bright, Gary R.  
APPLICANT: Premkumar, D. David

; APPLICANT: Chen, Yih-Tai  
; TITLE OF INVENTION: Novel Fusion Proteins And Assays For Molecular Binding  
; FILE REFERENCE: 01-1022-US  
; CURRENT APPLICATION NUMBER: US/10/211,088  
; CURRENT FILING DATE: 2002-10-15  
; PRIOR APPLICATION NUMBER: 60/309,395  
; PRIOR FILING DATE: 2001-08-01  
; PRIOR APPLICATION NUMBER: 60/341,589  
; PRIOR FILING DATE: 2001-12-13  
; NUMBER OF SEQ ID NOS: 366  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 141  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Binding domain  
US-10-211-088-141

Query Match 87.0%; Score 20; DB 6; Length 15;  
Best Local Similarity 60.0%; Pred. No. 5.1e+02;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5  
| | |  
Db 8 FSDLW 12

RESULT 7  
US-60-438-805-9  
; Sequence 9, Application US/60438805  
; GENERAL INFORMATION:  
; APPLICANT: KODAREK, THOMAS  
; TITLE OF INVENTION: MIXED ELEMENT CAPTURE AGENTS  
; FILE REFERENCE: UTSD:935USPI  
; CURRENT APPLICATION NUMBER: US/60/438,805  
; CURRENT FILING DATE: 2003-01-09  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 9  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
US-60-438-805-9

Query Match 87.0%; Score 20; DB 7; Length 19;  
Best Local Similarity 60.0%; Pred. No. 6.1e+02;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5  
| | |  
Db 7 FSDLW 11

RESULT 8  
PCT-US02-34021-343  
; Sequence 343, Application PC/TUS0234021  
; GENERAL INFORMATION:  
; APPLICANT: DGI Biotechnologies, Inc.  
; TITLE OF INVENTION: TARGET SPECIFIC SCREENING AND ITS USE FOR IDENTIFYING TARGET BIND  
; FILE REFERENCE: 2598-4009PC  
; CURRENT APPLICATION NUMBER: PCT/US02/34021  
; CURRENT FILING DATE: 2002-10-24  
; PRIOR APPLICATION NUMBER: 60/345,471  
; PRIOR FILING DATE: 2001-10-24  
; NUMBER OF SEQ ID NOS: 537  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 343  
; LENGTH: 20  
; TYPE: PRT

; ORGANISM: Escherichia coli  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; OTHER INFORMATION: DGI7-20M-4-G12  
PCT-US02-34021-343

Query Match 87.0%; Score 20; DB 1; Length 20;  
Best Local Similarity 60.0%; Pred. No. 6.4e+02;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5  
| | |  
Db 16 FFSWLW 20

RESULT 9  
US-10-203-138A-12722  
; Sequence 12722, Application US/10203138A  
; GENERAL INFORMATION:  
; APPLICANT: Molecular Dynamics, Inc.  
; APPLICANT: Penn, Sharon G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; FILE REFERENCE: PB 0004 WO 8  
; CURRENT APPLICATION NUMBER: US/10/203,138A  
; CURRENT FILING DATE: 2002-08-02  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 04 February 2000 (04.02.00)  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 26 May 2000 (26.05.00)  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 03 August 2000 (03.08.00)  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 03 October 2000 (03.10.00)  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 27 September 2000 (27.09.00)  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 21 September 2000 (21.09.00)  
; PRIOR APPLICATION NUMBER: US 09/608,408  
; PRIOR FILING DATE: 30 June 2000 (30.06.00)  
; NUMBER OF SEQ ID NOS: 15438  
; SOFTWARE: Molecular Dynamics Sequence Listing Engine  
; SEQ ID NO 12722  
; LENGTH: 22  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO AC009946.1  
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1  
; FEATURE:  
; OTHER INFORMATION: EST HUMAN HIT: AW452898.1, EVALUE 5.00e-03  
US-10-203-138A-12722

Query Match 87.0%; Score 20; DB 6; Length 22;  
Best Local Similarity 60.0%; Pred. No. 6.9e+02;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5  
| | |  
Db 6 FSQLW 10

RESULT 10  
US-09-281-717A-3  
; Sequence 3, Application US/09281717A  
; GENERAL INFORMATION:  
; APPLICANT: Baxter, John  
; APPLICANT: Darimont, Beatrice  
; APPLICANT: Feng, Weijun

; APPLICANT: Fletterick, Robert  
; APPLICANT: Kushner, Peter  
; APPLICANT: West, Brian  
; APPLICANT: Wagner, Richard  
; APPLICANT: Yamamoto, Keith  
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING NUCLEAR RECEPTOR  
; TITLE OF INVENTION: COACTIVATOR BINDING  
; FILE REFERENCE: 9811-008-999  
; CURRENT APPLICATION NUMBER: US/09/281.717A  
; CURRENT FILING DATE: 1999-03-30  
; PRIOR APPLICATION NUMBER: US 60/079,956  
; PRIOR FILING DATE: 1998-03-30  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 3  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; NAME/KEY: Variant  
; LOCATION: (2)...(3)  
; OTHER INFORMATION: Xaa is any amino acid  
US-09-281-717A-3

Query Match 82.6%; Score 19; DB 5; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3.5e+05; Indels 0; Gaps 0;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXLW 5  
| | | | |  
Db 1 FXXLW 5

RESULT 11  
US-10-225-567A-2041  
; Sequence 2041, Application US/10225567A  
; GENERAL INFORMATION:  
; APPLICANT: LifeSpan Biosciences  
; APPLICANT: Brown, Joseph P.  
; APPLICANT: Burmer, Glenna C.  
; APPLICANT: Roush, Christine L.  
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS  
; FILE REFERENCE: 1920-4-4  
; CURRENT APPLICATION NUMBER: US/10/225,567A  
; CURRENT FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 60/257,144  
; PRIOR FILING DATE: 2000-12-19  
; NUMBER OF SEQ ID NOS: 2292  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2041  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-225-567A-2041

Query Match 82.6%; Score 19; DB 6; Length 12;  
Best Local Similarity 60.0%; Pred. No. 6.8e+02;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5  
| | | | |  
Db 2 FLFLW 6

RESULT 12  
US-10-225-567A-2196  
; Sequence 2196, Application US/10225567A  
; GENERAL INFORMATION:  
; APPLICANT: LifeSpan Biosciences  
; APPLICANT: Brown, Joseph P.  
; APPLICANT: Burmer, Glenna C.  
; APPLICANT: Roush, Christine L.  
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS

; FILE REFERENCE: 1920-4-4  
; CURRENT APPLICATION NUMBER: US/10/225,567A  
; CURRENT FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 60/257,144  
; PRIOR FILING DATE: 2000-12-19  
; NUMBER OF SEQ ID NOS: 2292  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2196  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-225-567A-2196

Query Match 82.6%; Score 19; DB 6; Length 14;  
Best Local Similarity 60.0%; Pred. No. 7.7e+02;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5  
| | | | |  
Db 3 FLILW 7

RESULT 13  
US-10-225-567A-1920  
; Sequence 1920, Application US/10225567A  
; GENERAL INFORMATION:  
; APPLICANT: LifeSpan Biosciences  
; APPLICANT: Brown, Joseph P.  
; APPLICANT: Burmer, Glenna C.  
; APPLICANT: Roush, Christine L.  
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS  
; FILE REFERENCE: 1920-4-4  
; CURRENT APPLICATION NUMBER: US/10/225,567A  
; CURRENT FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 60/257,144  
; PRIOR FILING DATE: 2000-12-19  
; NUMBER OF SEQ ID NOS: 2292  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1920  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-225-567A-1920

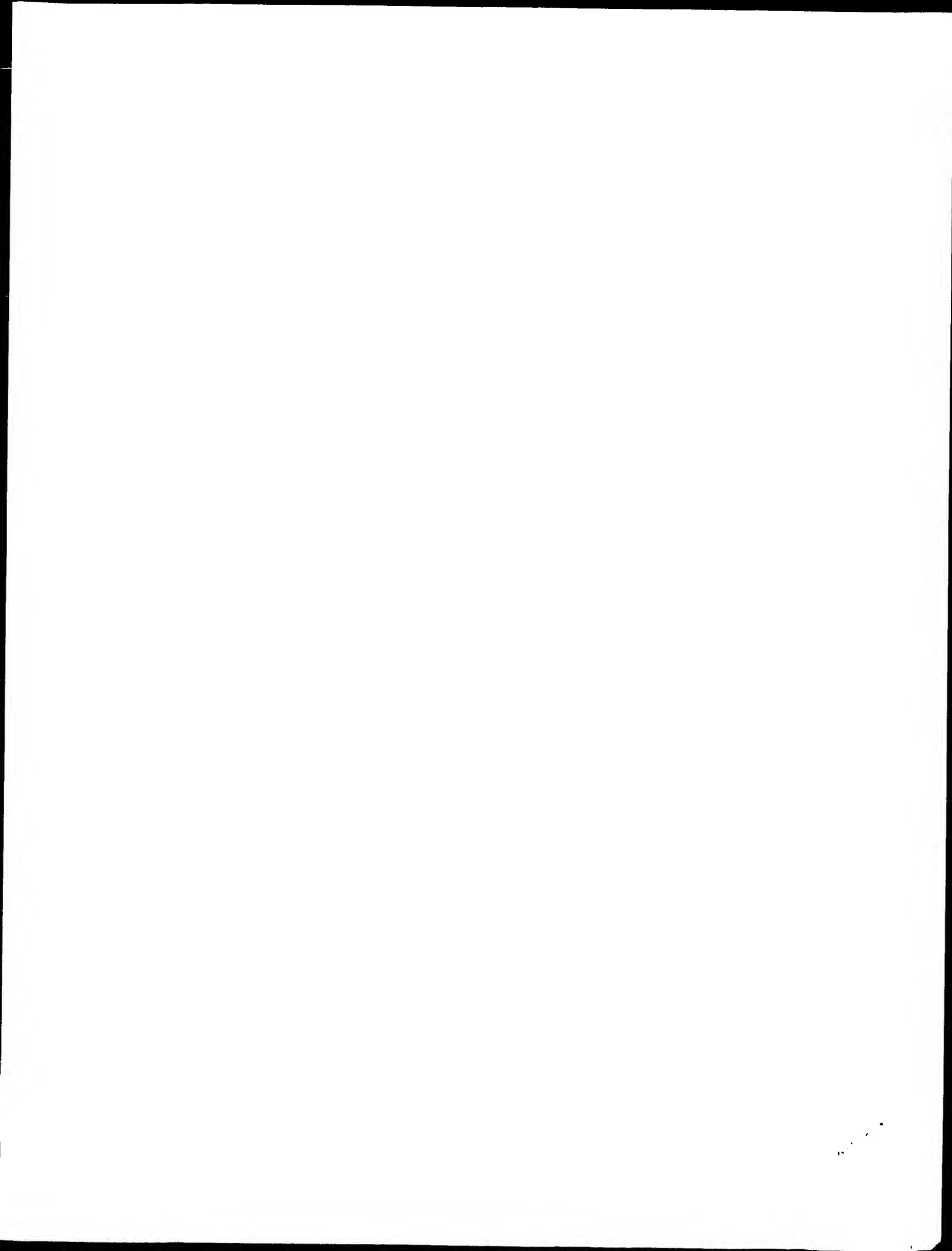
Query Match 82.6%; Score 19; DB 6; Length 15;  
Best Local Similarity 60.0%; Pred. No. 8.1e+02;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5  
| | | | |  
Db 9 FRLWL 13

RESULT 14  
US-10-283-599-199  
; Sequence 199, Application US/10283599  
; GENERAL INFORMATION:  
; APPLICANT: Daseux, Jean-Louis  
; APPLICANT: Sekul, Renate  
; APPLICANT: Butner, Klaus  
; APPLICANT: Cornut, Isabelle  
; APPLICANT: Metz, Gunther  
; APPLICANT: Dufourcq, Jean  
; TITLE OF INVENTION: GENE THERAPY APPROACHES TO  
; TITLE OF INVENTION: SUPPLY APOLIPOPROTEIN A-I AGONISTS AND THEIR  
; TITLE OF INVENTION: USE TO TREAT DYSLIPIDEMIC DISORDERS.  
; NUMBER OF SEQUENCES: 274  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA



```
;
;
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/283,599
; FILING DATE: 29-OCT-2002
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,136
; FILING DATE: 29-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0007-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 199:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: None
; FEATURE:
; NAME/KEY: Other
; LOCATION: 1..18
; OTHER INFORMATION: N-terminal acetylated and
; OTHER INFORMATION: C-terminal amidated
;
; US-10-283-599-199
;
; Query Match 82.6%; Score 19; DB 6; Length 18;
; Best Local Similarity 60.0%; Pred. No. 9.4e+02;
; Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;
; QY 1 FXXLW 5
; DB 6 FRELW 10
;
; RESULT 15
; US-10-319-786-54
; Sequence 54, Application US/10319786
; GENERAL INFORMATION:
; APPLICANT: Little, Roger G
; TITLE OF INVENTION: Biologically Active Peptides from
; Functional Domains of Bactericidal/Permeability-Increasing
; Protein and Uses Thereof
;
; NUMBER OF SEQUENCES: 98
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Allegretti, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/319,786
; FILING DATE: 13-Dec-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/473,344
; FILING DATE: 7-JUN-1995
; APPLICATION NUMBER: US 08/306,473
; FILING DATE: 15-SEP-1995
;
;
; APPLICATION NUMBER: US 08/209,762
; FILING DATE: 11-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: McDonnell, John J.
; REGISTRATION NUMBER: 26,949
; REFERENCE/DOCKET NUMBER: 93,1133-J
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: "BPI.7"
; SEQUENCE DESCRIPTION: SEQ ID NO: 54:
;
; US-10-319-786-54
;
; Query Match 82.6%; Score 19; DB 6; Length 20;
; Best Local Similarity 60.0%; Pred. No. 1e+03;
; Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;
; QY 1 FXXLW 5
; DB 8 FLKLW 12
;
; Search completed: February 12, 2003, 11:24:44
; Job time : 7.08333 secs
```



GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

QM protein - protein search, using sw model

Run on: February 12, 2003, 11:12:42 ; Search time 4.58333 Seconds  
(without alignments)  
32.098 Million cell updates/sec

Title: US-09-403-440A-1  
Perfect score: 23  
Sequence: 1 FXXLW 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 147762

Minimum DB seq length: 0  
Maximum DB seq length: 25

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A COMB.pcp.\*  
2: /cgn2\_6/ptodata/1/iaa/5B COMB.pcp.\*  
3: /cgn2\_6/ptodata/1/iaa/6A COMB.pcp.\*  
4: /cgn2\_6/ptodata/1/iaa/6B COMB.pcp.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTRUS COMB.pcp.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	91.3	11	1	US-08-277-660A-16
2	21	91.3	11	1	US-08-424-957-29
3	21	91.3	11	4	US-09-035-686-29
4	20	87.0	6	1	US-08-277-660A-2
5	20	87.0	6	1	US-08-277-660A-3
6	20	87.0	6	1	US-08-424-957-2
7	20	87.0	6	1	US-08-424-957-3
8	20	87.0	6	1	US-08-424-957-6
9	20	87.0	6	4	US-09-035-686-2
10	20	87.0	6	4	US-09-035-686-3
11	20	87.0	6	4	US-09-035-686-6
12	20	87.0	6	4	US-09-081-975-1
13	20	87.0	7	1	US-08-277-660A-27
14	20	87.0	7	1	US-08-424-957-15
15	20	87.0	7	1	US-08-424-957-19
16	20	87.0	7	4	US-09-035-686-15
17	20	87.0	7	4	US-09-035-686-19
18	20	87.0	7	4	US-09-638-202A-36
19	20	87.0	8	4	US-08-469-260A-252
20	20	87.0	9	1	US-08-350-884-8
21	20	87.0	9	1	US-08-350-884-11
22	20	87.0	9	1	US-08-350-884-14
23	20	87.0	9	1	US-08-709-173-8
24	20	87.0	9	1	US-08-709-173-11
25	20	87.0	9	1	US-08-709-173-14
26	20	87.0	9	1	US-08-638-911A-15
27	20	87.0	9	1	US-08-638-911A-18

Sequence 21, Appl  
Sequence 8, Appl  
Sequence 11, Appl  
Sequence 14, Appl  
Sequence 7, Appl  
Sequence 8, Appl  
Sequence 11, Appl  
Sequence 12, Appl  
Sequence 18, Appl  
Sequence 11, Appl  
Sequence 12, Appl  
Sequence 18, Appl  
Sequence 12, Appl  
Sequence 18, Appl  
Sequence 9, Appl  
Sequence 10, Appl  
Sequence 11, Appl  
Sequence 12, Appl  
Sequence 13, Appl  
Sequence 15, Appl

## ALIGNMENTS

RESULT 1  
US-08-277-660A-16  
; Sequence 16, Application US/08277660A  
; Patent No. 5702908  
; GENERAL INFORMATION:  
; APPLICANT: Picksley, Steven M.  
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53  
; TITLE OF INVENTION: Protein and Therapeutic Application Thereof  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert  
; STREET: Four Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States  
; ZIP: 94111-4187  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/277,660A  
; FILING DATE: 20-JUL-1994  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dreger, Walter H.  
; REGISTRATION NUMBER: 24,190  
; REFERENCE/DOCKET NUMBER: A-60244/WH  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 781-1989  
; TELEFAX: (415) 398-3249  
; TELEX: 910 277299  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
US-08-277-660A-16

Query Match 91.3%; Score 21; DB 1; Length 11;  
Best Local Similarity 60.0%; Pred. No. 1.5e+02;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXLW 5

Db 5 FSALW 9



SEQUENCE CHARACTERISTICS:  
 LENGTH: 6 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 US-08-277-660A-2

Query Match 87.0%; Score 20; DB 1; Length 6;  
 Best Local Similarity 60.0%; Pred. No. 2e+05;  
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5  
 | |  
 Db 2 FSDLW 6

RESULT 5  
 US-08-277-660A-3  
 ; Sequence 3, Application US/08277660A  
 ; Patent No. 5702908  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Picklesley, Steven M.  
 ; APPLICANT: Lane, David P.  
 ; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53  
 ; TITLE OF INVENTION: Protein and Therapeutic Application Thereof  
 ; NUMBER OF SEQUENCES: 27  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert  
 ; STREET: Four Embarcadero Center, Suite 3400  
 ; CITY: San Francisco  
 ; STATE: California  
 ; COUNTRY: United States  
 ; ZIP: 94111-4187  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/277,660A  
 ; FILING DATE: 20-JUL-1994  
 ; CLASSIFICATION: 514  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Dreger, Walter H.  
 ; REGISTRATION NUMBER: 24,190  
 ; REFERENCE/DOCKET NUMBER: A-60244/WH  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (415) 398-3249  
 ; TELEFAX: (415) 398-3249  
 ; TELEX: 910 277299  
 ; INFORMATION FOR SEQ ID NO: 3:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 6 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS:  
 ; TOPOLOGY: linear  
 ; US-08-277-660A-3

Query Match 87.0%; Score 20; DB 1; Length 6;  
 Best Local Similarity 60.0%; Pred. No. 2e+05;  
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5  
 | |  
 Db 2 FSLGW 6

RESULT 6  
 US-08-424-957-2  
 ; Sequence 2, Application US/08424957  
 ; Patent No. 5770377  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Picklesley, Steven M.

APPLICANT: Lane, David P.  
 TITLE OF INVENTION: Interruption of Binding of MDM2 and P53  
 TITLE OF INVENTION: Protein and Therapeutic Application Thereof  
 NUMBER OF SEQUENCES: 50  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert  
 STREET: Four Embarcadero Center, Suite 3400  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: United States  
 ZIP: 94111-4187  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/424,957  
 FILING DATE: 19-APR-1995  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/277,660  
 FILING DATE: 20-JUL-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Dreger, Walter H.  
 REGISTRATION NUMBER: 24,190  
 REFERENCE/DOCKET NUMBER: A-61228/WH  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 781-1989  
 TELEFAX: (415) 398-3249  
 TELEX: 910 277299  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 6 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: unknown  
 US-08-424-957-2

Query Match 87.0%; Score 20; DB 1; Length 6;  
 Best Local Similarity 60.0%; Pred. No. 2e+05;  
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5  
 | |  
 Db 2 FSDLW 6

RESULT 7  
 US-08-424-957-3  
 ; Sequence 3, Application US/08424957  
 ; Patent No. 5770377  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Picklesley, Steven M.  
 ; APPLICANT: Lane, David P.  
 ; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53  
 ; TITLE OF INVENTION: Protein and Therapeutic Application Thereof  
 ; NUMBER OF SEQUENCES: 50  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert  
 ; STREET: Four Embarcadero Center, Suite 3400  
 ; CITY: San Francisco  
 ; STATE: California  
 ; COUNTRY: United States  
 ; ZIP: 94111-4187  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/424,957  
 ; FILING DATE: 19-APR-1995

; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/277,660  
 ; FILING DATE: 20-JUL-1994  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Dreger, Walter H.  
 ; REGISTRATION NUMBER: 24,190  
 ; REFERENCE/DOCKET NUMBER: A-61228/WH/D  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (415) 781-1989  
 ; TELEFAX: (415) 398-3249  
 ; TELEX: 910 277299  
 ; INFORMATION FOR SEQ ID NO: 3:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 6 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS:  
 ; TOPOLOGY: unknown  
 ;  
 ; US-08-424-957-3

Query Match 87.0%; Score 20; DB 1; Length 6;  
 Best Local Similarity 60.0%; Pred. No. 2e+05;  
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5  
 Db 2 FSGLW 6

RESULT 8  
 ; US-08-424-957-6  
 ; Sequence 6, Application US/08424957  
 ; Patent No. 5770377  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Picksley, Steven M.  
 ; APPLICANT: Lane, David P.  
 ; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53  
 ; TITLE OF INVENTION: Protein and Therapeutic Application Thereof  
 ; NUMBER OF SEQUENCES: 50  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert  
 ; STREET: Four Embarcadero Center, Suite 3400  
 ; CITY: San Francisco  
 ; STATE: California  
 ; COUNTRY: United States  
 ; ZIP: 94111-4187  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/424,957  
 ; FILING DATE: 19-APR-1995  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/277,660  
 ; FILING DATE: 20-JUL-1994  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Dreger, Walter H.  
 ; REGISTRATION NUMBER: 24,190  
 ; REFERENCE/DOCKET NUMBER: A-61228/WH/D  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (415) 781-1989  
 ; TELEFAX: (415) 398-3249  
 ; TELEX: 910 277299  
 ; INFORMATION FOR SEQ ID NO: 6:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 6 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS:  
 ; TOPOLOGY: unknown  
 ;  
 ; US-08-424-957-6

Query Match 87.0%; Score 20; DB 1; Length 6;  
 Best Local Similarity 60.0%; Pred. No. 2e+05;  
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5  
 Db 2 FSGLW 6

RESULT 9  
 ; US-09-035-686-2  
 ; Sequence 2, Application US/09035686  
 ; Patent No. 6153391  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Picksley, Steven M.  
 ; APPLICANT: Lane, David P.  
 ; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53  
 ; TITLE OF INVENTION: Protein and Therapeutic Application Thereof  
 ; NUMBER OF SEQUENCES: 50  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert  
 ; STREET: Four Embarcadero Center, Suite 3400  
 ; CITY: San Francisco  
 ; STATE: California  
 ; COUNTRY: United States  
 ; ZIP: 94111-4187  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/035,686  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/424,957  
 ; FILING DATE: 19-APR-1995  
 ; APPLICATION NUMBER: US 08/277,660  
 ; FILING DATE: 20-JUL-1994  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Dreger, Walter H.  
 ; REGISTRATION NUMBER: 24,190  
 ; REFERENCE/DOCKET NUMBER: A-61228/WH/D  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (415) 781-1989  
 ; TELEFAX: (415) 398-3249  
 ; TELEX: 910 277299  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 6 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS:  
 ; TOPOLOGY: unknown  
 ;  
 ; US-09-035-686-2

Query Match 87.0%; Score 20; DB 4; Length 6;  
 Best Local Similarity 60.0%; Pred. No. 2e+05;  
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5  
 Db 2 FSGLW 6

RESULT 10  
 ; US-09-035-686-3  
 ; Sequence 3, Application US/09035686  
 ; Patent No. 6153391  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Picksley, Steven M.  
 ; APPLICANT: Lane, David P.

```
;
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/035,686
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; FILING DATE: 19-APR-1995
; APPLICATION NUMBER: US 08/424,957
; FILING DATE: 20-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-61228/WHd
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; US-09-035-686-3

Query Match 87.0%; Score 20; DB 4; Length 6;
Best Local Similarity 60.0%; Pred. No. 2e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5
Db 2 FSGLW 6

RESULT 11
US-09-035-686-6
; Sequence 6, Application US/09035686
; Patent No. 6153391
; GENERAL INFORMATION:
; APPLICANT: Pickaley, Steven M.
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/035,686
```

```
;
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/424,957
; FILING DATE: 19-APR-1995
; APPLICATION NUMBER: US 08/277,660
; FILING DATE: 20-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-61228/WHd
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; US-09-035-686-6

Query Match 87.0%; Score 20; DB 4; Length 6;
Best Local Similarity 60.0%; Pred. No. 2e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5
Db 2 FSGLW 6

RESULT 12
US-09-081-975-1
; Sequence 1, Application US/09081975
; Patent No. 6451979
; GENERAL INFORMATION:
; APPLICANT: Kaelin, William
; APPLICANT: Jost, Christine
; TITLE OF INVENTION: METHODS OF TREATMENT USING
; TITLE OF INVENTION: NBS-1, ANTIBODIES AND PROTEINS THERETO, AND USES OF THE
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon Peabody LLP
; STREET: 101 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/081,975
; FILING DATE: 12-MAY-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/046,207
; FILING DATE: 12-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Eisenstein, Ronald I
; REGISTRATION NUMBER: 30,628
; REFERENCE/DOCKET NUMBER: 47400
; TELEPHONE: 617-345-6054
; TELEFAX: 617-345-1300
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
```

```

;
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-081-975-1
Query Match 87.0%; Score 20; DB 4; Length 6;
Best Local Similarity 60.0%; Pred. No. 2e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5
Db 2 FSDLW 6

RESULT 13
US-08-277-660A-27
; Sequence 27, Application US/08277660A
; Patent No. 5702908
; GENERAL INFORMATION:
; APPLICANT: Picksley, Steven M.
; APPLICANT: Lane, David P.
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/277,660A
; FILING DATE: 20-JUL-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-60244/WHd
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-277-660A-27
Query Match 87.0%; Score 20; DB 1; Length 7;
Best Local Similarity 60.0%; Pred. No. 2e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5
Db 1 FSDLW 5

RESULT 14
US-08-424-957-15
; Sequence 15, Application US/08424957
; Patent No. 5770377
; GENERAL INFORMATION:
; APPLICANT: Picksley, Steven M.
; APPLICANT: Lane, David P.
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,957
; FILING DATE: 19-APR-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/277,660
; FILING DATE: 20-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-61228/WHd
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
US-08-424-957-15
Query Match 87.0%; Score 20; DB 1; Length 7;
Best Local Similarity 60.0%; Pred. No. 2e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5
Db 1 FSDLW 5

RESULT 15
US-08-424-957-19
; Sequence 19, Application US/08424957
; Patent No. 5770377
; GENERAL INFORMATION:
; APPLICANT: Picksley, Steven M.
; APPLICANT: Lane, David P.
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,957
; FILING DATE: 19-APR-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

```



```

; APPLICATION NUMBER: US 08/277,660
; FILING DATE: 20-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Drager, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-61228/WHd
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
;
US-08-424-957-19
Query Match 87.0%; Score 20; DB 1; Length 7;
Best Local Similarity 60.0%; Pred. No. 2e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy 1 PXXLW 5
Db 3 FSDLW 7

```

Search completed: February 12, 2003, 11:15:59  
Job time : 5.08333 secs

